

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 4278
 - Ceres seq_id 1580122
 - Location of start within SEQ ID NO 4275: at 28 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- Eukaryotic protein kinase domain
 - Location within SEQ ID NO 4278: from 1 to 86 aa.

- (Dp) Related Amino Acid Sequences

Maximum Length Sequence:

related to:

Clone IDs:

342142

- (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 4279
- Ceres seq_id 1580127

- (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 4280
- Ceres seq_id 1580128
- Location of start within SEQ ID NO 4279: at 1 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- Sperm histone P2
 - Location within SEQ ID NO 4280: from 43 to 101 aa.

- (Dp) Related Amino Acid Sequences

- (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 4281
- Ceres seq_id 1580129
- Location of start within SEQ ID NO 4279: at 65 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (Dp) Related Amino Acid Sequences

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 874 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..874
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

atcactaaca	aaacacacat	caaaaaacgat	tttacaagaa	aaaaatatca	gaaaaaatgt	60
cagagaccac	caagaatgcc	ttccaagccg	gtcaggccgc	tggcaaaagt	gaggagaaga	120
gcaatgttct	gtggacaag	gccaaaggatg	ctgctgctgc	agctggagct	tccgcgcaac	180
aggcgggaac	gagtatatcg	gatgcggcag	tgggaggtgc	tccatctggt	cctgaagctg	240
gccctcgaac	aatgaaattc	cttgacaatt	tccatgtgca	aacaaagaga	gagcatgttt	300
tgttgggaga	taacgagaat	ggtgagaacg	atgaggaagg	cggtgaggtt	gcaaacccaa	360
aatggatcac	cattaaaGca	gctctgctGc	tactgttagg	agctgccatt	gcagctgcat	420
ttgctgatcc	tttagtcgac	actgttaaca	acttctccgc	agccacaggg	attccgtctt	480
tcttcatttc	cttcactgct	ttgcctttgg	ccaccaattc	aagtgaagcc	gtgtctgcca	540
tcactcttcg	atccccgaaa	aagatcagaa	ccgcctcttt	aactttctcc	gagctatgcg	600
gtggagtgac	aatgaacaac	attctgtgtc	tctcgggtgt	cttagcaatc	gtctacgttc	660
gaggactgac	atgggaactc	tcatacaga	agtggtgtag	tctcatcggt	tgtctcgtga	720
tggcggtgtt	cgcgagtgtc	cgcacaactt	atcctctttg	gacatgtttc	atagcttaact	780
tgctttacc	attctccttg	ggctcgtgtc	atattcttga	ttactggttt	ggctcgtcgt	840
agatatcaat	ctctgttcaa	agagtttgtt	ctac			

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..261
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Glu	Thr	Asn	Lys	Asn	Ala	Phe	Gln	Ala	Gly	Gln	Ala	Ala	Gly
1				5					10				15		
Lys	Ala	Glu	Glu	Lys	Ser	Asn	Val	Leu	Leu	Asp	Lys	Ala	Lys	Asp	Ala
				20					25				30		
Ala	Ala	Ala	Ala	Gly	Ala	Ser	Ala	Gln	Gln	Ala	Gly	Lys	Ser	Ile	Ser
				35					40				45		
Asp	Ala	Ala	Val	Gly	Gly	Ala	Pro	Ser	Gly	Pro	Glu	Ala	Gly	Pro	Arg
				50					55				60		
Thr	Met	Lys	Phe	Leu	Asp	Asn	Phe	His	Val	Gln	Thr	Lys	Arg	Glu	His
				65					70				75		80
Ala	Leu	Leu	Gly	Asp	Asn	Glu	Asn	Gly	Glu	Asn	Asp	Glu	Glu	Gly	Gly
				85					90				95		
Glu	Val	Ala	Asn	Pro	Lys	Trp	Ile	Thr	Ile	Lys	Ala	Ala	Leu	Leu	Leu
				100					105				110		
Leu	Leu	Gly	Ala	Ala	Ile	Ala	Ala	Ala	Phe	Ala	Asp	Pro	Leu	Val	Asp
				115					120				125		
Thr	Val	Asn	Asn	Phe	Ser	Ala	Ala	Thr	Gly	Ile	Pro	Ser	Phe	Phe	Ile
				130					135				140		
Ser	Phe	Ile	Ala	Leu	Pro	Leu	Ala	Thr	Asn	Ser	Ser	Glu	Ala	Val	Ser
				145					150				155		160
Ala	Ile	Ile	Phe	Ala	Ser	Arg	Lys	Lys	Ile	Arg	Thr	Ala	Ser	Leu	Thr
				165					170				175		

Phe Ser Glu Leu Cys Gly Gly Val Thr Met Asn Asn Ile Leu Cys Leu
180 185 190
Ser Val Phe Leu Ala Ile Val Tyr Val Arg Gly Leu Thr Trp Asn Phe
195 200 205
Ser Ser Glu Val Leu Val Ile Leu Ile Val Cys Leu Val Met Gly Gly
210 215 220
Phe Ala Ser Phe Arg Thr Thr Tyr Pro Leu Trp Thr Cys Phe Ile Ala
225 230 235 240
Tyr Leu Leu Tyr Pro Phe Ser Leu Gly Leu Val Tyr Ile Leu Asp Tyr
245 250 255
Trp Phe Gly Trp Ser
260

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Lys Phe Leu Asp Asn Phe His Val Gln Thr Lys Arg Glu His Ala
1 5 10 15
Leu Leu Gly Asp Asn Glu Asn Gly Glu Asn Asp Glu Glu Gly Glu
20 25 30
Val Ala Asn Pro Lys Trp Ile Thr Ile Lys Ala Ala Leu Leu Leu
35 40 45
Leu Gly Ala Ala Ile Ala Ala Ala Phe Ala Asp Pro Leu Val Asp Thr
50 55 60
Val Asn Asn Phe Ser Ala Ala Thr Gly Ile Pro Ser Phe Phe Ile Ser
65 70 75 80
Phe Ile Ala Leu Pro Leu Ala Thr Asn Ser Ser Glu Ala Val Ser Ala
85 90 95
Ile Ile Phe Ala Ser Arg Lys Lys Ile Arg Thr Ala Ser Leu Thr Phe
100 105 110
Ser Glu Leu Cys Gly Gly Val Thr Met Asn Asn Ile Leu Cys Leu Ser
115 120 125
Val Phe Leu Ala Ile Val Tyr Val Arg Gly Leu Thr Trp Asn Phe Ser
130 135 140
Ser Glu Val Leu Val Ile Leu Ile Val Cys Leu Val Met Gly Gly Phe
145 150 155 160
Ala Ser Phe Arg Thr Thr Tyr Pro Leu Trp Thr Cys Phe Ile Ala Tyr
165 170 175
Leu Leu Tyr Pro Phe Ser Leu Gly Leu Val Tyr Ile Leu Asp Tyr Trp
180 185 190
Phe Gly Trp Ser
195

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..598
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

aaatttcaat	tttaagata	aaagtaaatg	aactggtaag	ccaChgnntt	tggttctgct	60
cttaccgttc	tcccaacttc	catatccaaa	ctgaaaagaca	ctgggttttg	ttttgctggg	120
aaaaggagaa	acttcacaaa	gatgccacct	ttgaatctct	tcactaacat	accagtgcac	180
gccgtcactt	gctcagacat	cctcaaggac	gccactaagg	ccgtcgctaa	aatcatcgcc	240
aaacctgaat	ccatgtgat	gatactgctt	aacagtggag	tgccccattg	atttgcgggt	300
acctagggaac	ctgctgcata	tgagaaattg	atatctattg	ggggattagg	acctggcgta	360
aacgggaagc	ttagcgagac	gatatctgag	attctccaaa	ttaagctctc	catagacagc	420
tctcgctttt	atacacaatt	ctacgattct	ccgcgacctt	tcttcggtta	caatggatca	480
actttctgaa	aagagcgcaa	ttcaaccttg	taatgatatt	tggttagaa	ctgtttgctt	540
attcatttca	aaagctgtaa	tctgaacca	taattataa	ttttacctcc	ctcaaaagc	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..54

(D) OTHER INFORMATION: / Ceres Seq. ID 1565547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ile	Ser	Ile	Leu	Lys	Ile	Lys	Val	Asn	Glu	Leu	Val	Ser	His	Xaa	Phe
1			5						10					15	
Trp	Phe	Cys	Ser	Tyr	Arg	Tyr	Pro	Asn	Phe	His	Ile	Gln	Thr	Glu	Arg
			20					25					30		
His	Trp	Phe	Trp	Phe	Cys	Arg	Glu	Lys	Glu	Lys	Leu	Gln	Lys	Asp	Ala
			35				40					45			
His	Phe	Glu	Ser	Leu	His										
			50												

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..54

(D) OTHER INFORMATION: / Ceres Seq. ID 1565548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Pro	Thr	Leu	Asn	Leu	Phe	Thr	Asn	Ile	Pro	Val	Asp	Ala	Val	Thr
1			5						10				15		
Cys	Ser	Asp	Ile	Leu	Lys	Asp	Ala	Thr	Lys	Ala	Val	Ala	Lys	Ile	Ile
			20					25					30		
Gly	Lys	Pro	Glu	Ser	Tyr	Val	Met	Ile	Leu	Leu	Asn	Ser	Gly	Val	Pro
			35				40					45			
Ile	Ala	Phe	Ala	Gly	Thr										
			50												

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..35

(D) OTHER INFORMATION: / Ceres Seq. ID 1565549
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
Met Asp Gln Leu Ser Glu Lys Arg Arg Ile Gln Pro Cys Asn Asp Ile
1 5 10 15
Trp Val Arg Thr Val Cys Leu Phe Ile Ser Lys Ala Val Ile Leu Asn
20 25 30
His Asn Leu
35

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1285 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1285

(D) OTHER INFORMATION: / Ceres Seq. ID 1565556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

gcagacgaat	gtttttggt	tcgagaattt	gctgaaatct	attcaacgta	tacagaggct	60
ggagctgggg	aagaaaagga	ttgtctatgg	agggagacgt	cggaaataggt	ttgggtatgcc	120
agaatactat	ggatgggaag	gcgagtaatg	gaaatggttt	agagaagact	gtacctttctt	180
gttgccctaa	ggctatggca	tgtgtacctg	aggatgatgc	taagtgtcac	tccactgttg	240
ttttctgggtg	gttttcggaa	cctcaccctc	gctctgggaa	aaaaggcggc	aaagcagctc	300
atttcaacaa	cctcatgttg	ccaggagaag	cacactcact	gaaagtgtag	aaagtcttgt	360
tcaaagacaa	gtcggatatt	caggaagctc	tagtgttcga	gtcagccacg	tacggaaaagg	420
tgcttgttct	agatggtatc	gtacagctga	ccgaaaaaga	tgaatgtgca	tatcaggaga	480
tgatagccca	tctgccttta	tgctctatat	cttccccctaa	aaatgttctt	gttgtttggtg	540
gaggtgatgg	tgggtgtctt	cgagagattt	ctcgccatag	tctgtttgag	gtttattgata	600
tctgtgagat	agacaagaatg	gttatagatg	tgtctaaaga	gttcttcccc	gagttagcgg	660
ttgggtttga	cgatctcctg	gttcaacctc	acattgggtga	tgtgtgtgta	tctctccogta	720
aatccccctga	agggaaagtat	gatgccatca	ttgttgattc	ttcagatccc	gtaggctcgt	780
ctcttgccgt	tgttgagaag	cotttcttcg	agacactggc	tagagcgttg	aagcctgggg	840
gagttctttg	taacatggca	gaaagtatgt	ggctccatac	tcatcttatt	gaagatatga	900
tctccatttg	cogtcaaaaca	tcaaaaagtg	ttcactatgc	gtggagcagc	gtccccacat	960
atccaaagcg	cgtgattggg	ttcgtcttgt	gctctactga	aggaccagct	gttgacttca	1020
agaaaccaat	caaccttatt	gagaaactag	acgggtgcgt	gacccataaa	agagaattga	1080
agttctataa	ctctgatatg	cacagagccg	catttgcctt	gcccacattc	CTcgggagag	1140
aagttagcttc	acttctggct	tcttgacttc	tgtttggctc	taccatatcc	ctcatatcaa	1200
actttgtaga	actctttgaag	aggaataata	aatcattgaa	ggctttgtat	ctctaagttt	1260
actcctttat	aaaaagactt	atatt				

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..359

(D) OTHER INFORMATION: / Ceres Seq. ID 1565557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Glu Gly Asp Val Gly Ile Gly Leu Val Cys Gln Asn Thr Met Asp
1 5 10 15
Gly Lys Ala Ser Asn Gly Asn Gly Leu Glu Lys Thr Val Pro Ser Cys
20 25 30
Cys Leu Lys Ala Met Ala Cys Val Pro Glu Asp Asp Ala Lys Cys His
35 40 45
Ser Thr Val Ser Ser Gly Trp Phe Ser Glu Pro His Pro Arg Ser Gly

1	Met	Asp	Gly	Lys	Ala	Ser	Asn	Gly	Asn	Gly	Leu	Glu	Lys	Thr	Val	Pro
				5						10					15	
Ser	Cys	Cys	Leu	Lys	Ala	Met	Ala	Cys	Val	Pro	Glu	Asp	Asp	Ala	Lys	
			20					25						30		
Cys	His	Ser	Thr	Val	Val	Ser	Gly	Trp	Phe	Ser	Glu	Pro	His	Pro	Arg	
		35					40						45			
Ser	Gly	Lys	Lys	Gly	Gly	Lys	Ala	Val	Tyr	Phe	Asn	Asn	Pro	Met	Trp	
	50					55					60					
Pro	Gly	Glu	Ala	His	Ser	Leu	Lys	Val	Glu	Lys	Val	Leu	Phe	Lys	Asp	
65					70					75				80		

Lys Ser Asp Phe Gln Glu Val Leu Val Phe Glu Ser Ala Thr Tyr Gly
85 90 95
Lys Val Leu Val Leu Asp Gly Ile Val Gln Leu Thr Glu Lys Asp Glu
100 105 110
Cys Ala Tyr Gln Glu Met Ile Ala His Leu Pro Leu Cys Ser Ile Ser
115 120 125
Ser Pro Lys Asn Val Leu Val Val Gly Gly Gly Asp Gly Gly Val Leu
130 135 140
Arg Glu Ile Ser Arg His Ser Ser Val Glu Val Ile Asp Ile Cys Glu
145 150 155 160
Ile Asp Lys Met Val Ile Asp Val Ser Lys Lys Phe Phe Pro Glu Leu
165 170 175
Ala Val Gly Phe Asp Asp Pro Arg Val Gln Leu His Ile Gly Asp Ala
180 185 190
Ala Glu Phe Leu Arg Lys Ser Pro Glu Gly Lys Tyr Asp Ala Ile Ile
195 200 205
Val Asp Ser Ser Asp Pro Val Gly Pro Ala Leu Ala Leu Val Glu Lys
210 215 220
Pro Phe Phe Glu Thr Leu Ala Arg Ala Leu Lys Pro Gly Gly Val Leu
225 230 235 240
Cys Asn Met Ala Glu Ser Met Trp Leu His Thr His Leu Ile Glu Asp
245 250 255
Met Ile Ser Ile Cys Arg Gln Thr Phe Lys Ser Val His Tyr Ala Trp
260 265 270
Ser Ser Val Pro Thr Tyr Pro Ser Gly Val Ile Gly Phe Val Leu Cys
275 280 285
Ser Thr Glu Gly Pro Ala Val Asp Phe Lys Asn Pro Ile Asn Pro Ile
290 295 300
Glu Lys Leu Asp Gly Ala Met Thr His Lys Arg Glu Leu Lys Phe Tyr
305 310 315 320
Asn Ser Asp Met His Arg Ala Ala Phe Ala Leu Pro Thr Phe Leu Arg
325 330 335
Arg Glu Val Ala Ser Leu Leu Ala Ser
340 345

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..323
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Cys Val Pro Glu Asp Asp Ala Lys Cys His Ser Thr Val Val
1 5 10 15
Ser Gly Trp Phe Ser Glu Pro His Pro Arg Ser Gly Lys Lys Gly Gly
20 25 30
Lys Ala Val Tyr Phe Asn Asn Pro Met Trp Pro Gly Glu Ala His Ser
35 40 45
Leu Lys Val Glu Lys Val Leu Phe Lys Asp Lys Ser Asp Phe Gln Glu
50 55 60
Val Leu Val Phe Glu Ser Ala Thr Tyr Gly Lys Val Leu Val Leu Asp
65 70 75 80
Gly Ile Val Gln Leu Thr Glu Lys Asp Glu Cys Ala Tyr Gln Glu Met
85 90 95
Ile Ala His Leu Pro Leu Cys Ser Ile Ser Ser Pro Lys Asn Val Leu
100 105 110
Val Val Gly Gly Gly Asp Gly Gly Val Leu Arg Glu Ile Ser Arg His

115										120										125																	
Ser	Ser	Val	Glu	Val	Ile	Asp	Ile	Cys	Glu	Ile	Asp	Lys	Met	Val	Ile	Ser	Ser	Val	Glu	Val	Ile	Asp	Lys	Met	Val	Ile	Ser	Ser	Val	Glu	Val	Ile	Asp	Lys	Met	Val	Ile
130																135										140											
Asp	Val	Ser	Lys	Lys	Phe	Phe	Pro	Glu	Leu	Ala	Val	Gly	Phe	Asp	Asp	150										155											
145																150										155											
Pro	Arg	Val	Gln	Leu	His	Ile	Gly	Asp	Ala	Ala	Glu	Phe	Leu	Arg	Lys	165										170											
																165										170											
Ser	Pro	Glu	Gly	Lys	Tyr	Asp	Ala	Ile	Ile	Val	Asp	Ser	Ser	Asp	Pro	180										185											
																180										185											
Val	Gly	Pro	Ala	Leu	Ala	Leu	Val	Glu	Lys	Pro	Phe	Phe	Glu	Thr	Leu	195										200											
																195										200											
Ala	Arg	Ala	Leu	Lys	Pro	Gly	Gly	Val	Leu	Cys	Asn	Met	Ala	Glu	Ser	210										215											
																210										215											
Met	Trp	Leu	His	Thr	His	Leu	Ile	Glu	Asp	Met	Ile	Ser	Ile	Cys	Arg	225										230											
																225										230											
Gln	Thr	Phe	Lys	Ser	Val	His	Tyr	Ala	Trp	Ser	Ser	Val	Pro	Thr	Tyr	245										250											
																245										250											
Pro	Ser	Gly	Val	Ile	Gly	Phe	Val	Leu	Cys	Ser	Thr	Glu	Gly	Pro	Ala	260										265											
																260										265											
Val	Asp	Phe	Lys	Asn	Pro	Ile	Asn	Pro	Ile	Glu	Lys	Leu	Asp	Gly	Ala	275										280											
																275										280											
Met	Thr	His	Lys	Arg	Glu	Leu	Lys	Phe	Tyr	Asn	Ser	Asp	Met	His	Arg	290										295											
																290										295											
Ala	Ala	Phe	Ala	Leu	Pro	Thr	Phe	Leu	Arg	Arg	Glu	Val	Ala	Ser	Leu	305										310											
																305										310											
Leu	Ala	Ser																																			

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1485
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

aacacctag	ttctgtttc	ctaacaagg	ctctactttt	tcttttagta	actactatgg	60
ctcatttct	cgagacacg	gaaccctcg	tattctccgg	gaagaaacga	aacgatcgcg	120
atgacaacga	cggtgacgc	ttgtgttgcga	agaaatcagc	actggcggtg	tgtgatcgccg	180
accctgcag	ggccatagcg	aatatccgac	atgagtttgg	ggagcacggg	ggagtaaacga	240
tgtccatgca	agcctccgac	accttcacgc	tcattggaac	ggatccatcg	aggcggtatgt	300
tcacgggaga	actgggacgc	gacaacgaac	tctacgtata	cagccgacac	ttcaacccca	360
ccgtgctcaa	ctcagccgt	cagatggtcg	ctctcgaaag	caacccaagc	gcctactgta	420
ccctatgcgg	tatgtcggcg	atatcgtcag	tgatgtgcga	actgtgcagc	agcgaggagac	480
acgtgggtcg	ggcaagcacg	ctctacggag	gaacacacgc	tttgcctctc	catcttctgc	540
cacggacatg	taacataacc	acctccttgc	ttgacataac	ggaccatggc	gcggtggcga	600
acggcatcgt	tgagggttag	acacaggttc	tctactttga	gtcgggtggca	aaccgcagcg	660
tgactgtgct	tgacatacct	gaactgagcc	gtatggcaca	cgagaaggcg	gtgacggtgg	720
tggttgacaa	cacattcgcc	cccatgtgtc	tgtctccggc	caagcttggg	cgagatgtgg	780
tggttcacag	tatctccaag	ttcatcagtg	gtggggctga	catcatcgca	ggggccgctgt	840
gtggagtgga	gaagctgggt	gaagagagat	atggatcttc	gtggcggaatc	tctgatctgt	900
ctaggtcccca	ccatgaacgc	caagtggtgt	ttcgagctgt	ccgagcgaat	ccctcactgt	960
ggcctacgca	tgagagagca	cagccacaga	gcccaagtgc	atgctgagag	aatgagggat	1020
ttgggagatg	aagtcatata	tccaggggtc	gagaccaccc	cgcagcacaa	gctcttcaaa	1080
ggtatggtga	atagagacata	tggatacggg	ggattgtgtg	cgatagacat	ggagacagag	1140
ggaaagccca	acaagctcat	ggcatatctc	cagaacgcga	ctcagtttgg	cttgatggcc	1200
gtcagtttgg	gttactacga	gacactcatg	tcttgcctcg	ggagcagcac	cagcagcgag	1260
cttgaccctc	cgcagaagga	agctgcaggg	atctctcctg	gtcttgttacg	aatatcggtg	1320

gggtatgtgg gtacattgga gcagaagtgg acacaattcg agaagcattc ctcagaatgt 1380
aaaatgtott cttctatata tgaagggtttt ctttccccc aataccaaca attcatcatc 1440
tgcggtatat gtatgatgtg gccaatgttc agtctcttat ttgtgc

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..316
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Ala	His	Phe	Leu	Glu	Thr	Gln	Glu	Pro	Leu	Val	Phe	Ser	Gly	Lys	
1			5					10						15		
Lys	Arg	Asn	Asp	Arg	Asp	Asp	Asn	Asp	Gly	Asp	Ala	Leu	Val	Ala	Lys	
			20					25						30		
Lys	Ser	Ala	Leu	Ala	Val	Cys	Asp	Ala	Asp	Pro	Ala	Ala	Ala	Ile	Ala	
			35				40					45				
Asn	Ile	Arg	His	Glu	Phe	Gly	Glu	His	Gly	Gly	Val	Asn	Met	Ser	Ile	
			50				55					60				
Glu	Ala	Ser	Ala	Thr	Phe	Thr	Val	Met	Glu	Pro	Asp	Thr	Met	Arg	Arg	
			65				70				75				80	
Met	Phe	Thr	Gly	Glu	Leu	Gly	Pro	Asp	Asn	Asp	Phe	Tyr	Val	Tyr	Ser	
															95	
Arg	His	Phe	Asn	Pro	Thr	Val	Leu	Asn	Leu	Ser	Arg	Gln	Met	Ala	Ala	
															110	
Leu	Glu	Gly	Thr	Gln	Ala	Ala	Tyr	Cys	Thr	Ser	Ser	Gly	Met	Ser	Ala	
															125	
Ile	Ser	Ser	Val	Met	Leu	Gln	Leu	Cys	Ser	Ser	Gly	Gly	His	Val	Val	
															140	
Ala	Ala	Ser	Thr	Leu	Tyr	Gly	Gly	Thr	His	Ala	Leu	Leu	Ser	His	Phe	
															160	
Leu	Pro	Arg	Thr	Cys	Asn	Ile	Thr	Thr	Ser	Phe	Val	Asp	Ile	Thr	Asp	
															175	
His	Gly	Ala	Val	Ala	Asn	Ala	Ile	Val	Glu	Gly	Arg	Thr	Gln	Val	Leu	
															190	
Tyr	Phe	Glu	Ser	Val	Ala	Asn	Pro	Thr	Leu	Thr	Val	Ala	Asp	Ile	Pro	
															205	
Glu	Leu	Ser	Arg	Met	Ala	His	Glu	Lys	Gly	Val	Thr	Val	Val	Val	Asp	
															220	
Asn	Thr	Phe	Ala	Pro	Met	Val	Leu	Ser	Pro	Ala	Lys	Leu	Gly	Ala	Asp	
															235	
Val	Val	Val	His	Ser	Ile	Ser	Lys	Phe	Ile	Ser	Gly	Gly	Ala	Asp	Ile	
															255	
Ile	Ala	Gly	Ala	Val	Cys	Gly	Ser	Glu	Lys	Leu	Val	Glu	Arg	Asp	Asp	
															270	
Gly	Ser	Ser	Trp	Arg	Ile	Ser	Asp	Ala	Ser	Arg	Ser	His	His	Glu	Arg	
															285	
Gln	Gly	Gly	Phe	Arg	Ala	Leu	Arg	Ala	Asn	Pro	Ser	Leu	Gly	Pro	Thr	
															300	
His	Glu	Arg	Gln	Gln	Pro	Gln	Ser	Pro	Ser	Val	Cys					
															315	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..255
 (D) OTHER INFORMATION: / Ceres Seq. ID 1565570
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Met Ser Ile Glu Ala Ser Ala Thr Phe Thr Val Met Glu Pro Asp Thr
1      5      10      15
Met Arg Arg Met Phe Thr Gly Glu Leu Gly Pro Asp Asn Asp Phe Tyr
      20      25      30
Val Tyr Ser Arg His Phe Asn Pro Thr Val Leu Asn Leu Ser Arg Gln
      35      40      45
Met Ala Ala Leu Glu Gly Thr Gln Ala Ala Tyr Cys Thr Ser Ser Gly
50      55      60
Met Ser Ala Ile Ser Ser Val Met Leu Gln Leu Cys Ser Ser Gly Gly
65      70      75      80
His Val Val Ala Ala Ser Thr Leu Tyr Gly Gly Thr His Ala Leu Leu
      85      90      95
Ser His Phe Leu Pro Arg Thr Cys Asn Ile Thr Thr Ser Phe Val Asp
      100      105      110
Ile Thr Asp His Gly Ala Val Ala Asn Ala Ile Val Glu Gly Arg Thr
      115      120      125
Gln Val Leu Tyr Phe Glu Ser Val Ala Asn Pro Thr Leu Thr Val Ala
130      135      140
Asp Ile Pro Glu Leu Ser Arg Met Ala His Glu Lys Gly Val Thr Val
145      150      155      160
Val Val Asp Asn Thr Phe Ala Pro Met Val Leu Ser Pro Ala Lys Leu
      165      170      175
Gly Ala Asp Val Val Val His Ser Ile Ser Lys Phe Ile Ser Gly Gly
      180      185      190
Ala Asp Ile Ile Ala Gly Ala Val Cys Gly Ser Glu Lys Leu Val Glu
195      200      205
Arg Asp Asp Gly Ser Ser Trp Arg Ile Ser Asp Ala Ser Arg Ser His
210      215      220
His Glu Arg Gln Gly Gly Phe Arg Ala Leu Arg Ala Asn Pro Ser Leu
225      230      235      240
Gly Pro Thr His Glu Arg Ala Gln Pro Gln Ser Pro Ser Val Cys
      245      250      255
```

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 244 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..244
 (D) OTHER INFORMATION: / Ceres Seq. ID 1565571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
Met Glu Pro Asp Thr Met Arg Arg Met Phe Thr Gly Glu Leu Gly Pro
1      5      10      15
Asp Asn Asp Phe Tyr Val Tyr Ser Arg His Phe Asn Pro Thr Val Leu
      20      25      30
Asn Leu Ser Arg Gln Met Ala Ala Leu Glu Gly Thr Gln Ala Ala Tyr
35      40      45
Cys Thr Ser Ser Gly Met Ser Ala Ile Ser Ser Val Met Leu Gln Leu
50      55      60
Cys Ser Ser Gly Gly His Val Val Ala Ala Ser Thr Leu Tyr Gly Gly
65      70      75      80
Thr His Ala Leu Leu Ser His Phe Leu Pro Arg Thr Cys Asn Ile Thr
```


(2) INFORMATION FOR SEO ID NO:16:

(A) LENGTH: 751 base pairs

(C) STRANDEDNESS: single

MOLECULE TYPE: DNA (g)

(A) NAME

(D) OTHER INFORMATION

gagaag gaacattcac tctcacgcgc ttcaactttc

(2) INFORMATION FOR SEQ ID NO:17:

(A) LENGTH: 182 amino acids

(C) STRANDEDNESS:

MOLECULE TYPE: peptid

(A) NAME

(D) OTHER INFORMATICS

Gly Glu Gly Thr Phe Thr Leu Thr Arg Phe

20 25 30
Lys Met Ala Asp Gln Leu Thr Asp Asp Gln Ile Ser Glu Phe Lys Glu
35 40 45
Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys
50 55 60
Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala
65 70 75 80
Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr
85 90 95
Ile Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp
100 105 110
Thr Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys
115 120 125
Asp Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val Met Thr
130 135 140
Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg
145 150 155 160
Glu Ala Asp Val Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu Phe Val
165 170 175
Lys Val Met Met Ala Lys
180

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala Asp Gln Leu Thr Asp Asp Gln Ile Ser Glu Phe Lys Glu Ala
1 5 10 15
Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys Glu
20 25 30
Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu
35 40 45
Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile
50 55 60
Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp Thr
65 70 75 80
Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys Asp
85 90 95
Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn
100 105 110
Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu
115 120 125
Ala Asp Val Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu Phe Val Lys
130 135 140
Val Met Met Ala Lys
145

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..113
(D) OTHER INFORMATION: / Ceres Seq. ID 1565579
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu Asp Met
1 5 10 15
Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp Phe Pro Glu
20 25 30
Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp Thr Asp Ser Glu Glu
35 40 45
Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys Asp Gln Asn Gly Phe
50 55 60
Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu Gly Glu Lys
65 70 75 80
Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala Asp Val Asp
85 90 95
Gly Asp Gly Gln Ile Asn Tyr Glu Glu Phe Val Lys Val Met Met Ala
100 105 110
Lys

- (2) INFORMATION FOR SEQ ID NO:20:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1602 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1602
(D) OTHER INFORMATION: / Ceres Seq. ID 1565612
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
agctactact gttgaagcga ttctcactaa aacctcgtaa cacatcgccct ttatctcttt 60
ctctagatct actgcgtatg gctactatca ccgttgttaa ggctagacag atctctcgaca 120
gtcgtgttaa tccacaccgt gaggtggata tccacacgtc aaatggtgtt aaggtttacag 180
cagctgttcc aagtggagct tccactggta tctatgaggg tcttgagctg agggatggag 240
gatctgacta ccttggaag ggtgtatcta aggctgttgg caatgtgaac aacatcatcg 300
ggccagcact tattggaag gacccaactc agcagactgc tattgacaac ttcatgtgtc 360
atgaacttga cggaacccaa aacgagtggg ggtggtgcaa gcaaaagctt ggagccaatg 420
cgattcttgc tgtgtctctt gctgtctgca aagctggggc tgttgtcagc ggcattctctc 480
tatacaagca cattgccaac ctgtctggta accccaagat tgtgctacca gtctctcgct 540
tcaacgtcat caatggttga tcccatgccg gaacaagctc tgcgtatcag gagtttatga 600
tctctctgtg tggagctgct tctttcaagg gagccatgaa gatgggtgtg gaagtttacc 660
accacttgaa gtctgtgatt aagaagaagt acggccagga tgcaccaaat gtgtgtgatg 720
aaggtggggt tgcaccaaac attcaggaga acaaggaggg tcttgaattg ctcaagactg 780
ctatcgagaa ggctggatgc actggaaaag ttgtcattgg aatggatgtt gccgcttcag 840
agttctactc agaagacaag acctacgact tgaacttcaa agaagagaa aacaatggct 900
ctcagaagat tctcgtgat gctctaaaag acctgtacaa gtccctttgc gctgagtacc 960
caatcgtgtc cattgaggac ccatttgacc aagatgactg ggagcactat gctaagatga 1020
ccaatcagtg tggaaaccgag gtccagaTtt gtcggtgatg atttgtttgt cactaacccc 1080
aagagagattg ctaaggccaat cgccgagaag tcttgcaatg ctctctcttt gaaggttaac 1140
caaatcggat ctgtaaccga gagtatcgag gcaggttaaga tgcgaagaa acgaggttgg 1200
ggagtgtatg ccagccacag aagtggtgaa accgaggaca cattcatctg tgaacttagcc 1260
gttggtctgt ctactggaca aatcaaaaac ggtgctcctt cgagatcaga gctgcttggc 1320
aagtaacaac agcttttgcg tattgaggag gagggtggat cagaggcaat ttacgctgga 1380
gtcaacttcc gcaaacctgt agaacctacg taatggagac ttttagaagc aaagtgtgtc 1440
tctttgtgac gaggagaaga tgacctgagt ttgatcattt gcttttaata aataaaacgt 1500
tctgttttga tttctttttt gtttggtttc ttactgtctt ttgtgaacct tttttgggaa 1560
aagttactca tttttgtaag ggaacatga gaatgctcg cc

- (2) INFORMATION FOR SEQ ID NO:21:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..351
(D) OTHER INFORMATION: / Ceres Seq. ID 1565613
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
Leu Leu Leu Leu Lys Arg Phe Ser Leu Lys Pro Ser Asn Thr Ser Pro
1 5 10 15
Leu Ser Leu Ser Leu Asp Leu Leu Ala Met Ala Thr Ile Thr Val Val
20 25 30
Lys Ala Arg Gln Ile Phe Asp Ser Arg Gly Asn Pro Thr Val Glu Val
35 40 45
Asp Ile His Thr Ser Asn Gly Val Lys Val Thr Ala Ala Val Pro Ser
50 55 60
Gly Ala Ser Thr Gly Ile Tyr Glu Ala Leu Glu Leu Arg Asp Gly Gly
65 70 75 80
Ser Asp Tyr Leu Gly Lys Gly Val Ser Lys Ala Val Gly Asn Val Asn
85 90 95
Asn Ile Ile Gly Pro Ala Leu Ile Gly Lys Asp Pro Thr Gln Gln Thr
100 105 110
Ala Ile Asp Asn Phe Met Val His Glu Leu Asp Gly Thr Gln Asn Glu
115 120 125
Trp Gly Trp Cys Lys Gln Lys Leu Gly Ala Asn Ala Ile Leu Ala Val
130 135 140
Ser Leu Ala Val Cys Lys Ala Gly Ala Val Val Ser Gly Ile Pro Leu
145 150 155 160
Tyr Lys His Ile Ala Asn Leu Ala Gly Asn Pro Lys Ile Val Leu Pro
165 170 175
Val Pro Ala Phe Asn Val Ile Asn Gly Gly Ser His Ala Gly Asn Lys
180 185 190
Leu Ala Met Gln Glu Phe Met Ile Leu Pro Val Gly Ala Ala Ser Phe
195 200 205
Lys Gly Ala Met Lys Met Gly Val Glu Val Tyr His His Leu Lys Ser
210 215 220
Val Ile Lys Lys Lys Tyr Gly Gln Asp Ala Thr Asn Val Gly Asp Glu
225 230 235 240
Gly Gly Phe Ala Pro Asn Ile Gln Glu Asn Lys Glu Gly Leu Glu Leu
245 250 255
Leu Lys Thr Ala Ile Glu Lys Ala Gly Tyr Thr Gly Lys Val Val Ile
260 265 270
Gly Met Asp Val Ala Ala Ser Glu Phe Tyr Ser Glu Asp Lys Thr Tyr
275 280 285
Asp Leu Asn Phe Lys Glu Glu Asn Asn Asn Gly Ser Gln Lys Ile Ser
290 295 300
Gly Asp Ala Leu Lys Asp Leu Tyr Lys Ser Phe Val Ala Glu Tyr Pro
305 310 315 320
Ile Val Ser Ile Glu Asp Pro Phe Asp Gln Asp Asp Trp Glu His Tyr
325 330 335
Ala Lys Met Thr Thr Glu Cys Gly Thr Glu Val Gln Ile Cys Arg
340 345 350

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 326 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..326

(D) OTHER INFORMATION: / Ceres Seq. ID 1565614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Met Ala Thr Ile Thr Val Val Lys Ala Arg Gln Ile Phe Asp Ser Arg
1      5      10      15
Gly Asn Pro Thr Val Glu Val Asp Ile His Thr Ser Asn Gly Val Lys
20     25     30
Val Thr Ala Ala Val Pro Ser Gly Ala Ser Thr Gly Ile Tyr Glu Ala
35     40     45
Leu Glu Leu Arg Asp Gly Gly Ser Asp Tyr Leu Gly Lys Gly Val Ser
50     55     60
Lys Ala Val Gly Asn Val Asn Asn Ile Ile Gly Pro Ala Leu Ile Gly
65     70     75     80
Lys Asp Pro Thr Gln Gln Thr Ala Ile Asp Asn Phe Met Val His Glu
85     90     95
Leu Asp Gly Thr Gln Asn Glu Trp Gly Trp Cys Lys Gln Lys Leu Gly
100    105    110
Ala Asn Ala Ile Leu Ala Val Ser Leu Ala Val Cys Lys Ala Gly Ala
115    120    125
Val Val Ser Gly Ile Pro Leu Tyr Lys His Ile Ala Asn Leu Ala Gly
130    135    140
Asn Pro Lys Ile Val Leu Pro Val Pro Ala Phe Asn Val Ile Asn Gly
145    150    155    160
Gly Ser His Ala Gly Asn Lys Leu Ala Met Gln Glu Phe Met Ile Leu
165    170    175
Pro Val Gly Ala Ala Ser Phe Lys Gly Ala Met Lys Met Gly Val Glu
180    185    190
Val Tyr His His Leu Lys Ser Val Ile Lys Lys Lys Tyr Gly Gln Asp
195    200    205
Ala Thr Asn Val Gly Asp Glu Gly Gly Phe Ala Pro Asn Ile Gln Glu
210    215    220
Asn Lys Glu Gly Leu Glu Leu Lys Thr Ala Ile Glu Lys Ala Gly
225    230    235    240
Tyr Thr Gly Lys Val Val Ile Gly Met Asp Val Ala Ala Ser Glu Phe
245    250    255
Tyr Ser Glu Asp Lys Thr Tyr Asp Leu Asn Phe Lys Glu Glu Asn Asn
260    265    270
Asn Gly Ser Gln Lys Ile Ser Gly Asp Ala Leu Lys Asp Leu Tyr Lys
275    280    285
Ser Phe Val Ala Glu Tyr Pro Ile Val Ser Ile Glu Asp Pro Phe Asp
290    295    300
Gln Asp Asp Trp Glu His Tyr Ala Lys Met Thr Thr Glu Cys Gly Thr
305    310    315    320
Glu Val Gln Ile Cys Arg
325

```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..234

(D) OTHER INFORMATION: / Ceres Seq. ID 1565615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

Met Val His Glu Leu Asp Gly Thr Gln Asn Glu Trp Gly Trp Cys Lys
1      5      10      15

```

Gln Lys Leu Gly Ala Asn Ala Ile Leu Ala Val Ser Leu Ala Val Cys
20 25 30
Lys Ala Gly Ala Val Val Ser Gly Ile Pro Leu Tyr Lys His Ile Ala
35 40 45
Asn Leu Ala Gly Asn Pro Lys Ile Val Leu Pro Val Pro Ala Phe Asn
50 55 60
Val Ile Asn Gly Gly Ser His Ala Gly Asn Lys Leu Ala Met Gln Glu
65 70 75 80
Phe Met Ile Leu Pro Val Gly Ala Ala Ser Phe Lys Gly Ala Met Lys
85 90 95
Met Gly Val Glu Val Tyr His His Leu Lys Ser Val Ile Lys Lys Lys
100 105 110
Tyr Gly Gln Asp Ala Thr Asn Val Gly Asp Glu Gly Gly Phe Ala Pro
115 120 125
Asn Ile Gln Glu Asn Lys Gly Gly Leu Glu Leu Lys Thr Ala Ile
130 135 140
Glu Lys Ala Gly Tyr Thr Gly Lys Val Val Ile Gly Met Asp Val Ala
145 150 155 160
Ala Ser Glu Phe Tyr Ser Glu Asp Lys Thr Tyr Asp Leu Asn Phe Lys
165 170 175
Glu Glu Asn Asn Asn Gly Ser Gln Lys Ile Ser Gly Asp Ala Leu Lys
180 185 190
Asp Leu Tyr Lys Ser Phe Val Ala Glu Tyr Pro Ile Val Ser Ile Glu
195 200 205
Asp Pro Phe Asp Gln Asp Asp Trp Glu His Tyr Ala Lys Met Thr Thr
210 215 220
Glu Cys Gly Thr Glu Val Gln Ile Cys Arg
225 230

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1292
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ataaaaatca	ttatccaaaa	aagtgcaccc	ttcttcgcgc	tagaaaaacat	tcggtaacc	60
atgtccgaa	gaatcacttg	ttcttcttca	cttggtctcac	ctctctctctt	ctctccgcttc	120
tttgcgaac	tcctctcgctc	ttactcctca	ccgaccaccca	tcgccgtctc	aggccgcaac	180
attcgcgcac	tatcaactctc	aaccactctt	cggtgcattt	gttcacactc	ttcatctgaa	240
atcatctccg	agcatctctc	gttctgcagg	gtttacaaaag	acggtctgat	cgaacgtctt	300
tcggcaccgc	aaacagtcctc	gggttctctca	aaaccacgaa	acgacgtctg	ttcaaaagac	360
gttgtctact	caacgggggca	taacctctcc	gttcgtctct	ttctccctca	caaatcaaca	420
caactgcgcg	ccggtaacaa	actccctcta	cttatctact	cccacggcgg	agcttgagata	480
aacgaatccc	ctttctcccc	aatctaccac	aatttctcca	cggaggtagt	taaatccgct	540
aactgcctcg	ccgtctcgggt	tcaataaccgc	cgtgcaccgg	aagatccggg	tcgggtctgc	600
tatgaagata	catggtctgc	tattcaatgg	attttctcac	attccgatgg	atctggtgaa	660
gaagattgga	ttacaacaata	cgtgatgttc	gaaaaagttt	ttctcgcggg	agatagtgc	720
ggtggttaata	tatctcatca	catggtgatg	agagctggta	aagagaagct	taagcctgaa	780
atcaaaagga	ctgtgattgt	gcataccagc	atttggggga	aagatccggg	cgatgagcac	840
gatgtgcaag	atagagagat	cagagacgga	gttgacagaa	tttggggaaa	aattgtgagt	900
ccgaatagt	ttgatggagc	ggatgatccg	tggtttaatg	tggttggtac	ccggctcgat	960
ttttccggga	tgggatgtga	gaagggtttt	gttgaggtgg	ctgggaaaag	tgtgttttgg	1020
cggaagagat	tagCttacgc	ggagaagcta	aagaagagtg	ggtggaagag	agaggtggaq	1080
gtgattgagg	aagaagatga	agaacattgc	ttccatctct	taaatccaag	ttctgaaaat	1140
gtccccagct	tcattgaagag	actgtgggag	tttatcaactg	gttaaacattg	ttcttttgtg	1200
gacacgaata	aattttgatg	taacctttga	atttgatttg	gttagataat	tatggttaag	1260

gaattaaata caggaataac tctgttctga ct

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 394 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..394

(D) OTHER INFORMATION: / Ceres Seq. ID 1565617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ile	Lys	Ile	Ile	Ile	Gln	Lys	Ser	Ala	Thr	Ser	Phe	Ala	Val	Glu	Asn	
1				5					10					15		
Ile	Pro	Val	Thr	Met	Leu	Arg	Arg	Ile	Thr	Cys	Ser	Ser	Ser	Leu	Ala	
				20					25					30		
Ser	Pro	Ser	Leu	Phe	Leu	Arg	Phe	Arg	Gln	Leu	Pro	Arg	Ser	Tyr		
				35					40					45		
Ser	Ser	Pro	Thr	Thr	Ile	Ala	Val	Ser	Gly	Arg	Asn	Ile	Arg	Arg	Leu	
				50					55					60		
Ser	Thr	Pro	Thr	Thr	Leu	Arg	Cys	Ile	Cys	Ser	His	Ser	Ser	Ser	Glu	
65					70				75					80		
Ile	Ile	Ser	Glu	His	Pro	Pro	Phe	Val	Arg	Val	Tyr	Lys	Asp	Gly	Arg	
				85					90					95		
Ile	Glu	Arg	Leu	Ser	Gly	Thr	Glu	Thr	Val	Pro	Ala	Ser	Leu	Asn	Pro	
				100					105					110		
Arg	Asn	Asp	Val	Val	Ser	Lys	Asp	Val	Val	Tyr	Ser	Pro	Gly	His	Asn	
				115					120					125		
Leu	Ser	Val	Arg	Leu	Phe	Leu	Pro	His	Lys	Ser	Thr	Gln	Leu	Ala	Ala	
				130					135					140		
Gly	Asn	Lys	Leu	Pro	Leu	Leu	Ile	Tyr	Phe	His	Gly	Gly	Ala	Trp	Ile	
145					150				155					160		
Asn	Glu	Ser	Pro	Phe	Ser	Pro	Ile	Tyr	His	Asn	Phe	Leu	Thr	Glu	Val	
				165					170					175		
Val	Lys	Ser	Ala	Asn	Cys	Leu	Ala	Val	Ser	Val	Gln	Tyr	Arg	Arg	Ala	
				180					185					190		
Pro	Glu	Asp	Pro	Val	Pro	Ala	Ala	Tyr	Glu	Asp	Thr	Trp	Ser	Ala	Ile	
				195					200					205		
Gln	Trp	Ile	Phe	Ser	His	Ser	Asp	Gly	Ser	Gly	Glu	Glu	Asp	Trp	Ile	
									215					220		
Asn	Lys	Tyr	Ala	Asp	Phe	Glu	Lys	Val	Phe	Leu	Ala	Gly	Asp	Ser	Ala	
225					230				235					240		
Gly	Gly	Asn	Ile	Ser	His	His	Met	Ala	Met	Arg	Ala	Gly	Lys	Glu	Lys	
				245					250					255		
Leu	Lys	Pro	Arg	Ile	Lys	Gly	Thr	Val	Ile	Val	His	Pro	Ala	Ile	Trp	
				260					265					270		
Gly	Lys	Asp	Pro	Val	Asp	Glu	His	Asp	Val	Gln	Asp	Arg	Glu	Ile	Arg	
				275					280					285		
Asp	Gly	Val	Ala	Glu	Ile	Trp	Glu	Lys	Ile	Val	Ser	Pro	Asn	Ser	Val	
				290					295					300		
Asp	Gly	Ala	Asp	Asp	Pro	Trp	Phe	Asn	Val	Val	Gly	Ser	Gly	Ser	Asp	
305					310				315					320		
Phe	Ser	Gly	Met	Gly	Cys	Glu	Lys	Val	Leu	Val	Glu	Val	Ala	Gly	Lys	
				325					330					335		
Asp	Val	Phe	Trp	Arg	Gln	Gly	Leu	Ala	Tyr	Ala	Glu	Lys	Leu	Lys	Lys	
				340					345					350		
Ser	Gly	Trp	Lys	Gly	Glu	Val	Glu	Val	Ile	Glu	Glu	Glu	Asp	Glu	Glu	
				355					360					365		
His	Cys	Phe	His	Leu	Leu	Asn	Pro	Ser	Ser	Glu	Asn	Ala	Pro	Ser	Phe	
				370					375					380		

370

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1179

(D) OTHER INFORMATION: / Ceres Seq. ID 1565633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
atcttaatta tactgatctt tatcgttgac tagatttaag aaacaaaaata ataagatgggt    60
tagggcacaat atagtgagca tggttctcct gatgcacgcc atcggtgggt ttcccttttca    120
tgcgaggggga ttaagtatga cttactacat gatgagctgt cctttcgctg aacagattgt    180
gaagaacagt gttaacaaat ctcttcaagc cgatcccaact ttagccogctg gtcttatccg    240
tatgtgtgtc cagcactggt tcatcgaggg atgtgatgag tcaattctgc tagattcaac    300
gaaagacaac actgcgggaaa aggattcgcc tgcgaatctg agtctacgtg gctacgagat    360
catcgatgat gcaaaggaga aaatcgagaa tagatgtcca ggagttgtat catgcgcaga    420
tatagttgcc atggctgcta gagatgctgt cttttgggct ggtggtccat attatgacat    480
accgaaagga aggtttgatg gtaaaagatc aaagatagaa gatacaagaa atctaccttc    540
accttttctt aatgcctctc aactcattca aacttttggc caacgttggt tcactccaca    600
agatgttgtt gctctctctg gacgacatac cctaggagtt gcacgatgct cctccttcaa    660
ggctagactt accgtcccaag actcttctatt agactcgact ttgcaaaaca ctctctctaa    720
aacatgcagc gggggtgaca atgcagagca accctttgat gCtaacgcgca acgatttcca    780
caatgcttac ttcaatgcgc ttcagatgaa atcaggagtc cctttttcag accaaacttt    840
attcaacaca ccaaggacca ggaatcttgt taacggctat gcatttaacc aaagccaagt    900
ctctcttgat ttocaaacgg ccatgcgcaa gatgagcaat ctgtatgta aacttggtct    960
tcaaggtgaa gtccgtcaaa attgtcggag tattaattag cttagaccac atctactttac    1020
gatttttgta tttataataa gttctctact cttgtatat gaagaatcat gaattcttca    1080
ggctactatg taaaaattgt gtactctcgt aatagcagt tgtatactta ttgcttgtgt    1140
ggttcagata tccatcaaaa agtaataatac ttgtgttgc
```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..314

(D) OTHER INFORMATION: / Ceres Seq. ID 1565634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
Met Val Arg Ala Asn Ile Val Ser Met Val Leu Leu Met His Ala Ile
1      5      10      15
Val Gly Phe Pro Phe His Ala Arg Gly Leu Ser Met Thr Tyr Tyr Met
20      25      30
Met Ser Cys Pro Phe Ala Glu Gln Ile Val Lys Asn Ser Val Asn Asn
35      40      45
Ala Leu Gln Ala Asp Pro Thr Leu Ala Ala Gly Leu Ile Arg Met Leu
50      55      60
Phe His Asp Cys Phe Ile Glu Gly Cys Asp Ala Ser Ile Leu Leu Asp
65      70      75      80
Ser Thr Lys Asp Asn Thr Ala Glu Lys Asp Ser Pro Ala Asn Leu Ser
85      90      95
Leu Arg Gly Tyr Glu Ile Ile Asp Asp Ala Lys Glu Lys Ile Glu Asn
100      105      110
Arg Cys Pro Gly Val Val Ser Cys Ala Asp Ile Val Ala Met Ala Ala
115      120      125
```

Arg Asp Ala Val Phe Trp Ala Gly Gly Pro Tyr Tyr Asp Ile Pro Lys
130 135 140
Gly Arg Phe Asp Gly Lys Arg Ser Lys Ile Glu Asp Thr Arg Asn Leu
145 150 155 160
Pro Ser Pro Phe Leu Asn Ala Ser Gln Leu Ile Gln Thr Phe Gly Gln
165 170 175
Arg Gly Phe Thr Pro Gln Asp Val Val Ala Leu Ser Gly Ala His Thr
180 185 190
Leu Gly Val Ala Arg Cys Ser Ser Phe Lys Ala Arg Leu Thr Val Pro
195 200 205
Asp Ser Ser Leu Asp Ser Thr Phe Ala Asn Thr Leu Ser Lys Thr Cys
210 215 220
Ser Ala Gly Asp Asn Ala Glu Gln Pro Phe Asp Ala Thr Arg Asn Asp
225 230 235 240
Phe Asp Asn Ala Tyr Phe Asn Ala Leu Gln Met Lys Ser Gly Val Leu
245 250 255
Phe Ser Asp Gln Thr Leu Phe Asn Thr Pro Arg Thr Arg Asn Leu Val
260 265 270
Asn Gly Tyr Ala Leu Asn Gln Ala Lys Phe Phe Phe Asp Phe Gln Gln
275 280 285
Ala Met Arg Lys Met Ser Asn Leu Asp Val Lys Leu Gly Ser Gln Gly
290 295 300
Glu Val Arg Gln Asn Cys Arg Ser Ile Asn
305 310

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..306

(D) OTHER INFORMATION: / Ceres Seq. ID 1565635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Val Leu Leu Met His Ala Ile Val Gly Phe Pro Phe His Ala Arg
1 5 10 15
Gly Leu Ser Met Thr Tyr Tyr Met Met Ser Cys Pro Phe Ala Glu Gln
20 25 30
Ile Val Lys Asn Ser Val Asn Asn Ala Leu Gln Ala Asp Pro Thr Leu
35 40 45
Ala Ala Gly Leu Ile Arg Met Leu Phe His Asp Cys Phe Ile Glu Gly
50 55 60
Cys Asp Ala Ser Ile Leu Leu Asp Ser Thr Lys Asp Asn Thr Ala Glu
65 70 75 80
Lys Asp Ser Pro Ala Asn Leu Ser Leu Arg Gly Tyr Glu Ile Ile Asp
85 90 95
Asp Ala Lys Glu Lys Ile Glu Asn Arg Cys Pro Gly Val Val Ser Cys
100 105 110
Ala Asp Ile Val Ala Met Ala Ala Arg Asp Ala Val Phe Trp Ala Gly
115 120 125
Gly Pro Tyr Tyr Asp Ile Pro Lys Gly Arg Phe Asp Gly Lys Arg Ser
130 135 140
Lys Ile Glu Asp Thr Arg Asn Leu Pro Ser Pro Phe Leu Asn Ala Ser
145 150 155 160
Gln Leu Ile Gln Thr Phe Gly Gln Arg Gly Phe Thr Pro Gln Asp Val
165 170 175
Val Ala Leu Ser Gly Ala His Thr Leu Gly Val Ala Arg Cys Ser Ser
180 185 190
Phe Lys Ala Arg Leu Thr Val Pro Asp Ser Ser Leu Asp Ser Thr Phe

195	200	205
Ala Asn Thr Leu Ser Lys Thr Cys Ser Ala Gly Asp Asn Ala Glu Gln		
210	215	220
Pro Phe Asp Ala Thr Arg Asn Asp Phe Asp Asn Ala Tyr Phe Asn Ala		
225	230	235
Leu Gln Met Lys Ser Gly Val Leu Phe Ser Asp Gln Thr Leu Phe Asn		
245	250	255
Thr Pro Arg Thr Arg Asn Leu Val Asn Gly Tyr Ala Leu Asn Gln Ala		
260	265	270
Lys Phe Phe Phe Asp Phe Gln Gln Ala Met Arg Lys Met Ser Asn Leu		
275	280	285
Asp Val Lys Leu Gly Ser Gln Gly Glu Val Arg Gln Asn Cys Arg Ser		
290	295	300

Ile Asn
305

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 302 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..302

(D) OTHER INFORMATION: / Ceres Seq. ID 1565636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	His	Ala	Ile	Val	Gly	Phe	Pro	Phe	His	Ala	Arg	Gly	Leu	Ser	Met
1			5					10					15		
Thr	Tyr	Tyr	Met	Met	Ser	Cys	Pro	Phe	Ala	Glu	Gln	Ile	Val	Lys	Asn
			20					25					30		
Ser	Val	Asn	Asn	Ala	Leu	Gln	Ala	Asp	Pro	Thr	Leu	Ala	Ala	Gly	Leu
			35				40					45			
Ile	Arg	Met	Leu	Phe	His	Asp	Cys	Phe	Ile	Glu	Gly	Cys	Asp	Ala	Ser
			50			55					60				
Ile	Leu	Leu	Asp	Ser	Thr	Lys	Asp	Asn	Thr	Ala	Glu	Lys	Asp	Ser	Pro
					70				75					80	
Ala	Asn	Leu	Ser	Leu	Arg	Gly	Tyr	Glu	Ile	Asp	Asp	Ala	Lys	Glu	
				85				90						95	
Lys	Ile	Glu	Asn	Arg	Cys	Pro	Gly	Val	Ser	Cys	Ala	Asp	Ile	Val	
			100				105					110			
Ala	Met	Ala	Ala	Arg	Asp	Ala	Val	Phe	Trp	Ala	Gly	Gly	Pro	Tyr	Tyr
			115				120					125			
Asp	Ile	Pro	Lys	Gly	Arg	Phe	Asp	Gly	Lys	Arg	Ser	Lys	Ile	Glu	Asp
			130			135					140				
Thr	Arg	Asn	Leu	Pro	Ser	Pro	Phe	Leu	Asn	Ala	Ser	Gln	Leu	Ile	Gln
					150				155					160	
Thr	Phe	Gly	Gln	Arg	Gly	Phe	Thr	Pro	Gln	Asp	Val	Val	Ala	Leu	Ser
			165					170						175	
Gly	Ala	His	Thr	Leu	Gly	Val	Ala	Arg	Cys	Ser	Ser	Phe	Lys	Ala	Arg
			180				185					190			
Leu	Thr	Val	Pro	Asp	Ser	Ser	Leu	Asp	Ser	Thr	Phe	Ala	Asn	Thr	Leu
			195				200					205			
Ser	Lys	Thr	Cys	Ser	Ala	Gly	Asp	Asn	Ala	Glu	Gln	Pro	Phe	Asp	Ala
			210			215					220				
Thr	Arg	Asn	Asp	Phe	Asp	Asn	Ala	Tyr	Phe	Asn	Ala	Leu	Gln	Met	Lys
			225			230			235					240	
Ser	Gly	Val	Leu	Phe	Ser	Asp	Gln	Thr	Leu	Phe	Asn	Thr	Pro	Arg	Thr
			245					250					255		
Arg	Asn	Leu	Val	Asn	Gly	Tyr	Ala	Leu	Asn	Gln	Ala	Lys	Phe	Phe	
			260				265					270			

Asp Phe Gln Gln Ala Met Arg Lys Met Ser Asn Leu Asp Val Lys Leu
275 280 285
Gly Ser Gln Gly Glu Val Arg Gln Asn Cys Arg Ser Ile Asn
290 295 300

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1200
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

gaaatctctt	atccattctt	ctcgtctctg	caaaatcccc	acttcacgaa	tcgcaaaaaga	60
tcaaggttta	ttgatctatt	gcgaaattag	ggtttgtaa	ttcgaatcgg	agattaataa	120
tagattttgt	gatggagtgt	tcatacgcga	tagaagaatc	ttgatttcga	tctcgatgaa	180
attaggagtc	gagggatttt	atttataatt	aagatggtga	atattaaaag	ccctttacgg	240
ctattcatag	aggattctat	taaggaatta	attaggggtt	tcaggagaca	aaggatcaaa	300
tggagaaatg	catttctctt	tggttctata	atgactacca	ttgtgttctt	gcttcataca	360
ccaacgtttt	cagtctcttc	tgatgaagaa	gaacccgagt	cttcttcgcc	tatttacttg	420
aatgggtctc	tgcatttgaa	tatccatatt	gtagtagtg	aagcaaaaag	tgaaaaattt	480
catactctta	gaacaagaac	tcctattgtg	caattgaatg	cttctgaagc	aagtgaagct	540
gttatttcga	gaaaaaggcg	aaaaaggaaa	aaaaagaaag	agacaaaaga	tgatctgatt	600
ctcaactgac	ctctctcagc	accacgacat	gtctatctt	ccctcagagag	acgtgctctt	660
tccttgcacc	cgaagaaaag	tcttacttat	gcaaaaactg	agattoacgc	tgccccggag	720
gtcataaatg	acacagatct	atttgcctca	ttgtttgaa	acctctctgt	tttcaaaaag	780
agctatgagc	tattggaact	gatactaaag	gtctacatat	atCctgacgc	agacaaccac	840
atcttccacg	aaccgcattt	gaacggtata	tatgcttcag	aaggttggtt	tatgaagcta	900
atggagtcga	acacacagtt	tgctacaaaag	aaccctgaga	aggctcaatt	gttctacatg	960
ccatatagtg	tgaacacagt	tcagaaaaat	atctttgttc	ctggatcaca	taacatcaaa	1020
ccctttatct	tcttttctag	aGactacgtc	aacatgctct	ccatcaataa	ccctctctgg	1080
aaccgcactc	atgggtcaga	tcatttctct	gtcgtctgcc	acgattgggt	atcgaaaatg	1140
ttctctatgt	aaagaccaat	gggtttactt	ccctcatttt	tatgttatga	tctctatttc	1200

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Val Asn Ile Lys Ser Pro Leu Arg Leu Phe Ile Glu Asp Ser Ile	
1 5 10 15	
Lys Glu Leu Ile Arg Gly Phe Arg Arg Gln Arg Ile Lys Trp Arg Asn	
20 25 30	
Ala Phe Leu Leu Gly Ser Ile Met Thr Thr Ile Val Val Leu Leu His	
35 40 45	
Thr Pro Thr Phe Ser Val Phe Ser Asp Glu Glu Thr Thr Glu Ser Ser	
50 55 60	
Ser Pro Ile Tyr Leu Asn Gly Ser Leu His Leu Asn Ile His Ile Val	
65 70 75 80	
Ser Ser Glu Ala Lys Val Glc Asn Phe His Thr Leu Arg Thr Arg Thr	
85 90 95	

Pro Ile Val Gln Leu Asn Ala Ser Glu Ala Ser Glu Ala Val Ile Ser
100 105 110
Arg Lys Arg Arg Lys Arg Lys Lys Arg Lys Lys Thr Lys Asp Asp Leu
115 120 125
Ile Leu Thr Asp Pro Pro Pro Ala Pro Arg His Val Leu Ser Ser Ser
130 135 140
Glu Arg Arg Ala Leu Ser Leu Pro Pro Lys Lys Ala Leu Thr Tyr Ala
145 150 155 160
Lys Leu Glu Ile Gln Arg Ala Pro Glu Val Ile Asn Asp Thr Asp Leu
165 170 175
Phe Ala Pro Leu Phe Arg Asn Leu Ser Val Phe Lys Arg Ser Tyr Glu
180 185 190
Leu Met Glu Leu Ile Leu Lys Val Tyr Ile Tyr Pro Asp Gly Asp Lys
195 200 205
Pro Ile Phe His Glu Pro His Leu Asn Gly Ile Tyr Ala Ser Glu Gly
210 215 220
Trp Phe Met Lys Leu Met Glu Ser Asn Thr Gln Phe Val Thr Lys Asn
225 230 235 240
Pro Glu Lys Ala His Leu Phe Tyr Met Pro Tyr Ser Val Lys Gln Leu
245 250 255
Gln Lys Ser Ile Phe Val Pro Gly Ser His Asn Ile Lys Pro Leu Ser
260 265 270
Ile Phe Leu Arg Asp Tyr Val Asn Met Leu Ser Ile Lys Tyr Pro Phe
275 280 285
Trp Asn Arg Thr His Gly Ser Asp His Phe Leu Val Ala Cys His Asp
290 295 300
Trp Val Ser Lys Met Phe Leu Cys
305 310

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..273

(D) OTHER INFORMATION: / Ceres Seq. ID 1565645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Thr Thr Ile Val Val Leu Leu His Thr Pro Thr Phe Ser Val Phe
1 5 10 15
Ser Asp Glu Glu Glu Thr Glu Ser Ser Ser Pro Ile Tyr Leu Asn Gly
20 25 30
Ser Leu His Leu Asn Ile His Ile Val Ser Ser Glu Ala Lys Val Glu
35 40 45
Asn Phe His Thr Leu Arg Thr Arg Thr Pro Ile Val Gln Leu Asn Ala
50 55 60
Ser Glu Ala Ser Glu Ala Val Ile Ser Arg Lys Arg Arg Lys Arg Lys
65 70 75 80
Lys Arg Lys Lys Thr Lys Asp Asp Leu Ile Leu Thr Asp Pro Pro Pro
85 90 95
Ala Pro Arg His Val Leu Ser Ser Ser Glu Arg Arg Ala Leu Ser Leu
100 105 110
Pro Pro Lys Lys Ala Leu Thr Tyr Ala Lys Leu Glu Ile Gln Arg Ala
115 120 125
Pro Glu Val Ile Asn Asp Thr Asp Leu Phe Ala Pro Leu Phe Arg Asn
130 135 140
Leu Ser Val Phe Lys Arg Ser Tyr Glu Leu Met Glu Leu Ile Leu Lys
145 150 155 160
Val Tyr Ile Tyr Pro Asp Gly Asp Lys Pro Ile Phe His Glu Pro His

	165		170		175
Leu Asn Gly Ile Tyr Ala Ser Glu Gly Trp Phe Met Lys Leu Met Glu					
	180		185		190
Ser Asn Thr Gln Phe Val Thr Lys Asn Pro Glu Lys Ala His Leu Phe					
	195		200		205
Tyr Met Pro Tyr Ser Val Lys Gln Leu Gln Lys Ser Ile Phe Val Pro					
	210		215		220
Gly Ser His Asn Ile Lys Pro Leu Ser Ile Phe Leu Arg Asp Tyr Val					
	225		230		235
Asn Met Leu Ser Ile Lys Tyr Pro Phe Trp Asn Arg Thr His Gly Ser					
	240		245		250
Asp His Phe Leu Val Ala Cys His Asp Trp Val Ser Lys Met Phe Leu					
	255		260		265
					270

Cys

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1231

(D) OTHER INFORMATION: / Ceres Seq. ID 1565646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```

aaccaaaaga atcacgacat tgaatcttct ttcatcttct tctccaagac atagtagcat      60
aagamaatga agatatcatc actaggatgg gtcttagtcc ttatcttcat ctctattacc      120
attgtttcga gtgcaccagc acctaaacct cctaaacctc agcctgcacc agcacctaca      180
ctctcotaac ctaagcccac accagcacct acacctccta aaacctaaacc caaacaggaca      240
ctcacacctc ctaaacctaa gcccacacca gcacctacac ctctctaaacc taagcctgca      300
ccagcaccag caccagcacc aacaccagca ccgaaacctc aaacctgcacc taaaccaggca      360
ccagtgaggag aagttgagga cgaaaccogag tttagctacg agacgaaagg aaacaaggggg      420
ccagcgaaat gggggaacact acatgcagag tggaaaaatgt gtggaatagg caaaatgcaa      480
tctctatttg atcttcggga caaaaaatgtg gtatgttagta ataaatttgg attgctctgt      540
agccagtatc tgccttctaa taccaccatt aagaacagag gcatgatatt catgttgaaa      600
ttcaaaggag gcaataaagg tatgtggtgc actatccgtg gtactagata tcaacttcaa      660
caacttcatt ggcactctcc ttccgaacat acaatcaatg gcaaaaggtt tgcgctagag      720
gaacacttgg ttcatgagag taaagatava cGctacgctg ttgtcgcttt ctatatacaat      780
ctcggagactg ctgaccctctg tctcttttgc ttggaaaaaac aattgaagaa gataactgat      840
acacatgcgt ccgagggaaca tgtcggaaatc attgatccca aaaaactcag ttttgaatca      900
aaacattatt atagatatct cggatcaact actgctctcc catgttctcga aaatgttatt      960
tgggtccgttt ccaaagagat tcgcactgtg tcaagtaaac aagtgaagct tctccgtgtg      1020
gctgtacacg atgcttccaga tctaaatgcc aggcgcgttc aagcagtcga taagcgcaag      1080
gtatatattt acaaaccaaa ggtaagtta atgaagaatc actgtaatat aagttcttac      1140
tagtaattctt taattcttta tatatgtaca ttatgaattg tacactaaaa tgatgttttt      1200
agggataaac tgatgactgt gttttgttat t

```

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..358

(D) OTHER INFORMATION: / Ceres Seq. ID 1565647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Lys Ile Ser Ser Leu Gly Trp Val Leu Val Leu Ile Phe Ile Ser

1 5 10 15
Ile Thr Ile Val Ser Ser Ala Pro Ala Pro Lys Pro Pro Lys Pro Lys
20 25 30
Pro Ala Pro Ala Pro Thr Pro Pro Lys Pro Lys Pro Thr Pro Ala Pro
35 40 45
Thr Pro Pro Lys Pro Lys Pro Lys Pro Ala Pro Thr Pro Pro Lys Pro
50 55 60
Lys Pro Thr Pro Ala Pro Thr Pro Pro Lys Pro Lys Pro Ala Pro Ala
65 70 75 80
Pro Ala Pro Ala Pro Thr Pro Ala Pro Lys Pro Lys Pro Ala Pro Lys
85 90 95
Pro Ala Pro Gly Gly Glu Val Glu Asp Glu Thr Glu Phe Ser Tyr Glu
100 105 110
Thr Lys Gly Asn Lys Gly Pro Ala Lys Trp Gly Thr Leu His Ala Glu
115 120 125
Trp Lys Met Cys Gly Ile Gly Lys Met Gln Ser Pro Ile Asp Leu Arg
130 135 140
Asp Lys Asn Val Val Val Ser Asn Lys Phe Gly Leu Leu Arg Ser Gln
145 150 155 160
Tyr Leu Pro Ser Asn Thr Thr Ile Lys Asn Arg Gly His Asp Ile Met
165 170 175
Leu Lys Phe Lys Gly Gly Asn Lys Gly Ile Gly Val Thr Ile Arg Gly
180 185 190
Thr Arg Tyr Gln Leu Gln Gln Leu His Trp His Ser Pro Ser Glu His
195 200 205
Thr Ile Asn Gly Lys Arg Phe Ala Leu Glu Glu His Leu Val His Glu
210 215 220
Ser Lys Asp Xaa Arg Tyr Ala Val Val Ala Phe Leu Tyr Asn Leu Gly
225 230 235 240
Ala Ser Asp Pro Phe Leu Phe Ser Leu Glu Lys Gln Leu Lys Lys Ile
245 250 255
Thr Asp Thr His Ala Ser Glu Glu His Val Gly Ile Ile Asp Pro Lys
260 265 270
Lys Leu Ser Phe Glu Ser Lys His Tyr Tyr Arg Tyr Ser Gly Ser Leu
275 280 285
Thr Ala Pro Pro Cys Ser Glu Asn Val Ile Trp Ser Val Ser Lys Glu
290 295 300
Ile Arg Thr Val Ser Ser Lys Gln Val Lys Leu Leu Arg Val Ala Val
305 310 315 320
His Asp Ala Ser Asp Ser Asn Ala Arg Pro Leu Gln Ala Val Asn Lys
325 330 335
Arg Lys Val Tyr Leu Tyr Lys Pro Lys Val Lys Leu Met Lys Lys Tyr
340 345 350
Cys Asn Ile Ser Ser Tyr
355

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..228

(D) OTHER INFORMATION: / Ceres Seq. ID 1565648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Cys Gly Ile Gly Lys Met Gln Ser Pro Ile Asp Leu Arg Asp Lys
1 5 10 15
Asn Val Val Val Ser Asn Lys Phe Gly Leu Leu Arg Ser Gln Tyr Leu
20 25 30

```

Pro Ser Asn Thr Thr Ile Lys Asn Arg Gly His Asp Ile Met Leu Lys
      35                      40                      45
Phe Lys Gly Gly Asn Lys Gly Ile Gly Val Thr Ile Arg Gly Thr Arg
      50                      55                      60
Tyr Gln Leu Gln Gln Leu His Trp His Ser Pro Ser Glu His Thr Ile
      65                      70                      75                      80
Asn Gly Lys Arg Phe Ala Leu Glu Glu His Leu Val His Glu Ser Lys
      85                      90                      95
Asp Xaa Arg Tyr Ala Val Val Ala Phe Leu Tyr Asn Leu Gly Ala Ser
      100                      105                      110
Asp Pro Phe Leu Phe Ser Leu Glu Lys Gln Leu Lys Lys Ile Thr Asp
      115                      120                      125
Thr His Ala Ser Glu Glu His Val Gly Ile Ile Asp Pro Lys Lys Leu
      130                      135                      140
Ser Phe Glu Ser Lys His Tyr Tyr Arg Tyr Ser Gly Ser Leu Thr Ala
      145                      150                      155                      160
Pro Pro Cys Ser Glu Asn Val Ile Trp Ser Val Ser Lys Glu Ile Arg
      165                      170                      175
Thr Val Ser Ser Lys Gln Val Lys Leu Leu Arg Val Ala Val His Asp
      180                      185                      190
Ala Ser Asp Ser Asn Ala Arg Pro Leu Gln Ala Val Asn Lys Arg Lys
      195                      200                      205
Val Tyr Leu Tyr Lys Pro Lys Val Lys Leu Met Lys Lys Tyr Cys Asn
      210                      215                      220
Ile Ser Ser Tyr
      225

```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..222

(D) OTHER INFORMATION: / Ceres Seq. ID 1565649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```

Met Gln Ser Pro Ile Asp Leu Arg Asp Lys Asn Val Val Ser Asn
1      5      10      15
Lys Phe Gly Leu Leu Arg Ser Gln Tyr Leu Pro Ser Asn Thr Thr Ile
      20      25      30
Lys Asn Arg Gly His Asp Ile Met Leu Lys Phe Lys Gly Gly Asn Lys
      35      40      45
Gly Ile Gly Val Thr Ile Arg Gly Thr Arg Tyr Gln Leu Gln Gln Leu
      50      55      60
His Trp His Ser Pro Ser Glu His Thr Ile Asn Gly Lys Arg Phe Ala
      65      70      75      80
Leu Glu Glu His Leu Val His Glu Ser Lys Asp Xaa Arg Tyr Ala Val
      85      90      95
Val Ala Phe Leu Tyr Asn Leu Gly Ala Ser Asp Pro Phe Leu Phe Ser
      100      105      110
Leu Glu Lys Gln Leu Lys Lys Ile Thr Asp Thr His Ala Ser Glu Glu
      115      120      125
His Val Gly Ile Ile Asp Pro Lys Lys Leu Ser Phe Glu Ser Lys His
      130      135      140
Tyr Tyr Arg Tyr Ser Gly Ser Leu Thr Ala Pro Pro Cys Ser Glu Asn
      145      150      155      160
Val Ile Trp Ser Val Ser Lys Glu Ile Arg Thr Val Ser Ser Lys Gln
      165      170      175
Val Lys Leu Leu Arg Val Ala Val His Asp Ala Ser Asp Ser Asn Ala

```


	180		185		190
Arg Pro Leu Gln Ala Val Asn Lys Arg Lys Val Tyr Leu Tyr Lys Pro					
	195		200		205
Lys Val Lys Leu Met Lys Lys Tyr Cys Asn Ile Ser Ser Tyr					
	210		215		220

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..943
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

aatttctttc	gacgaaactt	catttctcaa	tttcttttga	ttttgatcgc	ttcgaagaac	60
gaatcaattt	aggcctgcc	caaacaaacc	ctagaatacg	acaacgcacg	acgcgaaga	120
agtcgaagaa	gactactact	ataaacgacg	aagatcatta	cttcaactctt	caatcgagct	180
tttaaatattt	cagatcgtag	aagaaaatcg	aacttttgat	tctaaaacgcg	atgagaccga	240
ttcaatcgcc	tccaggagtt	tccgttcccg	tgaaaagccg	tccccctgcg	cgctctgac	300
ttaccttacc	gcttctctaa	cgcgatgttt	ctctcgctgt	acctcttctc	ctccacacta	360
cttccggtgg	ttccggtggc	tctagtggat	ctgcgcgcgt	ttctgggtgt	tcggcgctct	420
caacgaacac	tacacagctc	atagaaagcg	agaactattc	ggatttagtg	agaggtaacc	480
gtatcggaag	cggagSaggt	ggaacggtat	acaaagtgtg	tcaccgtccg	agttctctgc	540
tatatgcact	taagggtgata	tacggttaacc	acgaagagac	tgtgagacgt	cagatctgtg	600
gagagatcga	gattttacga	gatgtgaatc	atccaaacat	ttcacaacgt	ttggaagata	660
ccaccagacg	tgactaaact	acacctcgag	catttcaacg	tgagcgacaa	ccatctctgc	720
ggaaaaatcc	caagtggcgg	tctccttcag	acctttgaac	catctgcctt	cgctcacaac	780
atctgtcttt	gtggaaactcc	ccttaaggct	tgttaatttg	gtttaaactt	ggcggaagaa	840
taaaaaattat	gttgaattatg	ttatgatgat	gtgttcatta	tcaccgcgcaa	accaagttta	900
ttgtttcttt	gttatgaatt	taattttaatg	gcaagaattg	ggt		

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Arg Pro Ile Gln Ser Pro Pro Gly Val Ser Val Pro Val Lys Ser									
	5		10		15				
Arg Pro Arg Arg Arg Pro Asp Leu Thr Leu Pro Leu Pro Gln Arg Asp									
	20		25		30				
Val Ser Leu Ala Val Pro Leu Pro Leu Pro Thr Ser Gly Gly Ser									
	35		40		45				
Gly Gly Ser Ser Gly Ser Ala Pro Ser Ser Gly Gly Ser Ala Ser Ser									
	50		55		60				
Thr Asn Thr Asn Ser Ile Glu Ala Lys Asn Tyr Ser Asp Leu Val									
	65		70		75				
Arg Gly Asn Arg Ile Gly Ser Gly Xaa Gly Gly Thr Val Tyr Lys Val									
	85		90		95				
Ile His Arg Pro Ser Ser Arg Leu Tyr Ala Leu Lys Val Ile Tyr Gly									
	100		105		110				
Asn His Glu Glu Thr Val Arg Arg Gln Ile Cys Arg Glu Ile Glu Ile									
	115		120		125				

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Leu Arg Asp Val Asn His Pro Asn Ile Ser Gln Arg Leu Glu Asp Thr
130 135 140

Thr Ser Thr Asp

145

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1383 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1383

(D) OTHER INFORMATION: / Ceres Seq. ID 1565658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

aattcccatt cgtgtttttt cggattgcga gaatcctacg ttatttcttc acttttcatg      60
atcccaggga catcttagac cccaaatggt Gbktcgtcga tgttctttgg aaactgggttc      120
ctctataact gtccggatca gaaacacagc ctctctcagc aacagatgcc attttgcaga      180
tagttctcga ggcaatggct gctacttcat ctaacgtcct ttgcaatgct agcgagtcag      240
atctttgtct tgaatgattc gctgcatttc tacttaaatt tgtagccatt gcttcgattc      300
tcttagctgg agctgctggg gtaactatac cactcattgg caggaaccgt cgtttccttc      360
aaactgattg taatctcttt gtgactgcta aagcttttgc agctgggtgg attctcgcca      420
cgtgttttgt tcataatgtt gcgggtggca cggaaagctt gaagaaccog tgcctaccgg      480
atttcccttg gtctaagttt cctttcccgg gattcttttg gatgattgct gctttgatca      540
ctctgtttgt ggatttcagt gggactcagt actatgaacg gaagcaagag agggaagcta      600
gtgagtcctg tgaacccgtt ggccgtgaac aatcaccggg tattgttgtt cccatgattg      660
gagaaggaaac gaatgatggg aaagtgtttt gtgaagaaga cagtgttggg attcacattg      720
ttggcatcca tgctcatgct gctcatcata gacatagtc tctctcgtgt catgattcat      780
gtgaaggaca cagtaaaaac gacattggtc atgctcatgc tcatggggac gggcatggac      840
acggacatgg acacgtacac ggggttttgg atgctgttaa tggagctagg catatcgttg      900
tttctcaggt ttggagcttt ggaattgtgt cacattccat aatcatcggt ctatcccttg      960
gagtatctca gtctccttgc acaatccggc ctctaatcgc agcactatcc ttccaccaat      1020
tctttgaagg atttgcgctc ggtggatgca tctcccaagc gcaattcagg aacaaatcag      1080
cgaccataat ggcttgtttt ttccgctcca caaccocgat agggatcggg attggaacga      1140
cagtggtgct gccttttcaat tctcacagtg tcggagcatt ggtcactgaa ggtatcttgg      1200
actcgctctc agccggaaatt cttgtgtaca tggcttttagt ggatctcata gctgctgatt      1260
tcttgagtac aaaaatgagg tgtaacttta ggcttcaaat tgtatcttat gtaatgttgg      1320
tcttaggagc tggactcatg tcttctcttg ccatttgggc ttaattagag tataagattc      1380
cac

```

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 453 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..453

(D) OTHER INFORMATION: / Ceres Seq. ID 1565659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

Phe Pro Phe Val Phe Phe Arg Ile Ala Arg Ile Leu Arg Tyr Phe Phe
1      5      10      15
Thr Phe His Asp Pro Glu Asp Ile Leu Asp Pro Lys Cys Xaa Xaa Val
      20      25      30
Asp Val Leu Trp Lys Leu Val Pro Leu Tyr Leu Phe Gly Ser Glu Thr
      35      40      45
Gln Ser Leu Ser Ala Thr Glu Ser Ile Leu Gln Ile Val Pro Glu Ala
      50      55      60
Met Ala Ala Thr Ser Ser Asn Val Leu Cys Asn Ala Ser Glu Ser Asp

```

65		70		75		80
Leu Cys	Leu Asp	Asp Ser	Ala Ala	Phe Leu	Leu Lys	Phe Val
	85			90		95
Ala Ser	Ile Leu	Leu Ala	Gly Ala	Ala Gly	Val Thr	Ile Pro
	100			105		110
Gly Arg	Asn Arg	Arg Phe	Leu Gln	Thr Asp	Gly Asn	Leu Phe
	115			120		125
Ala Lys	Ala Phe	Ala Ala	Gly Val	Ile Leu	Ala Thr	Cys Phe
	130			135		140
Met Leu	Ala Gly	Gly Thr	Glu Ala	Leu Lys	Asn Pro	Cys Leu
	145			150		155
Phe Pro	Trp Ser	Lys Phe	Pro Phe	Pro Gly	Phe Phe	Ala Met
	165			170		175
Ala Leu	Ile Thr	Leu Phe	Val Asp	Phe Met	Gly Thr	Gln Tyr
	180			185		190
Arg Lys	Gln Glu	Arg Glu	Ala Ser	Glu Ser	Val Glu	Pro Phe
	195			200		205
Glu Gln	Ser Pro	Gly Ile	Val Val	Pro Met	Ile Gly	Glu Gly
	210			215		220
Asp Gly	Lys Val	Phe Gly	Glu Glu	Asp Ser	Gly Gly	Ile His
	225			230		235
Gly Ile	His Ala	His Ala	Ala His	His Arg	His Ser	His Pro
	245			250		255
His Asp	Ser Cys	Glu Gly	His Ser	Lys Ile	Asp Ile	Gly His
	260			265		270
Ala His	Gly His	Gly His	Gly His	Gly His	Gly Val	His His
	275			280		285
Leu Asp	Ala Val	Asn Gly	Ala Arg	His Ile	Val Val	Ser Gln
	290			295		300
Glu Leu	Gly Ile	Val Ser	His Ser	Ile Ile	Ile Gly	Leu Ser
	305			310		315
Val Ser	Gln Ser	Pro Cys	Thr Ile	Arg Pro	Leu Ile	Ala Ala
	325			330		335
Phe His	Gln Phe	Phe Glu	Gly Phe	Ala Leu	Gly Gly	Cys Ile
	340			345		350
Ala Gln	Phe Arg	Asn Lys	Ser Ala	Thr Ile	Met Ala	Cys Phe
	355			360		365
Leu Thr	Thr Pro	Ile Gly	Ile Gly	Ile Gly	Thr Ala	Val Ala
	370			375		380
Phe Asn	Ser His	Ser Val	Gly Ala	Leu Val	Thr Glu	Gly Ile
	385			390		395
Ser Leu	Ser Ala	Gly Ile	Leu Val	Tyr Met	Ala Leu	Val Asp
	405			410		415
Ala Ala	Asp Phe	Leu Ser	Thr Lys	Met Arg	Cys Asn	Phe Arg
	420			425		430
Ile Val	Ser Tyr	Val Met	Leu Phe	Leu Gly	Ala Gly	Leu Met
	435			440		445
Leu Ala	Ile Trp	Ala				
	450					

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..389
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```

Met Ala Ala Thr Ser Ser Asn Val Leu Cys Asn Ala Ser Glu Ser Asp
1      5      10      15
Leu Cys Leu Asp Asp Ser Ala Ala Phe Leu Leu Lys Phe Val Ala Ile
20      25      30
Ala Ser Ile Leu Leu Ala Gly Ala Ala Gly Val Thr Ile Pro Leu Ile
35      40      45
Gly Arg Asn Arg Arg Phe Leu Gln Thr Asp Gly Asn Leu Phe Val Thr
50      55      60
Ala Lys Ala Phe Ala Ala Gly Val Ile Leu Ala Thr Cys Phe Val His
65      70      75      80
Met Leu Ala Gly Gly Thr Glu Ala Leu Lys Asn Pro Cys Leu Pro Asp
85      90      95
Phe Pro Trp Ser Lys Phe Pro Phe Pro Gly Phe Phe Ala Met Ile Ala
100     105     110
Ala Leu Ile Thr Leu Phe Val Asp Phe Met Gly Thr Gln Tyr Tyr Glu
115     120     125
Arg Lys Gln Glu Arg Glu Ala Ser Glu Ser Val Glu Pro Phe Gly Arg
130     135     140
Glu Gln Ser Pro Gly Ile Val Val Pro Met Ile Gly Glu Gly Thr Asn
145     150     155     160
Asp Gly Lys Val Phe Gly Glu Glu Asp Ser Gly Gly Ile His Ile Val
165     170     175
Gly Ile His Ala His Ala Ala His His Arg His Ser His Pro Pro Gly
180     185     190
His Asp Ser Cys Glu Gly His Ser Lys Ile Asp Ile Gly His Ala His
195     200     205
Ala His Gly His Gly His Gly His Gly His Gly His Val His Gly Gly
210     215     220
Leu Asp Ala Val Asn Gly Ala Arg His Ile Val Val Ser Gln Val Leu
225     230     235     240
Glu Leu Gly Ile Val Ser His Ser Ile Ile Ile Gly Leu Ser Leu Gly
245     250     255
Val Ser Gln Ser Pro Cys Thr Ile Arg Pro Leu Ile Ala Ala Leu Ser
260     265     270
Phe His Gln Phe Phe Glu Gly Phe Ala Leu Gly Gly Cys Ile Ser Gln
275     280     285
Ala Gln Phe Arg Asn Lys Ser Ala Thr Ile Met Ala Cys Phe Phe Ala
290     295     300
Leu Thr Thr Pro Ile Gly Ile Gly Ile Gly Thr Ala Val Ala Ser Ser
305     310     315     320
Phe Asn Ser His Ser Val Gly Ala Leu Val Thr Glu Gly Ile Leu Asp
325     330     335
Ser Leu Ser Ala Gly Ile Leu Val Tyr Met Ala Leu Val Asp Leu Ile
340     345     350
Ala Ala Asp Phe Leu Ser Thr Lys Met Arg Cys Asn Phe Arg Leu Gln
355     360     365
Ile Val Ser Tyr Val Met Leu Phe Leu Gly Ala Gly Leu Met Ser Ser
370     375     380
Leu Ala Ile Trp Ala
385

```

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..309
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met	Leu	Ala	Gly	Gly	Thr	Glu	Ala	Leu	Lys	Asn	Pro	Cys	Leu	Pro	Asp
1			5						10				15		
Phe	Pro	Trp	Ser	Lys	Phe	Pro	Phe	Pro	Gly	Phe	Phe	Ala	Met	Ile	Ala
			20					25					30		
Ala	Leu	Ile	Thr	Leu	Phe	Val	Asp	Phe	Met	Gly	Thr	Gln	Tyr	Tyr	Glu
			35				40					45			
Arg	Lys	Gln	Glu	Arg	Glu	Ala	Ser	Glu	Ser	Val	Glu	Pro	Phe	Gly	Arg
			50			55					60				
Glu	Gln	Ser	Pro	Gly	Ile	Val	Val	Pro	Met	Ile	Gly	Glu	Gly	Thr	Asn
65					70				75					80	
Asp	Gly	Lys	Val	Phe	Gly	Glu	Glu	Asp	Ser	Gly	Gly	Ile	His	Ile	Val
				85					90				95		
Gly	Ile	His	Ala	His	Ala	Ala	His	His	Arg	His	Ser	His	Pro	Pro	Gly
			100				105						110		
His	Asp	Ser	Cys	Glu	Gly	His	Ser	Lys	Ile	Asp	Ile	Gly	His	Ala	His
			115				120					125			
Ala	His	Gly	His	Gly	His	Gly	His	Gly	His	Gly	His	Val	His	Gly	Gly
			130				135					140			
Leu	Asp	Ala	Val	Asn	Gly	Ala	Arg	His	Ile	Val	Val	Ser	Gln	Val	Leu
145					150				155						160
Glu	Leu	Gly	Ile	Val	Ser	His	Ser	Ile	Ile	Ile	Gly	Leu	Ser	Leu	Gly
				165					170					175	
Val	Ser	Gln	Ser	Pro	Cys	Thr	Ile	Arg	Pro	Leu	Ile	Ala	Ala	Leu	Ser
				180				185					190		
Phe	His	Gln	Phe	Phe	Glu	Gly	Phe	Ala	Leu	Gly	Gly	Cys	Ile	Ser	Gln
				195			200					205			
Ala	Gln	Phe	Arg	Asn	Lys	Ser	Ala	Thr	Ile	Met	Ala	Cys	Phe	Phe	Ala
						215					220				
Leu	Thr	Thr	Pro	Ile	Gly	Ile	Gly	Ile	Gly	Thr	Ala	Val	Ala	Ser	Ser
225					230				235					240	
Phe	Asn	Ser	His	Ser	Val	Gly	Ala	Leu	Val	Thr	Glu	Gly	Ile	Leu	Asp
				245				250					255		
Ser	Leu	Ser	Ala	Gly	Ile	Leu	Val	Tyr	Met	Ala	Leu	Val	Asp	Leu	Ile
			260				265						270		
Ala	Ala	Asp	Phe	Leu	Ser	Thr	Lys	Met	Arg	Cys	Asn	Phe	Arg	Leu	Gln
			275				280					285			
Ile	Val	Ser	Tyr	Val	Met	Leu	Phe	Leu	Gly	Ala	Gly	Leu	Met	Ser	Ser
			290			295					300				

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1728 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1728
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ctcgacacaca	cttctctctc	tctctctctg	cctcctttcg	gattcaaatc	tcagatctag	60
ctcaaccatg	gcgttgctcg	tcgagaagac	ctcaagtggc	cgtgaataca	aggtcaaaga	120
catgtctcaa	gccgatttgc	gtcgtctcga	actcgagctc	gccgaagttg	agatgcctgg	180
actcatggct	tgtcgtaccg	aattcggacc	ttctcagcca	ttcaaaaggc	ctagaatcac	240
cggatctctt	caacatgaca	tcctaaaccgc	cgtactcatc	gaaaccctaa	ctgctctcgg	300
tgtgaagtc	agatgggtgt	ctcgcacatc	cttctccact	caagaccacg	ccgcgcgacg	360
catcgctcgt	gactccgcgc	ctgttttcgc	ctggaaaggt	gagactcttc	aggagtaact	420
gtggtgtacc	gagcgtgctc	tagattgggg	tccaggtggt	ggtctctgac	tgAttgttga	480

tgatggtggt	gacgctactc	ttttgattca	tgagggtggt	aaagctgagg	agatctttga	540
gaagactggt	caagttcctg	atcctacttc	tactgataac	cctgagtttc	agatcgttgt	600
gtctattatc	aaggaaggtc	ttcaagttga	tcctaagaag	taccacaaga	taaggagag	660
acttgttggt	gtctctgagg	aaactaccac	tggtgttaag	aggctttacc	agatcgacga	720
aaatggaact	cttttgtctc	ctgcccattaa	cggttaacgac	ctctgcacca	agagcaagtt	780
cgacaacttg	tatggttgcc	gtcactcact	ccctgatggt	ctcatgaggg	ccactgtatgt	840
catgatcgct	ggaaggttg	ctgttatctg	tggataggt	gatggttgaa	agggttgtgtg	900
tgctgcatg	aagactgctg	gtgctagagt	catgttgact	gagattgtac	ccatctgtgc	960
ccctcaagct	ttgatggaag	gacttcaggt	tcttaccctt	gaggatgttg	tctcagaagc	1020
tgatatcttt	gtcaccacca	ccggttaacaa	agacatcatc	atggtogacc	acatgaggaa	1080
gatgaagaac	aacgctattg	tgtgcaacat	tggtcacttt	gacaatgaga	ttgacatgct	1140
tggaactgag	acttaccctg	gtgtgaagcg	tatcaccatc	aagccacaga	ctgcacaggtg	1200
gggtgtccca	gagaccaagg	ctggaatcat	tgtcttgctc	gagggtcgct	tgatgaactt	1260
gggtgtgctg	actggtcacc	caagtttctg	gatgtcttgc	tctttcacca	accaggtgat	1320
tgcccagctc	gagctctgga	acgagaaagc	aagcggaaag	tacgagaaga	aggtgtacgt	1380
ctcttccaag	catttggtat	agaaggttgc	attacttcac	ttggcgcaagc	ttggagccag	1440
gcttcaaaag	ctgtcaaaag	accaNaTctg	actacgtcag	catctccaatt	gagggaccat	1500
acaagcctcc	tcactacag	tactgagaga	gagagagagt	cgacaaagcg	gttcaggttc	1560
ggatctactt	gtggttttgt	gttgggttgt	gggtgaagag	tggaacagtt	tgagatattg	1620
gtctcttgat	gaagttgacc	aatatcatgt	attaataaag	gttatgtgct	tttgaaggtt	1680
gtgctgtgtt	tctccatttt	tcatgaaact	taaattagtt	tttggtttt		

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..489

(D) OTHER INFORMATION: / Ceres Seq. ID 1565663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ser	His	Thr	Leu	Leu	Ser	Leu	Ser	Leu	Cys	Leu	Leu	Ser	Asp	Ser	Asn
1			5						10					15	
Leu	Arg	Ser	Ser	Ser	Thr	Met	Ala	Leu	Leu	Val	Glu	Lys	Thr	Ser	Ser
			20					25					30		
Gly	Arg	Glu	Tyr	Lys	Val	Lys	Asp	Met	Ser	Gln	Ala	Asp	Phe	Gly	Arg
			35				40					45			
Leu	Glu	Leu	Glu	Leu	Ala	Glu	Val	Glu	Met	Pro	Gly	Leu	Met	Ala	Cys
			50				55				60				
Arg	Thr	Glu	Phe	Gly	Pro	Ser	Gln	Pro	Phe	Lys	Gly	Ala	Arg	Ile	Thr
65					70				75					80	
Gly	Ser	Leu	His	Met	Thr	Ile	Gln	Thr	Ala	Val	Leu	Ile	Glu	Thr	Leu
			85						90					95	
Thr	Ala	Leu	Gly	Ala	Glu	Val	Arg	Trp	Cys	Ser	Cys	Asn	Ile	Phe	Ser
			100					105					110		
Thr	Gln	Asp	His	Ala	Ala	Ala	Ile	Ala	Arg	Asp	Ser	Ala	Ala	Val	
			115				120					125			
Phe	Ala	Trp	Lys	Gly	Glu	Thr	Leu	Gln	Glu	Tyr	Trp	Trp	Cys	Thr	Glu
			130				135				140				
Arg	Ala	Leu	Asp	Trp	Gly	Pro	Gly	Gly	Pro	Asp	Leu	Ile	Val	Asp	
145					150				155					160	
Asp	Gly	Gly	Asp	Ala	Thr	Leu	Leu	Ile	His	Glu	Gly	Val	Lys	Ala	Glu
			165						170					175	
Glu	Ile	Phe	Glu	Lys	Thr	Gly	Gln	Val	Pro	Asp	Pro	Thr	Ser	Thr	Asp
			180					185					190		
Asn	Pro	Glu	Phe	Gln	Ile	Val	Leu	Ser	Ile	Ile	Lys	Glu	Gly	Leu	Gln
			195				200					205			
Val	Asp	Pro	Lys	Lys	Tyr	His	Lys	Met	Lys	Glu	Arg	Leu	Val	Gly	Val
210							215				220				

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Ser Glu Glu Thr Thr Thr Gly Val Lys Arg Leu Tyr Gln Met Gln Gln
225                                     230                               240
Asn Gly Thr Leu Leu Phe Pro Ala Ile Asn Val Asn Asp Ser Val Thr
                                     245                               255
Lys Ser Lys Phe Asp Asn Leu Tyr Gly Cys Arg His Ser Leu Pro Asp
260                                     265                               270
Gly Leu Met Arg Ala Thr Asp Val Met Ile Ala Gly Lys Val Ala Val
275                                     280                               285
Ile Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Ala Ala Met Lys
290                                     295                               300
Thr Ala Gly Ala Arg Val Ile Val Thr Glu Ile Asp Pro Ile Cys Ala
305                                     310                               315                               320
Leu Gln Ala Leu Met Glu Gly Leu Gln Val Leu Thr Leu Glu Asp Val
325                                     330                               335
Val Ser Glu Ala Asp Ile Phe Val Thr Thr Thr Gly Asn Lys Asp Ile
340                                     345                               350
Ile Met Val Asp His Met Arg Lys Met Lys Asn Asn Ala Ile Val Cys
355                                     360                               365
Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met Leu Gly Leu Glu Thr
370                                     375                               380
Tyr Pro Gly Val Lys Arg Ile Thr Ile Lys Pro Gln Thr Asp Arg Trp
385                                     390                               395                               400
Val Phe Pro Glu Thr Lys Ala Gly Ile Ile Val Leu Ala Glu Gly Arg
405                                     410                               415
Leu Met Asn Leu Gly Cys Ala Thr Gly His Pro Ser Phe Val Met Ser
420                                     425                               430
Cys Ser Phe Thr Asn Gln Val Ile Ala Gln Leu Glu Leu Trp Asn Glu
435                                     440                               445
Lys Ala Ser Gly Lys Tyr Glu Lys Lys Val Tyr Val Leu Pro Lys His
450                                     455                               460
Leu Asp Glu Lys Val Ala Leu Leu His Leu Gly Lys Leu Gly Ala Arg
465                                     470                               475                               480
Leu Thr Lys Leu Ser Lys Asp Xaa Ile
485

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(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..467
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

Met Ala Leu Leu Val Glu Lys Thr Ser Ser Gly Arg Glu Tyr Lys Val
1      5      10      15
Lys Asp Met Ser Gln Ala Asp Phe Gly Arg Leu Glu Leu Glu Leu Ala
20     25
Glu Val Glu Met Pro Gly Leu Met Ala Cys Arg Thr Glu Phe Gly Pro
35     40     45
Ser Gln Pro Phe Lys Gly Ala Arg Ile Thr Gly Ser Leu His Met Thr
50     55     60
Ile Gln Thr Ala Val Leu Ile Glu Thr Leu Thr Ala Leu Gly Ala Glu
65     70     75     80
Val Arg Trp Cys Ser Cys Asn Ile Phe Ser Thr Gln Asp His Ala Ala
85     90     95
Ala Ala Ile Ala Arg Asp Ser Ala Ala Val Phe Ala Trp Lys Gly Glu
100    105    110
Thr Leu Gln Glu Tyr Trp Trp Cys Thr Glu Arg Ala Leu Asp Trp Gly

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115	120	125
Pro Gly Gly Pro Asp Leu Ile Val Asp Asp Gly Gly Asp Ala Thr		
130	135	140
Leu Leu Ile His Glu Gly Val Lys Ala Glu Glu Ile Phe Glu Lys Thr		
145	150	155
Gly Gln Val Pro Asp Pro Thr Ser Thr Asp Asn Pro Glu Phe Gln Ile		
165	170	175
Val Leu Ser Ile Ile Lys Glu Gly Leu Gln Val Asp Pro Lys Lys Tyr		
180	185	190
His Lys Met Lys Glu Arg Leu Val Gly Val Ser Glu Glu Thr Thr Thr		
195	200	205
Gly Val Lys Arg Leu Tyr Gln Met Gln Gln Asn Gly Thr Leu Leu Phe		
210	215	220
Pro Ala Ile Asn Val Asn Asp Ser Val Thr Lys Ser Lys Phe Asp Asn		
225	230	235
Leu Tyr Gly Cys Arg His Ser Leu Pro Asp Gly Leu Met Arg Ala Thr		
245	250	255
Asp Val Met Ile Ala Gly Lys Val Ala Val Ile Cys Gly Tyr Gly Asp		
260	265	270
Val Gly Lys Gly Cys Ala Ala Ala Met Lys Thr Ala Gly Ala Arg Val		
275	280	285
Ile Val Thr Glu Ile Asp Pro Ile Cys Ala Leu Gln Ala Leu Met Glu		
290	295	300
Gly Leu Gln Val Leu Thr Leu Glu Asp Val Val Ser Glu Ala Asp Ile		
305	310	315
Phe Val Thr Thr Thr Gly Asn Lys Asp Ile Ile Met Val Asp His Met		
325	330	335
Arg Lys Met Lys Asn Asn Ala Ile Val Cys Asn Ile Gly His Phe Asp		
340	345	350
Asn Glu Ile Asp Met Leu Gly Leu Glu Thr Tyr Pro Gly Val Lys Arg		
355	360	365
Ile Thr Ile Lys Pro Gln Thr Asp Arg Trp Val Phe Pro Glu Thr Lys		
370	375	380
Ala Gly Ile Ile Val Leu Ala Glu Gly Arg Leu Met Asn Leu Gly Cys		
385	390	395
Ala Thr Gly His Pro Ser Phe Val Met Ser Cys Ser Phe Thr Asn Gln		
405	410	415
Val Ile Ala Gln Leu Glu Leu Trp Asn Glu Lys Ala Ser Gly Lys Tyr		
420	425	430
Glu Lys Lys Val Tyr Val Leu Pro Lys His Leu Asp Glu Lys Val Ala		
435	440	445
Leu Leu His Leu Gly Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Lys		
450	455	460
Asp Xaa Ile		
465		

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..449

(D) OTHER INFORMATION: / Ceres Seq. ID 1565665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met	Ser	Gln	Ala	Asp	Phe	Gly	Arg	Leu	Glu	Leu	Glu	Ala	Glu	Val
1				5				10					15	
Glu	Met	Pro	Gly	Leu	Met	Ala	Cys	Arg	Thr	Glu	Phe	Gly	Pro	Ser
				20				25					30	


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Pro Phe Lys Gly Ala Arg Ile Thr Gly Ser Leu His Met Thr Ile Gln
      35              40              45
Thr Ala Val Leu Ile Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg
      50              55              60
Trp Cys Ser Cys Asn Ile Phe Ser Thr Gln Asp His Ala Ala Ala Ala
      65              70              75              80
Ile Ala Arg Asp Ser Ala Ala Val Phe Ala Trp Lys Gly Glu Thr Leu
      85              90              95
Gln Glu Tyr Trp Trp Cys Thr Glu Arg Ala Leu Asp Trp Gly Pro Gly
      100             105             110
Gly Gly Pro Asp Leu Ile Val Asp Asp Gly Gly Asp Ala Thr Leu Leu
      115             120             125
Ile His Glu Gly Val Lys Ala Glu Glu Ile Phe Glu Lys Thr Gly Gln
      130             135             140
Val Pro Asp Pro Thr Ser Thr Asp Asn Pro Glu Phe Gln Ile Val Leu
      145             150             155             160
Ser Ile Ile Lys Glu Gly Leu Gln Val Asp Pro Lys Lys Tyr His Lys
      165             170             175
Met Lys Glu Arg Leu Val Gly Val Ser Glu Glu Thr Thr Thr Gly Val
      180             185             190
Lys Arg Leu Tyr Gln Met Gln Gln Asn Gly Thr Leu Leu Phe Pro Ala
      195             200             205
Ile Asn Val Asn Asp Ser Val Thr Lys Ser Lys Phe Asp Asn Leu Tyr
      210             215             220
Gly Cys Arg His Ser Leu Pro Asp Gly Leu Met Arg Ala Thr Asp Val
      225             230             235             240
Met Ile Ala Gly Lys Val Ala Val Ile Cys Gly Tyr Gly Asp Val Gly
      245             250             255
Lys Gly Cys Ala Ala Ala Met Lys Thr Ala Gly Ala Arg Val Ile Val
      260             265             270
Thr Glu Ile Asp Pro Ile Cys Ala Leu Gln Ala Leu Met Glu Gly Leu
      275             280             285
Gln Val Leu Thr Leu Glu Asp Val Val Ser Glu Ala Asp Ile Phe Val
      290             295             300
Thr Thr Thr Gly Asn Lys Asp Ile Ile Met Val Asp His Met Arg Lys
      305             310             315             320
Met Lys Asn Asn Ala Ile Val Cys Asn Ile Gly His Phe Asp Asn Glu
      325             330             335
Ile Asp Met Leu Gly Leu Glu Thr Tyr Pro Gly Val Lys Arg Ile Thr
      340             345             350
Ile Lys Pro Gln Thr Asp Arg Trp Val Phe Pro Glu Thr Lys Ala Gly
      355             360             365
Ile Ile Val Leu Ala Glu Gly Arg Leu Met Asn Leu Gly Cys Ala Thr
      370             375             380
Gly His Pro Ser Phe Val Met Ser Cys Ser Phe Thr Asn Gln Val Ile
      385             390             395             400
Ala Gln Leu Glu Leu Trp Asn Glu Lys Ala Ser Gly Lys Tyr Glu Lys
      405             410             415
Lys Val Tyr Val Leu Pro Lys His Leu Asp Glu Lys Val Ala Leu Leu
      420             425             430
His Leu Gly Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Lys Asp Xaa
      435             440             445
Ile

```

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1415

(D) OTHER INFORMATION: / Ceres Seq. ID 1565666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

gtgtttgtgt	atgtgtggaa	aattaatttc	ttctccgcac	gaatcccaaa	agtttgttga	60
aatttgcttc	caagaaatct	gcaattagaa	atttcatttc	gcgcgcacgc	tcttctcttc	120
ctgattctga	tttaattccag	atgtcttcc	gagtttacg	gagattagg	catcttcgcc	180
tcgaactcgaa	ctctgtctcg	cagcttcgc	gagagagtc	tggaacacgc	accgactctc	240
cgtatcgcac	cttttggta	gacggagatt	aactgggaca	aacttgacaa	aaggaggttc	300
tacattaatg	cgtgcgcct	cttcaactgt	gttacagtag	ctctgtatcc	tgtatcgcgt	360
gtgaaaacaa	ggcttcaagt	ttctctctaa	gagattgctg	agagaaggtc	ctttcttgta	420
gttaaaggaa	ttttaaagaa	tgatggtgtt	cctggtctgt	accgaggttt	tggtactgtc	480
attacaggtg	ctgtacactgc	aagaatcata	ttcttaactg	ctcttgagac	cactaagatt	540
ctctgcttta	agttgggttc	acctttggag	ttaaagtgaac	ctacacaagc	cgccattgca	600
aatggaattg	ctggcgcagc	agcatctctt	ttctcacagg	ctgtgtttgt	cccaattgat	660
gttgtagcc	aaaagtgtat	ggtaacaagga	tactcaggtc	atgctacata	tactggtggt	720
atcgatgttg	ccacaaaaat	cattaaagtc	tatggtgtaa	ggggattata	cagaggggtt	780
ggctgtctg	ttatgacct	ttctccttca	agtgccgctt	gggtggctag	ctatggatca	840
agccaaactg	ttatctggag	attcttaggt	tatggtgttg	actcggatgc	aactactgct	900
ctgtagtaag	caaaaattgt	tatggtccag	gctgctggag	gaattattgc	tggtgcaaca	960
gcactctcaa	ttacaacacc	attagacaca	atcaaaacgc	gactgcaggt	catgggacat	1020
caagaaaaat	gaccttcagc	gaaacaagtg	gtgaaaaaac	tgctagcaga	agatggcttg	1080
aaagattct	atagggggtt	gggcccacga	ttcttttagc	tgtcggtctg	gggaacctcg	1140
atgatattga	cttacgaata	cttaaaagct	ctgtgtgcaa	tagaagatta	gaagacttca	1200
ctactgttgc	ttggtttttc	ttcttctact	aactcgagta	gacgcacata	cttggattca	1260
aatctcggtg	attgggaagt	tccatgttga	caattggacc	attctttcaa	ctttggaagt	1320
tgagttcgt	tattgtaact	attctttcaa	cttaatttgc	gtattggagt	gtattcttacc	1380
agcagaagaa	aktGtagct	tacgtttctc	tgctt			

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..323

(D) OTHER INFORMATION: / Ceres Seq. ID 1565667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met	Asp	Thr	Pro	Pro	Thr	Ser	Arg	Ile	Ala	Ser	Phe	Gly	Gln	Thr	Glu	
1			5						10				15			
Ile	Asn	Trp	Asp	Lys	Leu	Asp	Lys	Arg	Arg	Phe	Tyr	Ile	Asn	Gly	Ala	
			20					25					30			
Gly	Leu	Phe	Thr	Gly	Val	Thr	Val	Ala	Leu	Tyr	Pro	Val	Ser	Val	Val	
			35				40				45					
Lys	Thr	Arg	Leu	Gln	Val	Ala	Ser	Lys	Glu	Ile	Ala	Glu	Arg	Ser	Ala	
			50				55				60					
Phe	Ser	Val	Val	Lys	Gly	Ile	Leu	Lys	Asn	Asp	Gly	Val	Pro	Gly	Leu	
65				70			75							80		
Tyr	Arg	Gly	Phe	Gly	Thr	Val	Ile	Thr	Gly	Ala	Val	Pro	Ala	Arg	Ile	
			85				90						95			
Ile	Phe	Leu	Thr	Ala	Leu	Glu	Thr	Thr	Lys	Ile	Ser	Ala	Phe	Lys	Leu	
			100				105						110			
Val	Ala	Pro	Leu	Glu	Leu	Ser	Glu	Pro	Thr	Gln	Ala	Ala	Ile	Ala	Asn	
			115				120					125				
Gly	Ile	Ala	Gly	Met	Thr	Ala	Ser	Leu	Phe	Ser	Gln	Ala	Val	Phe	Val	
			130				135				140					
Pro	Ile	Asp	Val	Val	Ser	Gln	Lys	Leu	Met	Val	Gln	Gly	Tyr	Ser	Gly	
145				150					155						160	

His Ala Thr Tyr Thr Gly Gly Ile Asp Val Ala Thr Lys Ile Ile Lys
165 170 175
Ser Tyr Gly Val Arg Gly Leu Tyr Arg Gly Phe Gly Leu Ser Val Met
180 185 190
Thr Tyr Ser Ser Pro Ser Ser Ala Ala Trp Trp Ala Ser Tyr Gly Ser Ser
195 200 205
Gln Arg Val Ile Trp Arg Phe Leu Gly Tyr Gly Asp Ser Asp Ala
210 215 220
Thr Thr Ala Pro Ser Lys Ser Lys Ile Val Met Val Gln Ala Ala Gly
225 230 235
Gly Ile Ile Ala Gly Ala Thr Ala Ser Ser Ile Thr Thr Pro Leu Asp
245 250 255
Thr Ile Lys Thr Arg Leu Gln Val Met Gly His Gln Glu Asn Arg Pro
260 265 270
Ser Ala Lys Gln Val Val Lys Lys Leu Leu Ala Glu Asp Gly Trp Lys
275 280 285
Gly Phe Tyr Arg Gly Leu Gly Pro Arg Phe Phe Ser Met Ser Ala Trp
290 295 300
Gly Thr Ser Met Ile Leu Thr Tyr Glu Tyr Leu Lys Arg Leu Cys Ala
305 310 315 320
Ile Glu Asp

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..191
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Thr Ala Ser Leu Phe Ser Gln Ala Val Phe Val Pro Ile Asp Val
1 5 10 15
Val Ser Gln Lys Leu Met Val Gln Gly Tyr Ser Gly His Ala Thr Tyr
20 25 30
Thr Gly Gly Ile Asp Val Ala Thr Lys Ile Ile Lys Ser Tyr Gly Val
35 40 45
Arg Gly Leu Tyr Arg Gly Phe Gly Leu Ser Val Met Thr Tyr Ser Pro
50 55 60
Ser Ser Ala Ala Trp Trp Ala Ser Tyr Gly Ser Ser Gln Arg Val Ile
65 70 75 80
Trp Arg Phe Leu Gly Tyr Gly Asp Ser Asp Ala Thr Thr Ala Pro
85 90 95
Ser Lys Ser Lys Ile Val Met Val Gln Ala Ala Gly Gly Ile Ile Ala
100 105 110
Gly Ala Thr Ala Ser Ser Ile Thr Thr Pro Leu Asp Thr Ile Lys Thr
115 120 125
Arg Leu Gln Val Met Gly His Gln Glu Asn Arg Pro Ser Ala Lys Gln
130 135 140
Val Val Lys Lys Leu Leu Ala Glu Asp Gly Trp Lys Gly Phe Tyr Arg
145 150 155 160
Gly Leu Gly Pro Arg Phe Phe Ser Met Ser Ala Trp Gly Thr Ser Met
165 170 175
Ile Leu Thr Tyr Glu Tyr Leu Lys Arg Leu Cys Ala Ile Glu Asp
180 185 190

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..170
(D) OTHER INFORMATION: / Ceres Seq. ID 1565669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met	Val	Gln	Gly	Tyr	Ser	Gly	His	Ala	Thr	Tyr	Thr	Gly	Gly	Ile	Asp	
1				5				10						15		
Val	Ala	Thr	Lys	Ile	Ile	Lys	Ser	Tyr	Gly	Val	Arg	Gly	Leu	Tyr	Arg	
			20				25						30			
Gly	Phe	Gly	Leu	Ser	Val	Met	Thr	Tyr	Ser	Pro	Ser	Ser	Ala	Ala	Trp	
			35				40						45			
Trp	Ala	Ser	Tyr	Gly	Ser	Ser	Gln	Arg	Val	Ile	Trp	Arg	Phe	Leu	Gly	
			50				55				60					
Tyr	Gly	Gly	Asp	Ser	Asp	Ala	Thr	Thr	Ala	Pro	Ser	Lys	Ser	Lys	Ile	
			65			70				75					80	
Val	Met	Val	Gln	Ala	Ala	Gly	Gly	Ile	Ile	Ala	Gly	Ala	Thr	Ala	Ser	
			85						90				95			
Ser	Ile	Thr	Thr	Pro	Leu	Asp	Thr	Ile	Lys	Thr	Arg	Leu	Gln	Val	Met	
			100				105						110			
Gly	His	Gln	Glu	Asn	Arg	Pro	Ser	Ala	Lys	Gln	Val	Val	Lys	Lys	Leu	
			115				120					125				
Leu	Ala	Glu	Asp	Gly	Trp	Lys	Gly	Phe	Tyr	Arg	Gly	Leu	Gly	Pro	Arg	
			130				135					140				
Phe	Phe	Ser	Met	Ser	Ala	Trp	Gly	Thr	Ser	Met	Ile	Leu	Thr	Tyr	Glu	
			145			150				155					160	
Tyr	Leu	Lys	Arg	Leu	Cys	Ala	Ile	Glu	Asp							
			165					170								

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1213
(D) OTHER INFORMATION: / Ceres Seq. ID 1565672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

gaccattttt	acacacagcc	aatcagagcc	ttgttttcac	gtctctttgc	gaggcgataa	60
tatttagatc	tgctcaccat	ttctcccgcca	tcgcgcgacg	aagaagaaa	atgggagaca	120
acaaccctaa	ccgatcagaa	cgagaacgtc	ttctcggaa	cgcgagaa	cttctcgagt	180
cacagatctc	aaacgggttca	aaagagtttg	caatctttag	tcaagagaca	gagccactcc	240
tcgaaggcac	cgatcaaatc	ctcgcgcgtc	tcgatgtctt	actctcatca	gcaccagaga	300
atcgtatcaa	aaaccaacca	aactgggtaca	aaatccttca	gatcgaagat	ctaaatgaat	360
catcaacaga	caacgatcta	atcaagaaac	aataccgtcg	ttctgtctct	cttctccacc	420
cagacaaaaa	ccgttttccct	ttcgcgcgac	aagctttcag	attcgtgtct	gatgcatggg	480
aagttctatc	aacacccttc	aagaaatctc	aattcgatgg	agatttgaat	ctcatctcca	540
ctaaagtata	tctcaacact	cagaaatcga	agaagaaaac	aacaacgaat	gagaagatgt	600
ctacgttttg	gacgcgcgtg	cgtactgtgt	acagttcttc	tgagtatcct	aggggtttat	660
aagagtagtt	tattagatgt	caaaactgtc	aaagaGcgtt	tcacgtctgc	agtattctct	720
agttgcctcc	gttgatacct	ggtaaagatg	agtattattg	ttgctggggt	ttttttccga	780
tggggtttgt	tggtgggttaa	ggaggagaag	cgccattcgc	taattggagta	gatgcagcta	840
agttccctta	ttggtatgct	ccggtttttc	catccggcgg	cgttgacgtc	ctctccaaagt	900
gtaattgggt	tagtttttgt	ggatgggtcag	gtggagcggc	gaagagagat	aatgagcgtg	960
tgaggagtaa	taatgggtgt	ggagttaatt	catagtgaac	accgaagaag	agaggaagag	1020
gaaggccgaa	gaagaatccg	gttttagtgt	ctcttttcaa	actccggtca	tgattgttaa	1080

aattatggag acaaaatttt aaaggcaagt tttttaagg caaggaagtt taggtacagc 1140
gtttgtgtc ttatgtataa cttattatg catttgtgt tattacggt gtgtaattgt 1200
gttatcttga ttt

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..347
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Pro	Phe	Leu	His	Thr	Ala	Asn	Gln	Ser	Leu	Val	Ser	Ser	Ser	Leu	Val
1			5				10			15					
Glu	Ala	Ile	Ile	Phe	Arg	Ser	Ala	His	His	Phe	Ser	Ala	Ile	Ala	Asp
			20				25						30		
Gly	Arg	Arg	Lys	Met	Gly	Asp	Asn	Asn	Pro	Asn	Arg	Ser	Glu	Ala	Glu
			35				40					45			
Arg	Leu	Leu	Gly	Ile	Ala	Gly	Lys	Leu	Leu	Glu	Ser	Arg	Asp	Leu	Asn
			50				55				60				
Gly	Ser	Lys	Glu	Phe	Ala	Ile	Leu	Ala	Gln	Glu	Thr	Glu	Pro	Leu	Leu
			65				70				75			80	
Glu	Gly	Thr	Asp	Gln	Ile	Leu	Ala	Val	Val	Asp	Val	Leu	Leu	Ser	Ser
				85					90					95	
Ala	Pro	Glu	Asn	Arg	Ile	Lys	Asn	Gln	Pro	Asn	Trp	Tyr	Lys	Ile	Leu
			100					105					110		
Gln	Ile	Glu	Asp	Leu	Asn	Glu	Ser	Ser	Thr	Asp	Asn	Asp	Leu	Ile	Lys
			115				120					125			
Lys	Gln	Tyr	Arg	Arg	Leu	Ala	Leu	Leu	His	Pro	Asp	Lys	Asn	Arg	
			130				135				140				
Phe	Pro	Phe	Ala	Asp	Gln	Ala	Phe	Arg	Phe	Val	Leu	Asp	Ala	Trp	Glu
			145				150				155			160	
Val	Leu	Ser	Thr	Pro	Ser	Lys	Lys	Ser	Gln	Phe	Asp	Gly	Asp	Leu	Asn
				165					170					175	
Leu	Ile	Phe	Thr	Lys	Val	Asn	Leu	Asn	Thr	Gln	Lys	Ser	Lys	Lys	Lys
			180					185					190		
Thr	Thr	Thr	Asn	Glu	Lys	Met	Ser	Thr	Phe	Trp	Thr	Ala	Cys	Pro	Tyr
			195					200				205			
Cys	Tyr	Ser	Leu	His	Glu	Tyr	Pro	Arg	Val	Tyr	Gln	Glu	Tyr	Cys	Ile
			210				215					220			
Arg	Cys	Gln	Asn	Cys	Gln	Arg	Ala	Phe	His	Ala	Ala	Ser	Ile	Pro	Gln
			225				230				235			240	
Leu	Pro	Pro	Leu	Ile	Pro	Gly	Lys	Asp	Glu	Tyr	Tyr	Cys	Cys	Trp	Gly
			245						250					255	
Phe	Phe	Pro	Met	Gly	Phe	Val	Gly	Gly	Lys	Gly	Gly	Glu	Ala	Ala	Ile
			260					265					270		
Ala	Asn	Gly	Val	Asp	Ala	Ala	Lys	Phe	Pro	Tyr	Trp	Met	Pro	Pro	Val
			275				280					285			
Phe	Ser	Ser	Gly	Gly	Val	Ala	Ala	Pro	Pro	Ser	Gly	Asn	Gly	Val	Ser
			290				295				300				
Phe	Asp	Gly	Trp	Ser	Gly	Gly	Ala	Ala	Lys	Arg	Asp	Asn	Glu	Ala	Val
			305				310				315			320	
Arg	Ser	Asn	Asn	Gly	Val	Gly	Val	Asn	Ser	Asp	Gly	Thr	Pro	Lys	Lys
			325					330					335		
Arg	Gly	Arg	Gly	Arg	Pro	Lys	Lys	Asn	Pro	Val					
			340				345								

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..311
(D) OTHER INFORMATION: / Ceres Seq. ID 1565674
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:
Met Gly Asp Asn Asn Pro Asn Arg Ser Glu Ala Glu Arg Leu Leu Gly
1 5 10 15
Ile Ala Glu Lys Leu Leu Glu Ser Arg Asp Leu Asn Gly Ser Lys Glu
20 25 30
Phe Ala Ile Leu Ala Gln Glu Thr Glu Pro Leu Leu Glu Gly Thr Asp
35 40 45
Gln Ile Leu Ala Val Val Asp Val Leu Leu Ser Ser Ala Pro Glu Asn
50 55 60
Arg Ile Lys Asn Gln Pro Asn Trp Tyr Lys Ile Leu Gln Ile Glu Asp
65 70 75 80
Leu Asn Glu Ser Ser Thr Asp Asn Asp Leu Ile Lys Lys Gln Tyr Arg
85 90 95
Arg Leu Ala Leu Leu His Pro Asp Lys Asn Arg Phe Pro Phe Ala
100 105 110
Asp Gln Ala Phe Arg Phe Val Leu Asp Ala Trp Glu Val Leu Ser Thr
115 120 125
Pro Ser Lys Lys Ser Gln Phe Asp Gly Asp Leu Asn Leu Ile Phe Thr
130 135 140
Lys Val Asn Leu Asn Thr Gln Lys Ser Lys Lys Lys Thr Thr Thr Asn
145 150 155 160
Glu Lys Met Ser Thr Phe Trp Thr Ala Cys Pro Tyr Cys Tyr Ser Leu
165 170 175
His Glu Tyr Pro Arg Val Tyr Gln Glu Tyr Cys Ile Arg Cys Gln Asn
180 185 190
Cys Gln Arg Ala Phe His Ala Ala Ser Ile Pro Gln Leu Pro Pro Leu
195 200 205
Ile Pro Gly Lys Asp Glu Tyr Tyr Cys Cys Trp Gly Phe Phe Pro Met
210 215 220
Gly Phe Val Gly Gly Lys Gly Gly Glu Ala Ala Ile Ala Asn Gly Val
225 230 235 240
Asp Ala Ala Lys Phe Pro Tyr Trp Met Pro Pro Val Phe Ser Ser Gly
245 250 255
Gly Val Ala Ala Pro Pro Ser Gly Asn Gly Val Ser Phe Asp Gly Trp
260 265 270
Ser Gly Gly Ala Ala Lys Arg Asp Asn Glu Ala Val Arg Ser Asn Asn
275 280 285
Gly Val Gly Val Asn Ser Asp Gly Thr Pro Lys Lys Arg Gly Arg Gly
290 295 300
Arg Pro Lys Lys Asn Pro Val
305 310
(2) INFORMATION FOR SEQ ID NO:55:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 470 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..470
(D) OTHER INFORMATION: / Ceres Seq. ID 1565683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:
cacttagggt tcatagcagc cagagagaga gacaagtgc agggatctac caaacgaagc 60
aacaatgggt aagttcttga agcagaacaa ggccgtgac ctcttcaag gacgttacgc 120
cggaagaaaa gccgtcatca tcaaatctct cgacgacggt aaccgtgac gTccttacgc 180
acactgcctc gtgcgcggac tgaagaagta cccgagcaaa gtcacccgca aagactcagc 240
taagaagaca gctaagaaat ctagggttaa gtgtttcatc aagcttggta attaccagca 300
tctgatgctc actcgtttaca cactcgacgt ggacgtgtct gtaaggacga tcacgggttac 360
cgctgcgtaa ggatttgatg atgacgggtt tctctctac attatgatgc tttgttgtaa 420
ctctctctct gtctttgctg ataataata aattgttact aatataatct

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1565684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Val Lys Phe Leu Lys Gln Asn Lys Ala Val Ile Leu Leu Gln Gly
1 5 10 15
Arg Tyr Ala Gly Lys Lys Ala Val Ile Ile Lys Ser Phe Asp Asp Gly
20 25 30
Asn Arg Asp Arg Pro Tyr Gly His Cys Leu Val Ala Gly Leu Lys Lys
35 40 45
Tyr Pro Ser Lys Val Ile Arg Lys Asp Ser Ala Lys Lys Thr Ala Lys
50 55 60
Lys Ser Arg Val Lys Cys Phe Ile Lys Leu Val Asn Tyr Gln His Leu
65 70 75 80
Met Pro Thr Arg Tyr Thr Leu Asp Val Ala Val Ser Val Arg Thr Ile
85 90 95
Thr Val Thr Val Val Glu Gly Phe Asp Asp Gly Phe Leu Phe Tyr
100 105 110
Ile Met Met Leu Phe Val Asn Ser Leu Ser Val Phe Ala Asp Lys
115 120 125

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1881 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1881

(D) OTHER INFORMATION: / Ceres Seq. ID 1565688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

atagattata gatataacc actgaattaa tattacggct tccaatatag gtgcatttaa 60
aacataacgt tccctctctt gtcttcttat ttttgcctc tgttctttag aactgcatt 120
aacgagagtg agagagagac acacacacac agcgagtga aatgtotcgc gagaagaaga 180
gtcaaaaact cctccaata acggaatgca gagacggaga gtacgattcg atagccgccg 240
attctgacgg gactcStgct tctctcaaga agctccttc ctactcttgc gctcgtcgct 300
gttgaagctg gaagcctttt acgtggacta atcctccttc tctcgtttacc attcgtcatt 360
atctcttacc tatctcgata cgaatctctt ggtatccgc tctcatctt catctcattc 420
gtcgtgtctca aaatccgcga tatcgaactt gtctctcgc cagtctcttc acggtacgag 480
atctaaacata gactgttttc ttgttagtag atcactttag tttttttccg atgaactatg 540
tttaggtttt acgcggcgga ttgtgagaaa gacagttttg aggtgtttga taagtgaag 600
aagaaagtgg tagtgacgcg gaatccgatt gtgatggtg aggcgtttgt gaagSatta 660
tcttgagggt gataaagttt tgggaacaga gattgaagtt aaccctaaaa ccaatagagc 720

cactggattt	gtgaagaagc	ctggtgttct	tgttggtgat	cttaagaggt	tagccatttt	780
aaaagagttt	ggtaacgaat	cacctgatct	cgccctcggt	gatcgaaact	ctgatcatga	840
tttcatgtct	ctctgcaaga	aaggttacat	gttccatgcg	accaagtcag	ccacaacgat	900
tccaaaagaa	cgcttaaaag	accgcatagt	cttccatgat	gggcggttag	cgcaacgtcc	960
aactccggtt	aacgcattta	tcacataacct	atggcttctt	tttggtttca	tcctctccat	1020
cattccggtc	tacttcaacc	tcctcttacc	tgaagatttt	gtccgttacc	ctctcagatg	1080
gctcgggatc	cacttaacca	ttcgtgggtc	tcgtctctca	cctccttccc	ctggaaactct	1140
tggaacaact	tatgtcctta	accacggtac	cgcgcttgat	cccatacgct	ttgctattgc	1200
tcctggacgt	aagatcttgt	gcgtcactta	cagtgtctct	cgtctctccc	ttatgtcttc	1260
tcctattctc	gctgttgccc	tcacccggtg	cogtgcacc	gatgctgcga	acatgagaaa	1320
actctctcag	aaagcgcgat	tggtgatatg	tcccgaaggc	acgacgtgca	gagaagagta	1380
tcctactgag	tttagcgctc	tattcgacga	gctaagcgac	cggtattgtg	cagtacgcgt	1440
gaactgtaaa	caaggaatgt	tcaacgggac	cacagttagg	gggtgaaagt	tttgggacct	1500
ttactctctc	ttcatgaacc	caagaccaag	ctatgaagcc	actttcttgg	actgtttgcc	1560
tgaagaagt	actgtcaacg	gtggtggcaa	gactctcata	gaggtggcta	attacttcca	1620
gaaagtattc	ggcgcggttt	tggtgcttca	atgcaccgaa	cttactcgca	aggataaata	1680
tccttttctt	ggaggttaag	acggcaaggt	agagctctac	aacaacacca	agaagtgaag	1740
atccaaacaa	gggttttttc	ttgttatgtc	gtatacgaat	tttcatgtgt	gtaattgctg	1800
gagctcttgt	catcattatg	gtacgttttt	gttatgtgta	atacgcagta	tatatgtttg	1860
aataaaacta	tggttcgggtg	g				

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..297
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met	Ser	Leu	Cys	Lys	Lys	Gly	Tyr	Met	Val	His	Ala	Thr	Lys	Ser	Ala
1				5					10					15	
Thr	Thr	Ile	Pro	Lys	Glu	Arg	Leu	Lys	Asn	Arg	Ile	Val	Phe	His	Asp
			20						25				30		
Gly	Arg	Leu	Ala	Gln	Arg	Pro	Thr	Pro	Leu	Asn	Ala	Ile	Ile	Thr	Tyr
			35				40					45			
Leu	Trp	Leu	Pro	Phe	Gly	Phe	Ile	Leu	Ser	Ile	Ile	Arg	Val	Tyr	Phe
			50			55					60				
Asn	Leu	Pro	Leu	Pro	Glu	Arg	Phe	Val	Arg	Tyr	Thr	Tyr	Glu	Met	Leu
			65			70				75				80	
Gly	Ile	His	Leu	Thr	Ile	Arg	Gly	His	Arg	Pro	Pro	Pro	Pro	Ser	Pro
			85						90					95	
Gly	Thr	Leu	Gly	Asn	Leu	Tyr	Val	Leu	Asn	His	Arg	Thr	Ala	Leu	Asp
			100					105					110		
Pro	Ile	Ile	Val	Ala	Ile	Ala	Leu	Gly	Arg	Lys	Ile	Cys	Cys	Val	Thr
			115				120					125			
Tyr	Ser	Val	Ser	Arg	Leu	Ser	Leu	Met	Leu	Ser	Pro	Ile	Pro	Ala	Val
			130				135					140			
Ala	Leu	Thr	Arg	Asp	Arg	Ala	Thr	Asp	Ala	Ala	Asn	Met	Arg	Lys	Leu
			145			150				155				160	
Leu	Glu	Lys	Gly	Asp	Leu	Val	Ile	Cys	Pro	Glu	Gly	Thr	Thr	Cys	Arg
			165						170					175	
Glu	Glu	Tyr	Leu	Leu	Arg	Phe	Ser	Ala	Leu	Phe	Ala	Glu	Leu	Ser	Asp
			180					185					190		
Arg	Ile	Val	Pro	Val	Ala	Met	Asn	Cys	Lys	Gln	Gly	Met	Phe	Asn	Gly
			195				200					205			
Thr	Thr	Val	Arg	Gly	Val	Lys	Phe	Thr	Trp	Asp	Pro	Tyr	Phe	Phe	Met
			210			215						220			
Asn	Pro	Arg	Pro	Ser	Tyr	Glu	Ala	Thr	Phe	Leu	Asp	Arg	Leu	Pro	Glu

225					230					235					240
Glu	Met	Thr	Val	Asn	Gly	Gly	Gly	Lys	Thr	Pro	Ile	Glu	Val	Ala	Asn
				245					250					255	
Tyr	Val	Gln	Lys	Val	Ile	Gly	Ala	Val	Leu	Gly	Phe	Glu	Cys	Thr	Glu
			260					265					270		
Leu	Thr	Arg	Lys	Asp	Lys	Tyr	Leu	Leu	Leu	Gly	Gly	Asn	Asp	Gly	Lys
			275				280					285			
Val	Glu	Ser	Ile	Asn	Asn	Thr	Lys	Lys							
	290				295										

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..289

(D) OTHER INFORMATION: / Ceres Seq. ID 1565690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Met	Val	His	Ala	Thr	Lys	Ser	Ala	Thr	Thr	Ile	Pro	Lys	Glu	Arg	Leu
1															
			5						10					15	
Lys	Asn	Arg	Ile	Val	Phe	His	Asp	Gly	Arg	Leu	Ala	Gln	Arg	Pro	Thr
			20					25					30		
Pro	Leu	Asn	Ala	Ile	Ile	Thr	Tyr	Leu	Trp	Leu	Pro	Phe	Gly	Phe	Ile
		35					40					45			
Leu	Ser	Ile	Ile	Arg	Val	Tyr	Phe	Asn	Leu	Pro	Leu	Pro	Glu	Arg	Phe
	50					55					60				
Val	Arg	Tyr	Thr	Tyr	Glu	Met	Leu	Gly	Ile	His	Leu	Thr	Ile	Arg	Gly
	65				70					75				80	
His	Arg	Pro	Pro	Pro	Pro	Ser	Pro	Gly	Thr	Leu	Gly	Asn	Leu	Tyr	Val
			85						90				95		
Leu	Asn	His	Arg	Thr	Ala	Leu	Asp	Pro	Ile	Ile	Val	Ala	Ile	Ala	Leu
		100					105						110		
Gly	Arg	Lys	Ile	Cys	Cys	Val	Thr	Tyr	Ser	Val	Ser	Arg	Leu	Ser	Leu
		115					120					125			
Met	Leu	Ser	Pro	Ile	Pro	Ala	Val	Ala	Leu	Thr	Arg	Asp	Arg	Ala	Thr
	130					135					140				
Asp	Ala	Ala	Asn	Met	Arg	Lys	Leu	Leu	Glu	Lys	Gly	Asp	Leu	Val	Ile
	145				150					155				160	
Cys	Pro	Glu	Gly	Thr	Thr	Cys	Arg	Glu	Glu	Tyr	Leu	Leu	Arg	Phe	Ser
			165						170					175	
Ala	Leu	Phe	Ala	Glu	Leu	Ser	Asp	Arg	Ile	Val	Pro	Val	Ala	Met	Asn
		180						185					190		
Cys	Lys	Gln	Gly	Met	Phe	Asn	Gly	Thr	Thr	Val	Arg	Gly	Val	Lys	Phe
		195					200					205			
Trp	Asp	Pro	Tyr	Phe	Phe	Phe	Met	Asn	Pro	Arg	Pro	Ser	Tyr	Glu	Ala
	210					215					220				
Thr	Phe	Leu	Asp	Arg	Leu	Pro	Glu	Glu	Met	Thr	Val	Asn	Gly	Gly	Gly
	225				230				235					240	
Lys	Thr	Pro	Ile	Glu	Val	Ala	Asn	Tyr	Val	Gln	Lys	Val	Ile	Gly	Ala
			245						250					255	
Val	Leu	Gly	Phe	Glu	Cys	Thr	Glu	Leu	Thr	Arg	Lys	Asp	Lys	Tyr	Leu
		260					265					270			
Leu	Leu	Gly	Gly	Asn	Asp	Gly	Lys	Val	Glu	Ser	Ile	Asn	Asn	Thr	Lys
		275				280						285			

Lys

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..219
(D) OTHER INFORMATION: / Ceres Seq. ID 1565691
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:
Met Leu Gly Ile His Leu Thr Ile Arg Gly His Arg Pro Pro Pro Pro
1 5 10 15
Ser Pro Gly Thr Leu Gly Asn Leu Tyr Val Leu Asn His Arg Thr Ala
20 25 30
Leu Asp Pro Ile Ile Val Ala Ile Ala Leu Gly Arg Lys Ile Cys Cys
35 40 45
Val Thr Tyr Ser Val Ser Arg Leu Ser Leu Met Leu Ser Pro Ile Pro
50 55 60
Ala Val Ala Leu Thr Arg Asp Arg Ala Thr Asp Ala Ala Asn Met Arg
65 70 75 80
Lys Leu Leu Glu Lys Gly Asp Leu Val Ile Cys Pro Glu Gly Thr Thr
85 90 95
Cys Arg Glu Glu Tyr Leu Leu Arg Phe Ser Ala Leu Phe Ala Glu Leu
100 105 110
Ser Asp Arg Ile Val Pro Val Ala Met Asn Cys Lys Gln Gly Met Phe
115 120 125
Asn Gly Thr Thr Val Arg Gly Val Lys Phe Trp Asp Pro Tyr Phe Phe
130 135 140
Phe Met Asn Pro Arg Pro Ser Tyr Glu Ala Thr Phe Leu Asp Arg Leu
145 150 155 160
Pro Glu Glu Met Thr Val Asn Gly Gly Gly Lys Thr Pro Ile Glu Val
165 170 175
Ala Asn Tyr Val Gln Lys Val Ile Gly Ala Val Leu Gly Phe Glu Cys
180 185 190
Thr Glu Leu Thr Arg Lys Asp Lys Tyr Leu Leu Leu Gly Gly Asn Asp
195 200 205
Gly Lys Val Glu Ser Ile Asn Asn Thr Lys Lys
210 215

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1065 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1065
(D) OTHER INFORMATION: / Ceres Seq. ID 1565692
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

aaagaagaaa	ttggtatccgc	cgttgatcgt	cggatctg	aacgaggaag	atgagctctc	60
tatcttaaa	gggttagttg	attacagagc	taagacagga	ttcaatccca	aaatgattg	120
ggatgcgttt	tgtagtttcc	tcggaagttc	tatcgttgag	agattotcca	aggatcaggt	180
tttgagtaaa	atcaggaagt	tgaaaaggag	gtttcatgtt	cactcggaga	aaatcaatca	240
agggaatgat	cccaaaat	ctaggtctag	tgattctgaa	gcctttgggt	tttcttcgat	300
gatttgggga	caaggtgatg	atgatgggat	ggataaggag	cacgaggtaa	acggaatagg	360
tgacgcggaa	aaccggaacta	acgagagcgg	ggaggagatg	ttgaaggagc	acgagggaga	420
agtggtcaat	actgaacttt	taaatgagaa	tGgggcagcc	aaaacaacag	agaatgggac	480
tagtagtgga	aaagagagac	atgatgagga	caatgatgat	gatgatgagt	tatgcgcggt	540
gcaggatgca	tttgaggcgg	tgatgtcgca	aggtttaagt	ggttatcaaa	agaagttgca	600
gcttgagaag	ctgatgaacc	ttggaatagg	taaaagaaga	gagttgagtg	atgaatggaa	660

agcggttatgt gttgaggaaa caagattcaa tatcaagaag cttagatttt cgcgaagct 720
tgcagaggca gctaatgata gttagatgaa accaatatgc ccttgtagca ttgggtgtg 780
tttaggttct tagtaagtca taagctctag tctgttcagt gtatttatct ttagatcctg 840
tctttcttct acctgggcaa gtgtttgtaa gatattccac ttttactcaa agtatccaca 900
agagccaatg tagtagagtg gcttgtgcaa gagtctagag tctagggtta ataagtgtgt 960
ttaaggcatg cttgtgtgtg tgcctaagag tgtagtgaag tagtataag aagagtgtgt 1020
gtgtgtcttg taattattat caagataatta acaatgtaga agatc

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..247

(D) OTHER INFORMATION: / Ceres Seq. ID 1565693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Lys	Lys	Lys	Leu	Asp	Pro	Pro	Leu	Ile	Val	Arg	Ile	Trp	Asn	Glu	Glu
1			5						10				15		
Asp	Glu	Leu	Ser	Ile	Leu	Lys	Gly	Leu	Val	Asp	Tyr	Arg	Ala	Lys	Thr
			20					25					30		
Gly	Phe	Asn	Pro	Lys	Ile	Asp	Trp	Asp	Ala	Phe	Cys	Ser	Phe	Leu	Gly
			35					40				45			
Ser	Ser	Ile	Val	Glu	Arg	Phe	Ser	Lys	Asp	Gln	Val	Leu	Ser	Lys	Ile
			50				55				60				
Arg	Lys	Leu	Lys	Arg	Arg	Phe	His	Val	His	Ser	Glu	Lys	Ile	Asn	Gln
			65				70			75			80		
Gly	Asn	Asp	Pro	Lys	Phe	Thr	Arg	Ser	Ser	Asp	Ser	Glu	Ala	Phe	Gly
			85					90				95			
Phe	Ser	Ser	Met	Ile	Trp	Gly	Gln	Gly	Asp	Asp	Gly	Met	Asp	Lys	
			100					105				110			
Glu	His	Glu	Val	Asn	Gly	Asn	Gly	Ala	Ala	Glu	Asn	Arg	Thr	Asn	Glu
			115				120					125			
Ser	Gly	Glu	Glu	Met	Leu	Lys	Glu	His	Glu	Glu	Glu	Val	Ala	Asn	Thr
			130				135					140			
Glu	Leu	Leu	Asn	Glu	Asn	Gly	Ala	Ala	Lys	Thr	Thr	Glu	Asn	Gly	Thr
			145				150					155			160
Ser	Ser	Gly	Lys	Glu	Arg	His	Asp	Glu	Asp	Asn	Asp	Asp	Asp	Asp	Glu
			165					170				175			
Leu	Cys	Ala	Val	Gln	Asp	Ala	Phe	Glu	Ala	Val	Met	Ser	Gln	Gly	Leu
			180					185				190			
Ser	Gly	Tyr	Gln	Lys	Lys	Leu	Gln	Leu	Glu	Lys	Leu	Met	Asn	Leu	Gly
			195					200				205			
Asn	Gly	Lys	Arg	Arg	Glu	Leu	Ser	Asp	Glu	Trp	Lys	Ala	Leu	Cys	Val
			210				215					220			
Glu	Glu	Thr	Arg	Phe	Asn	Ile	Lys	Lys	Leu	Arg	Phe	Ser	Ala	Lys	Leu
			225				230			235					240
Ala	Glu	Ala	Ala	Asn	Asp	Ser									
							245								

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1565694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Ile Trp Gly Gln Gly Asp Asp Asp Gly Met Asp Lys Glu His Glu
1 5 10 15
Val Asn Gly Asn Gly Ala Ala Glu Asn Arg Thr Asn Glu Ser Gly Glu
20 25 30
Glu Met Leu Lys Glu His Glu Glu Val Ala Asn Thr Glu Leu Leu
35 40 45
Asn Glu Asn Gly Ala Ala Lys Thr Thr Glu Asn Gly Thr Ser Ser Gly
50 55 60
Lys Glu Arg His Asp Glu Asp Asn Asp Asp Asp Glu Leu Cys Ala
65 70 75 80
Val Gln Asp Ala Phe Glu Ala Val Met Ser Gln Gly Leu Ser Gly Tyr
85 90 95
Gln Lys Lys Leu Gln Leu Glu Lys Leu Met Asn Leu Gly Asn Gly Lys
100 105 110
Arg Arg Glu Leu Ser Asp Glu Trp Lys Ala Leu Cys Val Glu Glu Thr
115 120 125
Arg Phe Asn Ile Lys Lys Leu Arg Phe Ser Ala Lys Leu Ala Glu Ala
130 135 140

Ala Asn Asp Ser

145

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1565695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Asp Lys Glu His Glu Val Asn Gly Asn Gly Ala Ala Glu Asn Arg
1 5 10 15
Thr Asn Glu Ser Gly Glu Glu Met Leu Lys Glu His Glu Glu Glu Val
20 25 30
Ala Asn Thr Glu Leu Leu Asn Glu Asn Gly Ala Ala Lys Thr Thr Glu
35 40 45
Asn Gly Thr Ser Ser Gly Lys Glu Arg His Asp Glu Asp Asn Asp Asp
50 55 60
Asp Asp Glu Leu Cys Ala Val Gln Asp Ala Phe Glu Ala Val Met Ser
65 70 75 80
Gln Gly Leu Ser Gly Tyr Gln Lys Lys Leu Gln Leu Glu Lys Leu Met
85 90 95
Asn Leu Gly Asn Gly Lys Arg Arg Glu Leu Ser Asp Glu Trp Lys Ala
100 105 110
Leu Cys Val Glu Glu Thr Arg Phe Asn Ile Lys Lys Leu Arg Phe Ser
115 120 125
Ala Lys Leu Ala Glu Ala Ala Asn Asp Ser
130 135

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1498 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1498

(D) OTHER INFORMATION: / Ceres Seq. ID 1565723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

aaattcaaatg	gaccttttttc	ttcaaatctc	cagctttctg	catagatcca	tgaccatgag	60
agtctgtttc	ttagaacgaa	aattgaaaaa	atatctttac	attattcggg	agtcataagg	120
atactcgttg	tgggtgacgt	gacctcgatg	tgctcaagctg	tgggtagcaa	tgtgtaccct	180
ttgattctcg	ttccaggaaa	cggaggtaac	cagctagagg	tacggctgga	cagagaatac	240
aaagcaagta	gtgtctgggt	tagcagctgg	ttatatccga	ttcataagaa	gagtggtgga	300
tgtgttaggc	tatggttcga	tgacagcagt	ttattgtctc	ccttcaccag	gtgcttcagc	360
gatcgatgta	tgttgtaact	tgacctgat	ttggatgatt	accaaagtgc	tcttggtgtc	420
caaaaccggc	ttctctattt	cggttcgacc	aaatcacttc	tatacctgca	ccctcgcttc	480
cgagatgcc	cattctacat	ggaacatttg	gtgaaagctc	tagagaaaaa	atgttggtat	540
gttaacgacc	aaaccatcct	aggagctcca	tatgatttca	ggtagcgctc	ggctgcttcg	600
ggccaccogt	cccggtgtgc	ctcacagttc	ctacaagacc	tcaacaattt	ggtggaaaaa	660
actagcagcg	agaacgaagg	aaagccagtg	atactcctct	cccatacgct	aggaggactt	720
ttcgctctcc	atttctctaa	cgtaccaccc	ccttcattgg	gcgcgaagta	catcaaacac	780
tttgtgtcac	tcgctgcgcc	atggggtggg	acgatctctc	agatgaagac	atttgcctct	840
ggcaacacac	tcggtgtccc	tttagttaac	cctttgcttg	tcagacggca	tcagaggacc	900
tcogagagta	accaatggct	acttccatct	accaaagtgt	ttcacgacag	aactaaaccg	960
cttgtcgtaa	ctccccaggt	taactacaca	gcttacgaga	tggatcggtt	ttttgcagac	1020
attggattct	cacaaggagt	tgtgccttac	aagacaagag	tgttgccctt	aacagaggag	1080
ctgatgactc	cgggagtgcc	agtcacttgc	atatattgga	gaggagtgtg	tacaccggag	1140
gttttgatgt	gttgaaagg	aggattcgat	aagcaaccag	agattaagta	tggagatgga	1200
gatgggacgt	ttaaatttgc	gagcttagca	gctttgaaag	tcgatagctt	gaacaccgta	1260
gagattgatt	gagtttgcga	tacatctata	cttaaaagac	agatcgcat	taaaagagatt	1320
atgaagcaga	tttcaattat	taattatgaa	ttagccaatg	ttaatggcgt	caatgaatga	1380
gagcagtcga	ctatttcacc	atttttagtt	gtacatttta	agataaagag	ataatttaca	1440
tatatctcac	ggtttgcttt	aggcactcct	tatagaagaa	aaaaagaatt	aaaaaccg	

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 432 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..432

(D) OTHER INFORMATION: / Ceres Seq. ID 1565724

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met	Lys	Lys	Ile	Ser	Ser	His	Tyr	Ser	Val	Val	Ile	Ile	Leu	Val
1			5					10					15	
Val	Val	Thr	Met	Thr	Ser	Met	Cys	Gln	Ala	Val	Gly	Ser	Asn	Val
			20					25					30	
Pro	Leu	Ile	Leu	Val	Pro	Gly	Asn	Gly	Gly	Asn	Gln	Leu	Glu	Val
			35					40					45	
Leu	Asp	Arg	Glu	Tyr	Lys	Pro	Ser	Ser	Val	Trp	Cys	Ser	Ser	Trp
			50					55			60			
Tyr	Pro	Ile	His	Lys	Lys	Ser	Gly	Gly	Trp	Phe	Arg	Leu	Trp	Phe
			65					70			75			80
Ala	Ala	Val	Leu	Leu	Ser	Pro	Phe	Thr	Arg	Cys	Phe	Ser	Asp	Arg
			85					90					95	
Met	Leu	Tyr	Tyr	Asp	Pro	Asp	Leu	Asp	Asp	Tyr	Gln	Asn	Ala	Pro
			100					105					110	
Val	Gln	Thr	Arg	Val	Pro	His	Phe	Gly	Ser	Thr	Lys	Ser	Leu	Leu
			115					120					125	
Leu	Asp	Pro	Arg	Leu	Arg	Asp	Ala	Thr	Ser	Tyr	Met	Glu	His	Leu
			130					135			140			
Lys	Ala	Leu	Glu	Lys	Lys	Cys	Gly	Tyr	Val	Asn	Asp	Gln	Thr	Ile
			145					150			155			160
Gly	Ala	Pro	Tyr	Asp	Phe	Arg	Tyr	Gly	Leu	Ala	Ala	Ser	Gly	His

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(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

FEATURE:

(B) LOCATION: 1..413

SEQUENCE DESCRIPTION: SEQ ID NO:67:

Thr Ser Met Cys Gln Ala Val Gly Ser Asn

Met	Thr	Ser	Met	Cys	Gln	Ala	Val	Gly	Ser	Asn	Val	Tyr	Pro	Leu	Ile
1				5					10					15	
Leu	Val	Pro	Gly	Asn	Gly	Gly	Asn	Gln	Leu	Glu	Val	Arg	Leu	Asp	Arg
			20					25					30		
Glu	Tyr	Lys	Pro	Ser	Ser	Val	Trp	Cys	Ser	Ser	Trp	Leu	Tyr	Pro	Ile
		35					40					45			
His	Lys	Lys	Ser	Gly	Gly	Trp	Phe	Arg	Leu	Trp	Phe	Asp	Ala	Ala	Val
	50					55					60				
Leu	Leu	Ser	Pro	Phe	Thr	Arg	Cys	Phe	Ser	Asp	Arg	Met	Met	Leu	Tyr
					70					75				80	
Tyr	Asp	Pro	Asp	Leu	Asp	Asp	Tyr	Gln	Asn	Ala	Pro	Gly	Val	Gln	Thr
				85					90					95	
Arg	Val	Pro	His	Phe	Gly	Ser	Thr	Lys	Ser	Leu	Leu	Tyr	Leu	Asp	Pro
			100					105					110		

Arg Leu Arg Asp Ala Thr Ser Tyr Met Glu His Leu Val Lys Ala Leu
115 120 125
Glu Lys Lys Cys Gly Tyr Val Asn Asp Gln Thr Ile Leu Gly Ala Pro
130 135 140
Tyr Asp Phe Arg Tyr Gly Leu Ala Ala Ser Gly His Pro Ser Arg Val
145 150 155 160
Ala Ser Gln Phe Leu Gln Asp Leu Lys Gln Leu Val Glu Lys Thr Ser
165 170 175
Ser Glu Asn Glu Gly Lys Pro Val Ile Leu Leu Ser His Ser Leu Gly
180 185 190
Gly Leu Phe Val Leu His Phe Leu Asn Arg Thr Thr Pro Ser Trp Arg
195 200 205
Arg Lys Tyr Ile Lys His Phe Val Ala Leu Ala Ala Pro Trp Gly Gly
210 215 220
Thr Ile Ser Gln Met Lys Thr Phe Ala Ser Gly Asn Thr Leu Gly Val
225 230 235 240
Pro Leu Val Asn Pro Leu Leu Val Arg Arg His Gln Arg Thr Ser Glu
245 250 255
Ser Asn Gln Trp Leu Leu Pro Ser Thr Lys Val Phe His Asp Arg Thr
260 265 270
Lys Pro Leu Val Val Thr Pro Gln Val Asn Tyr Thr Ala Tyr Glu Met
275 280 285
Asp Arg Phe Phe Ala Asp Ile Gly Phe Ser Gln Gly Val Val Pro Tyr
290 295 300
Lys Thr Arg Val Leu Pro Leu Thr Glu Glu Leu Met Thr Pro Gly Val
305 310 315 320
Pro Val Thr Cys Ile Tyr Gly Arg Gly Val Asp Thr Pro Glu Val Leu
325 330 335
Met Tyr Gly Lys Gly Gly Phe Asp Lys Gln Pro Glu Ile Lys Tyr Gly
340 345 350
Asp Gly Asp Gly Thr Val Asn Leu Ala Ser Leu Ala Ala Leu Lys Val
355 360 365
Asp Ser Leu Asn Thr Val Glu Ile Asp Gly Val Ser His Thr Ser Ile
370 375 380
Leu Lys Asp Glu Ile Ala Leu Lys Glu Ile Met Lys Gln Ile Ser Ile
385 390 395 400
Ile Asn Tyr Glu Leu Ala Asn Val Asn Ala Val Asn Glu
405 410

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 410 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..410

(D) OTHER INFORMATION: / Ceres Seq. ID 1565726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met Cys Gln Ala Val Gly Ser Asn Val Tyr Pro Leu Ile Leu Val Pro
1 5 10 15
Gly Asn Gly Gly Asn Gln Leu Glu Val Arg Leu Asp Arg Glu Tyr Lys
20 25 30
Pro Ser Ser Val Trp Cys Ser Ser Trp Leu Tyr Pro Ile His Lys Lys
35 40 45
Ser Gly Gly Trp Phe Arg Leu Trp Phe Asp Ala Ala Val Leu Leu Ser
50 55 60
Pro Phe Thr Arg Cys Phe Ser Asp Arg Met Met Leu Tyr Tyr Asp Pro
65 70 75 80
Asp Leu Asp Asp Tyr Gln Asn Ala Pro Gly Val Gln Thr Arg Val Pro

	85		90		95
His Phe Gly Ser Thr Lys Ser Leu Leu Tyr Leu Asp Pro Arg Leu Arg	100	105	110		
Asp Ala Thr Ser Tyr Met Glu His Leu Val Lys Ala Leu Glu Lys Lys	115	120	125		
Cys Gly Tyr Val Asn Asp Gln Thr Ile Leu Gly Ala Pro Tyr Asp Phe	130	135	140		
Arg Tyr Gly Leu Ala Ala Ser Gly His Pro Ser Arg Val Ala Ser Gln	145	150	155	160	
Phe Leu Gln Asp Leu Lys Gln Leu Val Glu Lys Thr Ser Ser Glu Asn	165	170	175		
Glu Gly Lys Pro Val Ile Leu Leu Ser His Ser Leu Gly Gly Leu Phe	180	185	190		
Val Leu His Phe Leu Asn Arg Thr Thr Pro Ser Trp Arg Arg Lys Tyr	195	200	205		
Ile Lys His Phe Val Ala Leu Ala Ala Pro Trp Gly Gly Thr Ile Ser	210	215	220		
Gln Met Lys Thr Phe Ala Ser Gly Asn Thr Leu Gly Val Pro Leu Val	225	230	235	240	
Asn Pro Leu Leu Val Arg Arg His Gln Arg Thr Ser Glu Ser Asn Gln	245	250	255		
Trp Leu Leu Pro Ser Thr Lys Val Phe His Asp Arg Thr Lys Pro Leu	260	265	270		
Val Val Thr Pro Gln Val Asn Tyr Thr Ala Tyr Glu Met Asp Arg Phe	275	280	285		
Phe Ala Asp Ile Gly Phe Ser Gln Gly Val Val Pro Tyr Lys Thr Arg	290	295	300		
Val Leu Pro Leu Thr Glu Glu Leu Met Thr Pro Gly Val Pro Val Thr	305	310	315	320	
Cys Ile Tyr Gly Arg Gly Val Asp Thr Pro Glu Val Leu Met Tyr Gly	325	330	335		
Lys Gly Gly Phe Asp Lys Gln Pro Glu Ile Lys Tyr Gly Asp Gly Asp	340	345	350		
Gly Thr Val Asn Leu Ala Ser Leu Ala Ala Leu Lys Val Asp Ser Leu	355	360	365		
Asn Thr Val Glu Ile Asp Gly Val Ser His Thr Ser Ile Leu Lys Asp	370	375	380		
Glu Ile Ala Leu Lys Glu Ile Met Lys Gln Ile Ser Ile Ile Asn Tyr	385	390	395	400	
Glu Leu Ala Asn Val Asn Ala Val Asn Glu	405	410			

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1280
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

acaatttcagg	gaaaatcttc	aaagtgtttg	cagagaaatc	taaatctcatc	aacagttttt	60
tacaaaagaa	atggaagcag	gagaagcaaa	acagagtgtg	ctcttctcta	ctccctataa	120
gatgggaaga	tccaatcttt	cccatagggt	tggtcttagca	ccattgacga	gacagagatc	180
gtacggaaac	gttctctcagc	ctcacgctgc	catatattac	tctcagagaa	cgactccagg	240
aggtttttct	atcaactgaag	ccactggagt	tccagatata	gctcaaggat	atcaagatac	300
tctcgggata	tggaactaaag	agcatgtgga	ggcatgggaag	ccaatcgttg	atgctgtaca	360
tgccaaaggt	ggtatcttct	tctgtcagat	ctggcatgtt	ggccgcgttt	ctaatagcgg	420
gttttcagcca	aatggaaaaa	ctcctatctc	ttgttcggat	aagccattga	tgccctcaaat	480

tgcgtctaat	ggcatcgatg	aagctctctt	tacccctcca	agacggcttg	gtatcgaaaga	540
aatccccggc	attgtcaatg	attttaggct	tgcgtcaaga	aatgctatgg	aagctgggtt	600
tgatggagtt	gagattcata	gagctaattg	ctatctgatt	gaccagttca	tgaaggatac	660
gggtgaatgat	agaactgatg	aatacggtgg	atcattgcaa	aaccgttgca	aatttctctt	720
agaaatagtc	gatgcagttg	ctaaggagat	cggaccagac	cgtgttgtaa	tcaggctctc	780
tccattttgt	gactacatgg	aatctggaga	cactaatcca	ggagcattag	ggctttatat	840
ggcggaatct	ttgaacaaa	acggaatcct	ctactgtcat	gtgattgaag	cgagaatgaa	900
aacaatggga	gaagtacatg	cttgtcctca	cacactaatg	ccgatgagga	aagcgtttaa	960
ggggactttt	atctccgcag	gaggtttcac	gagggaaagt	gggaatgagg	ctgtgtcaaa	1020
gggaagaact	gatttgggtg	cttatggctg	atggtttcta	gccaacccgg	acctgcaaaa	1080
gaggtttcaa	gtggatgcac	cgctgaataa	gtacgataga	ccaacgtttt	acacttctga	1140
tccagtcgtc	gggttacacc	attacccttt	cctcgatata	acagctttaa	attgttatca	1200
ataatgtaat	gtagtggtgt	tcctttatat	aagatgtaat	aagtttctgg	cttttcat	1260
atacttttta	agtttaagcc					

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..372
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met	Glu	Asn	Gly	Glu	Ala	Lys	Gln	Ser	Val	Pro	Leu	Leu	Thr	Pro	Tyr
1			5					10					15		
Lys	Met	Gly	Arg	Phe	Asn	Leu	Ser	His	Arg	Val	Val	Leu	Ala	Pro	Leu
			20					25					30		
Thr	Arg	Gln	Arg	Ser	Tyr	Gly	Asn	Val	Pro	Gln	Pro	His	Ala	Ala	Ile
			35				40					45			
Tyr	Tyr	Ser	Gln	Arg	Thr	Thr	Pro	Gly	Gly	Phe	Leu	Ile	Thr	Glu	Ala
			50				55				60				
Thr	Gly	Val	Ser	Asp	Thr	Ala	Gln	Gly	Tyr	Gln	Asp	Thr	Pro	Gly	Ile
			65				70			75				80	
Trp	Thr	Lys	Glu	His	Val	Glu	Ala	Trp	Lys	Pro	Ile	Val	Asp	Ala	Val
			85						90				95		
His	Ala	Lys	Gly	Gly	Ile	Phe	Phe	Cys	Gln	Ile	Trp	His	Val	Gly	Arg
			100					105					110		
Val	Ser	Asn	Ser	Gly	Phe	Gln	Pro	Asn	Gly	Lys	Ala	Pro	Ile	Ser	Cys
			115					120				125			
Ser	Asp	Lys	Pro	Leu	Met	Pro	Gln	Ile	Arg	Ser	Asn	Gly	Ile	Asp	Glu
			130				135				140				
Ala	Leu	Phe	Thr	Pro	Pro	Arg	Arg	Leu	Gly	Ile	Glu	Glu	Ile	Pro	Gly
			145				150				155			160	
Ile	Val	Asn	Asp	Phe	Arg	Leu	Ala	Ala	Arg	Asn	Ala	Met	Glu	Ala	Gly
			165						170				175		
Phe	Asp	Gly	Val	Glu	Ile	His	Arg	Ala	Asn	Gly	Tyr	Leu	Ile	Asp	Gln
			180					185					190		
Phe	Met	Lys	Asp	Thr	Val	Asn	Asp	Arg	Thr	Asp	Glu	Tyr	Gly	Gly	Ser
			195					200				205			
Leu	Gln	Asn	Arg	Cys	Lys	Phe	Pro	Leu	Glu	Ile	Val	Asp	Ala	Val	Ala
			210				215				220				
Lys	Glu	Ile	Gly	Pro	Asp	Arg	Val	Gly	Ile	Arg	Leu	Ser	Pro	Phe	Ala
			225					230			235				
Asp	Tyr	Met	Glu	Ser	Gly	Asp	Thr	Asn	Pro	Gly	Ala	Leu	Gly	Leu	Tyr
			245					250					255		
Met	Ala	Glu	Ser	Leu	Asn	Lys	Tyr	Gly	Ile	Leu	Tyr	Cys	His	Val	Ile
			260					265					270		
Glu	Ala	Arg	Met	Lys	Thr	Met	Gly	Glu	Val	His	Ala	Cys	Pro	His	Thr

275	280	285
Leu Met Pro Met Arg Lys Ala Phe Lys Gly Thr Phe Ile Ser Ala Gly		
290	295	300
Gly Phe Thr Arg Glu Asp Gly Asn Glu Ala Val Ser Lys Gly Arg Thr		
305	310	315
Asp Leu Val Ala Tyr Gly Arg Trp Phe Leu Ala Asn Pro Asp Leu Pro		
	325	330
Lys Arg Phe Gln Val Asp Ala Pro Leu Asn Lys Tyr Asp Arg Pro Thr		
	340	345
Phe Tyr Thr Ser Asp Pro Val Val Gly Tyr Thr Asp Tyr Pro Phe Leu		
	355	360
Glu Ser Thr Ala		365
370		

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 355 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..355

(D) OTHER INFORMATION: / Ceres Seq. ID 1565748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Gly Arg Phe Asn Leu Ser His Arg Val Val Leu Ala Pro Leu Thr	
1	5
Arg Gln Arg Ser Tyr Gly Asn Val Pro Gln Pro His Ala Ala Ile Tyr	10
	20
Tyr Ser Gln Arg Thr Thr Pro Gly Gly Phe Leu Ile Thr Glu Ala Thr	25
	35
Gly Val Ser Asp Thr Ala Gln Gly Tyr Gln Asp Thr Pro Gly Ile Trp	40
	50
Thr Lys Glu His Val Glu Ala Trp Lys Pro Ile Val Asp Ala Val His	55
	65
Ala Lys Gly Gly Ile Phe Phe Cys Gln Ile Trp His Val Gly Arg Val	70
	85
Ser Asn Ser Gly Phe Gln Pro Asn Gly Lys Ala Pro Ile Ser Cys Ser	90
	100
Asp Lys Pro Leu Met Pro Gln Ile Arg Ser Asn Gly Ile Asp Glu Ala	105
	115
Leu Phe Thr Pro Pro Arg Arg Leu Gly Ile Glu Glu Ile Pro Gly Ile	120
	130
Val Asn Asp Phe Arg Leu Ala Ala Arg Asn Ala Met Glu Ala Gly Phe	135
	145
Asp Gly Val Glu Ile His Arg Ala Asn Gly Tyr Leu Ile Asp Gln Phe	150
	165
Met Lys Asp Thr Val Asn Asp Arg Thr Asp Glu Tyr Gly Gly Ser Leu	170
	180
Gln Asn Arg Cys Lys Phe Pro Leu Glu Ile Val Asp Ala Val Ala Lys	185
	195
Glu Ile Gly Pro Asp Arg Val Gly Ile Arg Leu Ser Pro Phe Ala Asp	200
	210
Tyr Met Glu Ser Gly Asp Thr Asn Pro Gly Ala Leu Gly Leu Tyr Met	215
	225
Ala Glu Ser Leu Asn Lys Tyr Gly Ile Leu Tyr Cys His Val Ile Glu	230
	245
Ala Arg Met Lys Thr Met Gly Glu Val His Ala Cys Pro His Thr Leu	250
	260
Met Pro Met Arg Lys Ala Phe Lys Gly Thr Phe Ile Ser Ala Gly Gly	265
	275
	280
	285

Phe Thr Arg Glu Asp Gly Asn Glu Ala Val Ser Lys Gly Arg Thr Asp
290 295 300
Leu Val Ala Tyr Gly Arg Trp Phe Leu Ala Asn Pro Asp Leu Pro Lys
305 310 315 320
Arg Phe Gln Val Asp Ala Pro Leu Asn Lys Tyr Asp Arg Pro Thr Phe
325 330 335
Tyr Thr Ser Asp Pro Val Val Gly Tyr Thr Asp Tyr Pro Phe Leu Glu
340 345 350
Ser Thr Ala
355

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1565749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met Pro Gln Ile Arg Ser Asn Gly Ile Asp Glu Ala Leu Phe Thr Pro
1 5 10 15
Pro Arg Arg Leu Gly Ile Glu Glu Ile Pro Gly Ile Val Asn Asp Phe
20 25 30
Arg Leu Ala Ala Arg Asn Ala Met Glu Ala Gly Phe Asp Gly Val Glu
35 40 45
Ile His Arg Ala Asn Gly Tyr Leu Ile Asp Gln Phe Met Lys Asp Thr
50 55 60
Val Asn Asp Arg Thr Asp Glu Tyr Gly Gly Ser Leu Gln Asn Arg Cys
65 70 75 80
Lys Phe Pro Leu Glu Ile Val Asp Ala Val Ala Lys Glu Ile Gly Pro
85 90 95
Asp Arg Val Gly Ile Arg Leu Ser Pro Phe Ala Asp Tyr Met Glu Ser
100 105 110
Gly Asp Thr Asn Pro Gly Ala Leu Gly Leu Tyr Met Ala Glu Ser Leu
115 120 125
Asn Lys Tyr Gly Ile Leu Tyr Cys His Val Ile Glu Ala Arg Met Lys
130 135 140
Thr Met Gly Glu Val His Ala Cys Pro His Thr Leu Met Pro Met Arg
145 150 155 160
Lys Ala Phe Lys Gly Thr Phe Ile Ser Ala Gly Gly Phe Thr Arg Glu
165 170 175
Asp Gly Asn Glu Ala Val Ser Lys Gly Arg Thr Asp Leu Val Ala Tyr
180 185 190
Gly Arg Trp Phe Leu Ala Asn Pro Asp Leu Pro Lys Arg Phe Gln Val
195 200 205
Asp Ala Pro Leu Asn Lys Tyr Asp Arg Pro Thr Phe Tyr Thr Ser Asp
210 215 220
Pro Val Val Gly Tyr Thr Asp Tyr Pro Phe Leu Glu Ser Thr Ala
225 230 235

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1012 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1012

(D) OTHER INFORMATION: / Ceres Seq. ID 1565769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

acttcagcaa	aaccactaca	ctttctttat	ctctcagatt	ttctcaagaa	gattgtgtgg	60
aagatgatga	gacggaagat	ttttctcttt	gggtgattcca	tcactgaaga	atccttttagt	120
gacggtggct	gggtgtcttc	ttctgcgcgt	cttctccgct	gcaaggctga	tatggtgcta	180
cgaggataca	gtggatataa	cacgaggtgg	gcactgaaag	tggtggagag	agtttttccg	240
gtggcagaag	aagacggcgg	agattctccg	gcagctgtga	ctgttttctt	tggagcggaac	300
gacgctgttc	ttccggagag	atgctcgggg	tttcagcatg	tgccacttca	cgagtacaag	360
cagaatcttc	gtctatttgt	ttcgtttctc	aagaatcgtt	ggccacaaac	ggccattatt	420
cttataactc	cgctccaat	agacgaagag	gcccgcctca	gatatactta	tatcgaaaaa	480
acaacggggg	tgccggaag	aacgaatgaa	gtagccggac	tatacgcaaa	agcatgtata	540
gcagtagctg	aggaatgtca	aatttcggtc	actgatcttt	ggtccaaaaa	gcagcAaakt	600
scaaaattggs	aaacagaatg	tctatgggg	gggttacatt	tgagtccggg	cggtaacaaa	660
gtattgtttg	aagaagttagc	aaagaagctt	aaagaagaag	gcattggagc	tgaggactta	720
gcctgtggatc	ttccctctat	agaagatgtt	gaccctaagg	atcctctcaa	atcctttgat	780
gagttttgat	gctttatatt	actaccatgc	agtttgggtc	ttctatcttt	gAttacttct	840
taatttcgat	attaatttag	ggaatgtgac	attattaggc	actttgtgag	aatctttttg	900
tgagaaatctt	tttaccgtttg	aggcactttg	gagagagagg	gcactttggc	atcttttttt	960
agaggagatt	gaaccaattt	gcccctgaag	tgatgaaaaa	acaataattt	tt	

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..262

(D) OTHER INFORMATION: / Ceres Seq. ID 1565770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Thr	Ser	Ala	Lys	Pro	Leu	His	Leu	Ser	Tyr	Leu	Ser	Asp	Phe	Leu	Lys
1			5					10				15			
Lys	Ile	Val	Trp	Lys	Met	Met	Arg	Arg	Lys	Ile	Phe	Leu	Phe	Gly	Asp
		20						25				30			
Ser	Ile	Thr	Glu	Glu	Ser	Phe	Ser	Asp	Gly	Gly	Trp	Gly	Ala	Ser	Leu
		35					40				45				
Ala	Asp	Leu	Leu	Arg	Arg	Lys	Ala	Asp	Met	Val	Leu	Arg	Gly	Tyr	Ser
	50					55					60				
Gly	Tyr	Asn	Thr	Arg	Trp	Ala	Leu	Lys	Val	Val	Glu	Arg	Val	Phe	Pro
	65				70				75					80	
Val	Ala	Glu	Glu	Asp	Gly	Gly	Asp	Ser	Pro	Ala	Ala	Val	Thr	Val	Phe
			85					90						95	
Phe	Gly	Ala	Asn	Asp	Ala	Cys	Leu	Pro	Glu	Arg	Cys	Ser	Gly	Phe	Gln
			100					105					110		
His	Val	Pro	Leu	His	Glu	Tyr	Lys	Gln	Asn	Leu	Arg	Ser	Ile	Val	Ser
		115					120					125			
Phe	Leu	Lys	Asn	Arg	Trp	Pro	Gln	Thr	Ala	Ile	Ile	Leu	Ile	Thr	Pro
		130				135						140			
Pro	Pro	Ile	Asp	Glu	Glu	Ala	Arg	Leu	Arg	Tyr	Pro	Tyr	Ile	Glu	Asn
	145					150				155				160	
Thr	Thr	Gly	Leu	Pro	Glu	Arg	Thr	Asn	Glu	Val	Ala	Gly	Leu	Tyr	Ala
			165						170					175	
Lys	Ala	Cys	Ile	Ala	Val	Ala	Glu	Glu	Cys	Gln	Ile	Ser	Val	Thr	Asp
			180					185					190		
Leu	Trp	Ser	Lys	Met	Gln	Gln	Xaa	Xaa	Asn	Trp	Xaa	Thr	Glu	Cys	Leu
		195					200					205			
Trp	Asp	Gly	Leu	His	Leu	Ser	Arg	Val	Gly	Asn	Lys	Val	Leu	Phe	Glu
		210				215					220				
Glu	Val	Ala	Lys	Lys	Leu	Lys	Glu	Glu	Gly	Ile	Gly	Ala	Glu	Asp	Leu

225 230 235 240
Ala Val Asp Leu Pro Leu Ile Glu Asp Val Asp Pro Lys Asp Pro Leu
 245 250 255
Lys Ser Phe Asp Glu Phe
 260

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..241
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Met Met Arg Arg Lys Ile Phe Leu Phe Gly Asp Ser Ile Thr Glu Glu
1 5 10 15
Ser Phe Ser Asp Gly Gly Trp Gly Ala Ser Leu Ala Asp Leu Leu Arg
 20 25 30
Arg Lys Ala Asp Met Val Leu Arg Gly Tyr Ser Gly Tyr Asn Thr Arg
 35 40 45
Trp Ala Leu Lys Val Val Glu Arg Val Phe Pro Val Ala Glu Glu Asp
 50 55 60
Gly Gly Asp Ser Pro Ala Ala Val Thr Val Phe Phe Gly Ala Asn Asp
65 70 75 80
Ala Cys Leu Pro Glu Arg Cys Ser Gly Phe Gln His Val Pro Leu His
 85 90 95
Glu Tyr Lys Gln Asn Leu Arg Ser Ile Val Ser Phe Leu Lys Asn Arg
 100 105 110
Trp Pro Gln Thr Ala Ile Ile Leu Ile Thr Pro Pro Pro Ile Asp Glu
 115 120 125
Glu Ala Arg Leu Arg Tyr Pro Tyr Ile Glu Asn Thr Thr Gly Leu Pro
 130 135 140
Glu Arg Thr Asn Glu Val Ala Gly Leu Tyr Ala Lys Ala Cys Ile Ala
145 150 155 160
Val Ala Glu Glu Cys Gln Ile Ser Val Thr Asp Leu Trp Ser Lys Met
 165 170 175
Gln Gln Xaa Xaa Asn Trp Xaa Thr Glu Cys Leu Trp Asp Gly Leu His
 180 185 190
Leu Ser Arg Val Gly Asn Lys Val Leu Phe Glu Glu Val Ala Lys Lys
 195 200 205
Leu Lys Glu Glu Gly Ile Gly Ala Glu Asp Leu Ala Val Asp Leu Pro
 210 215 220
Leu Ile Glu Asp Val Asp Pro Lys Asp Pro Leu Lys Ser Phe Asp Glu
225 230 235 240
Phe

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..240
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met	Arg	Arg	Lys	Ile	Phe	Leu	Phe	Gly	Asp	Ser	Ile	Thr	Glu	Glu	Ser
1			5						10				15		
Phe	Ser	Asp	Gly	Trp	Gly	Ala	Ser	Leu	Ala	Asp	Leu	Leu	Arg	Arg	
		20					25					30			
Lys	Ala	Asp	Met	Val	Leu	Arg	Gly	Tyr	Ser	Gly	Tyr	Asn	Thr	Arg	Trp
		35					40					45			
Ala	Leu	Lys	Val	Val	Glu	Arg	Val	Phe	Pro	Val	Ala	Glu	Glu	Asp	Gly
	50					55				60					
Gly	Asp	Ser	Pro	Ala	Ala	Val	Thr	Val	Phe	Phe	Gly	Ala	Asn	Asp	Ala
65					70				75				80		
Cys	Leu	Pro	Glu	Arg	Cys	Ser	Gly	Phe	Gln	His	Val	Pro	Leu	His	Glu
			85						90				95		
Tyr	Lys	Gln	Asn	Leu	Arg	Ser	Ile	Val	Ser	Phe	Leu	Lys	Asn	Arg	Trp
			100						105				110		
Pro	Gln	Thr	Ala	Ile	Ile	Leu	Ile	Thr	Pro	Pro	Pro	Ile	Asp	Glu	Glu
			115					120				125			
Ala	Arg	Leu	Arg	Tyr	Pro	Tyr	Ile	Glu	Asn	Thr	Thr	Gly	Leu	Pro	Glu
	130					135					140				
Arg	Thr	Asn	Glu	Val	Ala	Gly	Leu	Tyr	Ala	Lys	Ala	Cys	Ile	Ala	Val
145					150				155					160	
Ala	Glu	Glu	Cys	Gln	Ile	Ser	Val	Thr	Asp	Leu	Trp	Ser	Lys	Met	Gln
			165						170					175	
Gln	Xaa	Xaa	Asn	Trp	Xaa	Thr	Glu	Cys	Leu	Trp	Asp	Gly	Leu	His	Leu
	180						185						190		
Ser	Arg	Val	Gly	Asn	Lys	Val	Leu	Phe	Glu	Glu	Val	Ala	Lys	Lys	Leu
	195						200					205			
Lys	Glu	Glu	Gly	Ile	Gly	Ala	Glu	Asp	Leu	Ala	Val	Asp	Leu	Pro	Leu
	210					215					220				
Ile	Glu	Asp	Val	Asp	Pro	Lys	Asp	Pro	Leu	Lys	Ser	Phe	Asp	Glu	Phe
225					230				235					240	

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..976
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

aaaaactttc	tgttatcccc	tctttctctt	attctctctc	tctcgcctac	tctccctctt	60
aaAgtttttt	ttttaaaccag	actctccctc	taagtatttc	gttcgcaatt	aaaaaagaaa	120
acaaaatctt	tataaaatct	gattttctct	ttttaccctg	attattttga	tttgactgtt	180
ttacgacagt	caatatattca	attttattat	tgggtgctga	cgtggcatgc	atccaataga	240
gtatcaccat	gaaccacaaa	acgatgcgtc	ttccccccac	tcgcgtttcta	acggcgggata	300
acgcgcaaga	acgagacgccc	tctatctcct	cgttcaccga	taatcccgccg	gaatacgcca	360
agtttccctc	tccgcccgtc	aaacttggtc	ctccgcgggt	taatcccatat	tccaagaagt	420
cttcaaccgc	acgacggcgc	cgcgtcgggt	cgaaccaact	gatgttagcc	ggttatctga	480
gccacgagta	cctcacccaa	ggcacactct	tcggagagca	atggaaccag	gctcgagccc	540
aagccgagtc	cagtaagata	aagccgagcc	atactgttga	gtccggtgag	gaatgtgagc	600
cgaaccggaa	gaggtataga	gaggttgcta	attctctcgc	gtccagatggg	gcccaactgc	660
ccggcatcgt	caatctcgcc	cagcttgccc	gattttctca	actgtgatgc	gcgtaaatccg	720
gtgtccacgt	ggagacagat	caattgctct	tcttcggcca	acgagagacag	ccttaaaacc	780
gaaacctctt	tctctctctt	tttttttcaa	atgttttttt	agaatctctc	ctgtaaaagt	840
gactcgctgc	ctctctcttc	tctatcctgc	cttctcgcga	aatcgactga	gaaaatttag	900
ggtttgttgt	tgaggtagat	gctctctctt	tgtacatcac	aaatatcaat	tagccaatgg	960
attatgtttt	cagatc					

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
- (A) NAME/KEY: peptide
 - (B) LOCATION: 1..152
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1565778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met Asn Thr Lys Thr Met Arg Leu Pro Pro Arg Arg Val Leu Thr Ala
1 5 10 15
Asp Lys Arg Lys Glu Arg Asp Ala Phe Ile Ser Ser Val Thr Asp Asn
20 25 30
Pro Pro Glu Ile Ala Lys Phe Pro Ser Pro Pro Pro Lys Leu Val Pro
35 40 45
Pro Pro Val Asn Pro Ile Ser Lys Lys Ser Ser Thr Ala Ala Ala Glu
50 55 60
Pro Ile Gly Ser Asn Gln Leu Met Leu Ala Gly Tyr Leu Ser His Glu
65 70 75 80
Tyr Leu Thr Gln Gly Thr Leu Phe Gly Glu Gln Trp Asn Gln Ala Arg
85 90 95
Ala Gln Ala Glu Ser Ser Lys Ile Lys Pro Ser His Thr Val Glu Pro
100 105 110
Ala Glu Glu Cys Glu Pro Lys Arg Lys Arg Tyr Arg Glu Val Ala Asn
115 120 125
Leu Leu Arg Ser Asp Gly Ala Gln Leu Pro Gly Ile Val Asn Pro Ala
130 135 140
Gln Leu Ala Arg Phe Leu Lys Leu
145 150

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
- (A) NAME/KEY: peptide
 - (B) LOCATION: 1..147
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1565779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Arg Leu Pro Pro Arg Arg Val Leu Thr Ala Asp Lys Arg Lys Glu
1 5 10 15
Arg Asp Ala Phe Ile Ser Ser Val Thr Asp Asn Pro Pro Glu Ile Ala
20 25 30
Lys Phe Pro Ser Pro Pro Pro Lys Leu Val Pro Pro Pro Val Asn Pro
35 40 45
Ile Ser Lys Lys Ser Ser Thr Ala Ala Ala Glu Pro Ile Gly Ser Asn
50 55 60
Gln Leu Met Leu Ala Gly Tyr Leu Ser His Glu Tyr Leu Thr Gln Gly
65 70 75 80
Thr Leu Phe Gly Glu Gln Trp Asn Gln Ala Arg Ala Gln Ala Glu Ser
85 90 95
Ser Lys Ile Lys Pro Ser His Thr Val Glu Pro Ala Glu Glu Cys Glu
100 105 110
Pro Lys Arg Lys Arg Tyr Arg Glu Val Ala Asn Leu Leu Arg Ser Asp
115 120 125
Gly Ala Gln Leu Pro Gly Ile Val Asn Pro Ala Gln Leu Ala Arg Phe

130 135 140
Leu Lys Leu
145
(2) INFORMATION FOR SEQ ID NO:80:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..81
(D) OTHER INFORMATION: / Ceres Seq. ID 1565780
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:
Met Leu Ala Gly Tyr Leu Ser His Glu Tyr Leu Thr Gln Gly Thr Leu
1 5 10 15
Phe Gly Glu Gln Trp Asn Gln Ala Arg Ala Gln Ala Glu Ser Ser Lys
20 25 30
Ile Lys Pro Ser His Thr Val Glu Pro Ala Glu Glu Cys Glu Pro Lys
35 40 45
Arg Lys Arg Tyr Arg Glu Val Ala Asn Leu Leu Arg Ser Asp Gly Ala
50 55 60
Gln Leu Pro Gly Ile Val Asn Pro Ala Gln Leu Ala Arg Phe Leu Lys
65 70 75 80
Leu

(2) INFORMATION FOR SEQ ID NO:81:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1305
(D) OTHER INFORMATION: / Ceres Seq. ID 1565787
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:
agccgatttc tagattctcc tccaccacca ttttaccctt cttttaaatt ccttccttca 60
atcaaaattc gaattatttc tcaaacctct tctttatata ctaaaacgtc tcaacatgaac 120
aagaagaata aatagaaca aagaagatga acaagaacaa gattgatgtt aagatcgaga 180
cgaagaaga atcgatggat gaggggcstg agccaatcgt ccgagtcag tccttagccg 240
agagcaacct ctccctctct cccgacccgtt acatcaaaac agcgtctcta cgcgccacca 300
cgacccaaga cgctccctacc gcgaccaaca tcccaatcat agaccttgaa ggactctctc 360
ggaagaaggg ttgtctgatt acgtcatcat ggctcggata tccggagcct gccgtgggtg 420
ggggttcttc caggtgggtga accacggggt caaacccggag ctgatggacg cggtcaggga 480
saattggaga gaggtttttc atatgcccgt taatgcccac gagacttact caaactcacc 540
aagaacctac gaaggtcatg gaagtagact aggtgttgag aaaagcaagt cttgattgga 600
gtgatattta ctttctccat ctctctctcc atcatttgaa agacttcaac aagtggtcctt 660
cttttccctc caccataaga gaagtatcgt atgaatacgg cgaagagcta gtgaagctaa 720
gtgggagaat tatgaggta ttatogacaa acttgggact aaaaaggat aagtttcaag 780
aagcattggg aggtgaaaac atggggcggt gtttgagggt taattattac ccaaatgcc 840
ctcgacctgt gctggctctt gctctctctc cacactccga tctggcggt atgacattc 900
tcttaccgga cgatcaagtc ttccgtctcc aggttcgtga agatgacacg tggatcccg 960
tcaagctcca tccccatgct ttcactgcta atattgggtga tcaaatacag atactaagca 1020
actcaacata caagagtgtg gagcatagag tgatagtga cctggacaag gagagagattt 1080
cacttgccct ctctctcaat cctaaaaggc atattTccga tccaacctat acaagaacttt 1140
gtatcaactc ataactctcc ttatataccct cccatgacct ttcactcaga tagactcttt 1200
atcagaactc aaggtccaca aggcataatcc catgttgat ctcataattc tcctcgttga 1260
ttgtttttct tttatttctt ccttaaaaga aaaattaagt tttttg

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met	Asn	Lys	Asn	Lys	Ile	Asp	Val	Lys	Ile	Glu	Thr	Lys	Lys	Gly	Ser	
1			5						10					15		
Met	Asp	Glu	Trp	Xaa	Glu	Pro	Ile	Val	Arg	Val	Gln	Ser	Leu	Ala	Glu	
		20						25					30			
Ser	Asn	Leu	Ser	Ser	Leu	Pro	Asp	Arg	Tyr	Ile	Lys	Pro	Ala	Ser	Leu	
		35					40					45				
Arg	Pro	Thr	Thr	Thr	Glu	Asp	Ala	Pro	Thr	Ala	Thr	Asn	Ile	Pro	Ile	
		50			55						60					
Ile	Asp	Leu	Glu	Gly	Leu	Ser	Arg	Lys	Lys	Gly	Cys	Leu	Met	Thr	Ser	
		65			70					75				80		
Ser	Trp	Leu	Gly	Tyr	Arg	Arg	Leu	Ala	Val	Gly	Gly	Gly	Ser	Ser	Arg	
			85						90					95		

Trp

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Met	Arg	Val	Leu	Ser	Thr	Asn	Leu	Gly	Leu	Lys	Glu	Asp	Lys	Phe	Gln	
1			5						10					15		
Glu	Ala	Phe	Gly	Gly	Glu	Asn	Ile	Gly	Ala	Cys	Leu	Arg	Val	Asn	Tyr	
		20						25					30			
Tyr	Pro	Lys	Cys	Pro	Arg	Pro	Val	Leu	Ala	Leu	Gly	Leu	Ser	Pro	His	
		35					40					45				
Ser	Asp	Pro	Gly	Gly	Met	Thr	Ile	Leu	Leu	Pro	Asp	Asp	Gln	Val	Phe	
		50				55					60					
Gly	Leu	Gln	Val	Arg	Lys	Asp	Asp	Thr	Trp	Ile	Thr	Val	Lys	Pro	His	
		65			70					75				80		
Pro	His	Ala	Phe	Ile	Val	Asn	Ile	Gly	Asp	Gln	Ile	Gln	Ile	Leu	Ser	
			85						90					95		
Asn	Ser	Thr	Tyr	Lys	Ser	Val	Glu	His	Arg	Val	Ile	Val	Asn	Ser	Asp	
		100						105					110			
Lys	Glu	Arg	Val	Ser	Leu	Ala	Phe	Phe	Tyr	Asn	Pro	Lys	Ser	Asp	Ile	
		115					120					125				
Ser	Asp	Pro	Thr	Ile	Thr	Arg	Thr	Cys	Ile	Asn	Ser					
		130							135				140			

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..87
 (D) OTHER INFORMATION: / Ceres Seq. ID 1565790
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:
Met Thr Ile Leu Leu Pro Asp Asp Gln Val Phe Gly Leu Gln Val Arg
1 5 10 15
Lys Asp Asp Thr Trp Ile Thr Val Lys Pro His Pro His Ala Phe Ile
 20 25 30
Val Asn Ile Gly Asp Gln Ile Gln Ile Leu Ser Asn Ser Thr Tyr Lys
 35 40 45
Ser Val Glu His Arg Val Ile Val Asn Ser Asp Lys Glu Arg Val Ser
 50 55 60
Leu Ala Phe Phe Tyr Asn Pro Lys Ser Asp Ile Ser Asp Pro Thr Ile
65 70 75 80
Thr Arg Thr Cys Ile Asn Ser
 85

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1648 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1648
(D) OTHER INFORMATION: / Ceres Seq. ID 1565799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

acatgttctc	tccgcgcctga	atcatgtcaa	tctccacaaa	aagatctttg	ataaaaaaga	60
ttgagcccta	attccttgat	gtttgttgaa	tcgcacagca	gataaaaaaa	aatggtgttg	120
gcggagctcg	gcggccggat	aacccgcgcc	atacagcaga	tgaacaatgt	gacaataatc	180
gatgaaaagg	ttttgaatga	tttcttaaac	gagattactc	gcgctttgtc	ccagtcocgt	240
gtttcttttt	gccttgttga	aaagatgcag	accaatatta	agaagatcgt	taacctcgac	300
gatctagcag	ctggcccacaa	caaacgcctg	atcatcgagc	aggctatctt	caaggaaact	360
tgtaggatcg	tggatccagg	aaagcctgcc	tttgcgccca	aaaaggccaa	acctagtgtg	420
gtgatgttgc	tcggtttaca	aggtgctgga	aaaaccacaa	catgtaccaa	gtatgcttac	480
tatcatcaga	agaaagggtg	caaagcagct	ctagtgtgtg	cggatacttt	cagggccggt	540
gcctttgtatc	agctgaaaca	gaatgccacc	aaggctaaag	tcccctttta	tggaagctac	600
acagaaatccg	atcctgtgaa	aattgtgtgt	gagggagttg	ataggttcaa	gaagaaaaag	660
tgtgatctta	ttattgttga	caccagtggt	cgccataaac	aagcagcttc	tctctttgaa	720
gaaatgcgtc	aagtgtgtga	agcaacggaa	ccagatcttg	ttatatttgt	tatggatagc	780
agtatgtgtc	aagctgcatt	tgaacaagct	gaagctttta	aggaacctgt	atctgttgga	840
gctgtaaatta	ttactaaagt	ggacggccat	gccaaaggag	gtggtgctct	tagcgtggtt	900
gcagctacaa	aaagtctcgt	gatattcatt	ggaacaggag	agcatatgga	tgagtttgaa	960
gtgtttgacg	ttaaacattt	tgtcagccgt	ctcttaggaa	aggggtgatg	gtctgggactc	1020
gtggaataac	tacaagaggt	ggtacctaaa	gatctacaga	atgaacttgt	agaaaaatctc	1080
tctcagggtg	actttacgtt	gaaagatgat	tacgaccagt	tccagtgctc	tctgcggatt	1140
ccacttaatc	agcttttctc	gatgctgcct	ggaattagtg	ctgaaatgat	gcgcaagga	1200
catggtgaag	aaaagccaggt	gaagatgaag	cgatacatga	caatgatgga	ttctatgaca	1260
aataaagzac	tgcacagccc	aaacccaaag	atttttaacg	agtcaggagt	aatgagagta	1320
gcgagagggg	cagggaaggt	agtaagagaa	gtgatggaga	gtttggaaga	gtacaagagg	1380
atagcaaaaga	caatgaaggt	gatcaagatc	ccaaagaacg	gagacatgag	caagggtcata	1440
ccgcctcaga	tgtcaaaaac	gatgggcggc	atgagcggtc	tcgacagatc	catgaagcac	1500
atgggttcgg	ctaaggacat	gatgggaatg	tttgtggcgg	gaggcaagta	gtttctatct	1560
ttcttgCaca	cagtgcacgt	agggcagatg	taaaactttt	gttacatact	gtattagtag	1620
cttataattt	taacacatcc	taacgacc				

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..479
(D) OTHER INFORMATION: / Ceres Seq. ID 1565800
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met	Val	Leu	Ala	Glu	Leu	Gly	Gly	Arg	Ile	Thr	Arg	Ala	Ile	Gln	Gln
1			5						10				15		
Met	Asn	Asn	Val	Thr	Ile	Ile	Asp	Glu	Lys	Val	Leu	Asn	Asp	Phe	Leu
			20					25					30		
Asn	Glu	Ile	Thr	Arg	Ala	Leu	Leu	Gln	Ser	Asp	Val	Ser	Phe	Gly	Leu
			35				40				45				
Val	Glu	Lys	Met	Gln	Thr	Asn	Ile	Lys	Lys	Ile	Val	Asn	Leu	Asp	Asp
	50					55				60					
Leu	Ala	Ala	Gly	His	Asn	Lys	Arg	Leu	Ile	Ile	Glu	Gln	Ala	Ile	Phe
	65				70				75					80	
Lys	Glu	Leu	Cys	Arg	Met	Leu	Asp	Pro	Gly	Lys	Pro	Ala	Phe	Ala	Pro
			85					90					95		
Lys	Lys	Ala	Lys	Pro	Ser	Val	Val	Met	Phe	Val	Gly	Leu	Gln	Gly	Ala
			100					105					110		
Gly	Lys	Thr	Thr	Thr	Cys	Thr	Lys	Tyr	Ala	Tyr	Tyr	His	Gln	Lys	Lys
			115					120					125		
Gly	Tyr	Lys	Ala	Ala	Leu	Val	Cys	Ala	Asp	Thr	Phe	Arg	Ala	Gly	Ala
			130				135				140				
Phe	Asp	Gln	Leu	Lys	Gln	Asn	Ala	Thr	Lys	Ala	Lys	Ile	Pro	Phe	Tyr
	145				150				155					160	
Gly	Ser	Tyr	Thr	Glu	Ser	Asp	Pro	Val	Lys	Ile	Ala	Val	Glu	Gly	Val
			165					170					175		
Asp	Arg	Phe	Lys	Lys	Glu	Lys	Cys	Asp	Leu	Ile	Ile	Val	Asp	Thr	Ser
			180					185					190		
Gly	Arg	His	Lys	Gln	Ala	Ala	Ser	Leu	Phe	Glu	Glu	Met	Arg	Gln	Val
			195				200					205			
Ala	Glu	Ala	Thr	Glu	Pro	Asp	Leu	Val	Ile	Phe	Val	Met	Asp	Ser	Ser
			210			215					220				
Ile	Gly	Gln	Ala	Ala	Phe	Glu	Gln	Ala	Glu	Ala	Phe	Lys	Glu	Thr	Val
			225		230				235					240	
Ser	Val	Gly	Ala	Val	Ile	Ile	Thr	Lys	Met	Asp	Gly	His	Ala	Lys	Gly
			245					250					255		
Gly	Gly	Ala	Leu	Ser	Ala	Val	Ala	Ala	Thr	Lys	Ser	Pro	Val	Ile	Phe
			260				265						270		
Ile	Gly	Thr	Gly	Glu	His	Met	Asp	Glu	Phe	Glu	Val	Phe	Asp	Val	Lys
			275				280					285			
Pro	Phe	Val	Ser	Arg	Leu	Leu	Gly	Lys	Gly	Asp	Trp	Ser	Gly	Leu	Val
			290			295					300				
Asp	Lys	Leu	Gln	Glu	Val	Val	Pro	Lys	Asp	Leu	Gln	Asn	Glu	Leu	Val
			305			310				315				320	
Glu	Asn	Leu	Ser	Gln	Gly	Asn	Phe	Thr	Leu	Arg	Ser	Met	Tyr	Asp	Gln
			325						330					335	
Phe	Gln	Cys	Ser	Leu	Arg	Ile	Pro	Leu	Asn	Gln	Leu	Phe	Ser	Met	Leu
			340					345					350		
Pro	Gly	Ile	Ser	Ala	Glu	Met	Met	Pro	Lys	Gly	His	Gly	Glu	Glu	Ser
			355				360					365			
Arg	Val	Lys	Met	Lys	Arg	Tyr	Met	Thr	Met	Met	Asp	Ser	Met	Thr	Asn
			370			375					380				
Lys	Glu	Leu	Asp	Ser	Pro	Asn	Pro	Lys	Ile	Phe	Asn	Glu	Ser	Arg	Ile
			385			390				395				400	
Met	Arg	Ile	Ala	Arg	Gly	Ser	Gly	Arg	Leu	Val	Arg	Glu	Val	Met	Glu

(2) INFORMATION FOR SEQ ID NO:87:

(A) LENGTH: 463 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..463

(D) OTHER INFORMATION: / Ceres Seq. ID 1565801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met	Asn	Asn	Val	5	Thr	Ile	Ile	Asp	Glu	Lys	Val	Leu	Asn	Asp	Phe	Leu
1	Asn	Glu	Ile	Thr	Arg	Ala	Leu	Leu	Gln	Ser	Asp	Val	Ser	Phe	Gly	Leu
				20					25					30		
Val	Glu	Lys	Met	Gln	Thr	Asn	Ile	Lys	Lys	Ile	Val	Asn	Leu	Asp	Asp	
		35					40					45				
Leu	Ala	Ala	Gly	His	Asn	Lys	Arg	Leu	Ile	Ile	Glu	Gln	Ala	Ile	Phe	
	50					55					60					
Lys	Glu	Leu	Cys	Arg	Met	Leu	Asp	Pro	Gly	Lys	Pro	Ala	Phe	Ala	Pro	
65					70					75					80	
Lys	Lys	Ala	Lys	Pro	Ser	Val	Val	Met	Phe	Val	Gly	Leu	Gln	Gly	Ala	
				85					90					95		
Gly	Lys	Thr	Thr	Thr	Cys	Thr	Lys	Tyr	Ala	Tyr	Tyr	His	Gln	Lys	Lys	
				100				105					110			
Gly	Tyr	Lys	Ala	Ala	Leu	Val	Cys	Ala	Asp	Thr	Phe	Arg	Ala	Gly	Ala	
		115				120						125				
Phe	Asp	Gln	Leu	Lys	Gln	Asn	Ala	Thr	Lys	Ala	Lys	Ile	Pro	Phe	Tyr	
	130					135					140					
Gly	Ser	Tyr	Thr	Glu	Ser	Asp	Pro	Val	Lys	Ile	Ala	Val	Glu	Gly	Ala	
145					150					155					160	
Asp	Arg	Phe	Lys	Lys	Glu	Lys	Cys	Asp	Leu	Ile	Ile	Val	Asp	Thr	Ser	
				165					170					175		
Gly	Arg	His	Lys	Gln	Ala	Ala	Ser	Leu	Phe	Glu	Glu	Met	Arg	Gln	Val	
				180				185					190			
Ala	Glu	Ala	Thr	Thr	Glu	Pro	Asp	Leu	Val	Ile	Phe	Val	Met	Asp	Ser	Ser
		195					200						205			
Ile	Gly	Gln	Ala	Ala	Phe	Glu	Gln	Ala	Glu	Ala	Phe	Lys	Glu	Thr	Val	
	210					215					220					
Ser	Val	Gly	Ala	Val	Ile	Ile	Thr	Lys	Met	Asp	Gly	His	Ala	Lys	Gly	
225					230					235					240	
Gly	Gly	Ala	Leu	Ser	Ala	Val	Ala	Ala	Thr	Lys	Ser	Pro	Val	Ile	Phe	
				245					250					255		
Ile	Gly	Thr	Gly	Glu	His	Met	Asp	Glu	Phe	Glu	Val	Phe	Asp	Val	Lys	
			260				265						270			
Pro	Phe	Val	Ser	Arg	Leu	Leu	Gly	Lys	Gly	Asp	Trp	Ser	Gly	Leu	Val	
		275					280					285				
Asp	Lys	Leu	Gln	Glu	Val	Val	Pro	Lys	Asp	Leu	Gln	Asn	Glu	Leu	Val	
	290					295					300					
Glu	Asn	Leu	Ser	Gln	Gly	Asn	Phe	Thr	Leu	Arg	Ser	Met	Tyr	Asp	Gln	
305					310					315					320	

Phe	Gln	Cys	Ser	Leu	Arg	Ile	Pro	Leu	Asn	Gln	Leu	Phe	Ser	Met	Leu	
			325						330					335		
Pro	Gly	Ile	Ser	Ala	Glu	Met	Met	Pro	Lys	Gly	His	Gly	Glu	Glu	Ser	
			340					345					350			
Arg	Val	Lys	Met	Lys	Arg	Tyr	Met	Thr	Met	Met	Asp	Ser	Met	Thr	Asn	
		355					360					365				
Lys	Glu	Leu	Asp	Ser	Pro	Asn	Pro	Lys	Ile	Phe	Asn	Glu	Ser	Arg	Ile	
	370					375				380						
Met	Arg	Ile	Ala	Arg	Gly	Ser	Gly	Arg	Leu	Val	Arg	Glu	Val	Met	Glu	
	385				390					395				400		
Met	Leu	Glu	Glu	Tyr	Lys	Arg	Ile	Ala	Lys	Thr	Met	Lys	Gly	Ile	Lys	
			405					410						415		
Ile	Pro	Lys	Asn	Gly	Asp	Met	Ser	Lys	Val	Ile	Pro	Pro	Gln	Met	Leu	
			420					425					430			
Lys	Gln	Met	Gly	Gly	Met	Ser	Gly	Leu	Gln	Ser	Leu	Met	Lys	Gln	Met	
		435					440					445				
Gly	Ser	Ala	Lys	Asp	Met	Met	Gly	Met	Phe	Gly	Gly	Gly	Gly	Lys		
	450					455					460					

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..428

(D) OTHER INFORMATION: / Ceres Seq. ID 1565802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Met	Gln	Thr	Asn	Ile	Lys	Lys	Ile	Val	Asn	Leu	Asp	Asp	Leu	Ala	Ala	
1			5					10					15			
Gly	His	Asn	Lys	Arg	Leu	Ile	Ile	Glu	Gln	Ala	Ile	Phe	Lys	Glu	Leu	
			20					25					30			
Cys	Arg	Met	Leu	Asp	Pro	Gly	Lys	Pro	Ala	Phe	Ala	Pro	Lys	Lys	Ala	
		35				40					45					
Lys	Pro	Ser	Val	Val	Met	Phe	Val	Gly	Leu	Gln	Gly	Ala	Gly	Lys	Thr	
	50					55					60					
Thr	Thr	Cys	Thr	Lys	Tyr	Ala	Tyr	Tyr	His	Gln	Lys	Lys	Gly	Tyr	Lys	
	65				70				75					80		
Ala	Ala	Leu	Val	Cys	Ala	Asp	Thr	Phe	Arg	Ala	Gly	Ala	Phe	Asp	Gln	
			85					90					95			
Leu	Lys	Gln	Asn	Ala	Thr	Lys	Ala	Lys	Ile	Pro	Phe	Tyr	Gly	Ser	Tyr	
			100					105					110			
Thr	Glu	Ser	Asp	Pro	Val	Lys	Ile	Ala	Val	Glu	Gly	Val	Asp	Arg	Phe	
		115				120						125				
Lys	Lys	Glu	Lys	Cys	Asp	Leu	Ile	Ile	Val	Asp	Thr	Ser	Gly	Arg	His	
	130				135						140					
Lys	Gln	Ala	Ala	Ser	Leu	Phe	Glu	Glu	Met	Arg	Gln	Val	Ala	Glu	Ala	
	145				150					155				160		
Thr	Glu	Pro	Asp	Leu	Val	Ile	Phe	Val	Met	Asp	Ser	Ser	Ile	Gly	Gln	
			165					170						175		
Ala	Ala	Phe	Glu	Gln	Ala	Glu	Ala	Phe	Lys	Glu	Thr	Val	Ser	Val	Gly	
		180						185					190			
Ala	Val	Ile	Ile	Thr	Lys	Met	Asp	Gly	His	Ala	Lys	Gly	Gly	Gly	Ala	
		195				200					205					
Leu	Ser	Ala	Val	Ala	Ala	Thr	Lys	Ser	Pro	Val	Ile	Phe	Ile	Gly	Thr	
		210				215					220					
Gly	Glu	His	Met	Asp	Glu	Phe	Glu	Val	Phe	Asp	Val	Lys	Pro	Phe	Val	
	225				230				235					240		
Ser	Arg	Leu	Leu	Gly	Lys	Gly	Asp	Trp	Ser	Gly	Leu	Val	Asp	Lys	Leu	

(2) INFORMATION FOR SEO ID NO:89:

(A) LENGTH: 1687 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:
```

(A) NAME/KEY: -

(B) LOCATION: 1..1687

(D) OTHER INFORMATION: / Ceres Seq. ID 1565810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

aggaaacaaa	caaatctcca	tctctctcca	ttagagctgt	aagcagccat	agcctaaaca	60
aacctctaac	aatggtctca	atggtctcgc	tttaagcaaa	aactccattc	ctctctcaac	120
cactaaccaa	atcatctcca	aactccgac	tcccctctgc	cgcgctctcc	ttcccttcca	180
aatccctcca	cgcgcgcctc	ggatacaatc	gagccggatt	aaatgcttcc	gacgctggta	240
agcttgtaga	ctgctcatgt	gaagagcaac	agcgacgaga	gaagaaacac	gagcgcgcg	300
atttgccacg	tgttgagctg	agcggcttat	acttgcgaat	gatcatctga	tttaagcgaag	360
gtgtggaaac	tcaactggga	gggtttatg	gagataccga	tgctctccaa	actctctcga	420
ttaaactcgt	acgtcttgga	gacgctctcg	tcgttaacat	tcctcgctgc	attgtctctc	480
ctattgcaga	tgaacaaaaa	gcagctatgc	gcgagctctac	actgtctcgt	ttttccaatt	540
ccagtggtaa	ccccctctct	atctacgag	atattgagat	ttataagact	ccaaagggaag	600
aaagtagtag	tgaacactgg	gttcacgacg	ctccagtggt	gcctactcgt	gacgagggaa	660
taactaatgc	tggaactcgt	ctcatctggg	gtgatcttga	gggtcttgag	ccagtagaag	720
acaatgattg	gttgatcgt	ttcaggctgt	cgctcgtcga	gttaccgtaa	gagttggaga	780
acgctaatgc	ggctggcggt	tttgcctctc	acgtgagaa	tccgttcat	aatgtctcgt	840
ctctctttaa	gactgaact	cttagagac	ttcttgagat	tggttcaaaa	aacctattc	900
tttgctctca	tcggttaggt	gggtttacaa	aggtgatga	tggtctctta	gattggagaa	960
tgaagcaaca	gcgaaggtt	tacaggagt	gtgtctctga	tcctggagac	acagtggttt	1020
cgatattccc	ctgacatagt	cattacgctg	gtccaaccca	agtgctagtg	caacgaaagg	1080
ctagaaatca	tgcgtggtct	aacctttaca	tgtgvggtcg	tgatcctgat	gggaagggtc	1140
atccagtaga	gaacgctgat	tttcaagatg	ctgatcatgg	aaacaaagta	ctaaagctag	1200
caccagagat	cgaacgactc	aaatcatttc	ctttcagggt	tgtctgcatat	gacagaacgc	1260
aaggcgaagt	ggcttttctc	gtacctcgca	ggctccaagg	tttcttgttc	atctccggca	1320
ctaaatgctg	ccacattggca	aagaaacaac	aaaaccccg	agacgcttgt	atgtgcccaag	1380
gttgatggaa	agtttctgtg	gtactactat	agagcttgac	tcctggcggt	aattgtgaag	1440
taccagaagt	ggttccggtg	taagacaaaa	ctgtctggat	caaatgtgtg	cgtttgtgtt	1500
ctgaacgctt	gttgacacaa	tatgttgtgt	attggggag	aagcctatgt	ataactcgc	1560

ttgacctttt tccaaataaa atacagaaga aaaaaagact gtttttcggt tgcaagataa 1620
tttacgaaac ttgtaatat ttgggcctcaa actttgtacc atattaatga aacgattgtg 1680
tttaccat

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..463

(D) OTHER INFORMATION: / Ceres Seq. ID 1565811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met	Ala	Ser	Met	Ala	Ala	Val	Leu	Ser	Lys	Thr	Pro	Phe	Leu	Ser	Gln
1			5						10				15		
Pro	Leu	Thr	Lys	Ser	Ser	Pro	Asn	Ser	Asp	Leu	Pro	Phe	Ala	Ala	Val
			20					25					30		
Ser	Phe	Pro	Ser	Lys	Ser	Leu	Arg	Arg	Arg	Val	Gly	Ser	Ile	Arg	Ala
		35					40					45			
Gly	Leu	Ile	Ala	Pro	Asp	Gly	Gly	Lys	Leu	Val	Glu	Leu	Ile	Val	Glu
	50					55					60				
Glu	Pro	Lys	Arg	Arg	Glu	Lys	Lys	His	Glu	Ala	Ala	Asp	Leu	Pro	Arg
	65				70				75				80		
Val	Glu	Leu	Thr	Ala	Ile	Asp	Leu	Gln	Trp	Met	His	Val	Leu	Ser	Glu
			85						90				95		
Gly	Trp	Thr	Ser	Pro	Leu	Gly	Gly	Phe	Met	Arg	Glu	Ser	Glu	Phe	Leu
			100					105					110		
Gln	Thr	Leu	His	Phe	Asn	Ser	Leu	Arg	Leu	Asp	Asp	Gly	Ser	Val	Val
			115				120					125			
Asn	Met	Ser	Val	Pro	Ile	Val	Leu	Ala	Ile	Asp	Asp	Glu	Gln	Lys	Ala
	130					135					140				
Arg	Ile	Gly	Glu	Ser	Thr	Arg	Val	Ala	Leu	Phe	Asn	Ser	Asp	Gly	Asn
	145				150					155				160	
Pro	Val	Ser	Ile	Leu	Ser	Asp	Ile	Glu	Ile	Tyr	Lys	His	Pro	Lys	Glu
			165						170					175	
Glu	Arg	Ile	Ala	Arg	Thr	Trp	Gly	Thr	Thr	Ala	Pro	Gly	Leu	Pro	Tyr
			180				185						190		
Val	Asp	Glu	Ala	Ile	Thr	Asn	Ala	Gly	Asn	Trp	Leu	Ile	Gly	Gly	Asp
	195						200					205			
Leu	Glu	Val	Leu	Glu	Pro	Val	Lys	Tyr	Asn	Asp	Gly	Leu	Asp	Arg	Phe
	210					215					220				
Arg	Leu	Ser	Pro	Ala	Glu	Leu	Arg	Lys	Glu	Leu	Glu	Lys	Arg	Asn	Ala
	225				230					235				240	
Asp	Ala	Val	Phe	Ala	Phe	Gln	Leu	Arg	Asn	Pro	Val	His	Asn	Gly	His
			245						250				255		
Ala	Leu	Leu	Met	Thr	Asp	Thr	Arg	Arg	Arg	Leu	Leu	Glu	Met	Gly	Tyr
			260				265						270		
Lys	Asn	Pro	Ile	Leu	Leu	Leu	His	Pro	Leu	Gly	Gly	Phe	Thr	Lys	Ala
	275						280					285			
Asp	Asp	Val	Pro	Leu	Asp	Trp	Arg	Met	Lys	Gln	His	Glu	Lys	Val	Leu
	290					295					300				
Glu	Asp	Gly	Val	Leu	Asp	Pro	Glu	Thr	Thr	Val	Val	Ser	Ile	Phe	Pro
			310						315					320	
Ser	Pro	Met	His	Tyr	Ala	Gly	Pro	Thr	Glu	Val	Gln	Trp	His	Ala	Lys
			325						330				335		
Ala	Arg	Ile	Asn	Ala	Gly	Ala	Asn	Phe	Tyr	Ile	Val	Gly	Arg	Asp	Pro
			340					345					350		
Ala	Gly	Met	Gly	His	Pro	Val	Glu	Lys	Arg	Asp	Leu	Tyr	Asp	Ala	Asp
	355						360					365			

His Gly Lys Lys Val Leu Ser Met Ala Pro Gly Leu Glu Arg Leu Asn
370 375 380
Ile Leu Pro Phe Arg Val Ala Ala Tyr Asp Lys Thr Gln Gly Lys Met
385 390 395
Ala Phe Phe Asp Pro Ser Arg Pro Gln Asp Phe Leu Phe Ile Ser Gly
405 410 415
Thr Lys Met Arg Thr Leu Ala Lys Asn Asn Glu Asn Pro Pro Asp Gly
420 425 430
Phe Met Cys Pro Gly Gly Trp Lys Val Leu Val Asp Tyr Tyr Glu Ser
435 440 445
Leu Thr Pro Ala Gly Asn Gly Arg Leu Pro Glu Val Val Pro Val
450 455 460

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..460

(D) OTHER INFORMATION: / Ceres Seq. ID 1565812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Met Ala Ala Val Leu Ser Lys Thr Pro Phe Leu Ser Gln Pro Leu Thr
1 5 10 15
Lys Ser Ser Pro Asn Ser Asp Leu Pro Phe Ala Ala Val Ser Phe Pro
20 25 30
Ser Lys Ser Leu Arg Arg Arg Val Gly Ser Ile Arg Ala Gly Leu Ile
35 40 45
Ala Pro Asp Gly Gly Lys Leu Val Glu Leu Ile Val Glu Glu Pro Lys
50 55 60
Arg Arg Glu Lys Lys His Glu Ala Ala Asp Leu Pro Arg Val Glu Leu
65 70 75 80
Thr Ala Ile Asp Leu Gln Trp Met His Val Leu Ser Glu Gly Trp Thr
85 90 95
Ser Pro Leu Gly Gly Phe Met Arg Glu Ser Glu Phe Leu Gln Thr Leu
100 105 110
His Phe Asn Ser Leu Arg Leu Asp Asp Gly Ser Val Val Asn Met Ser
115 120 125
Val Pro Ile Val Leu Ala Ile Asp Asp Glu Gln Lys Ala Arg Ile Gly
130 135 140
Glu Ser Thr Arg Val Ala Leu Phe Asn Ser Asp Gly Asn Pro Val Ser
145 150 155 160
Ile Leu Ser Asp Ile Glu Ile Tyr Lys His Pro Lys Glu Glu Arg Ile
165 170 175
Ala Arg Thr Trp Gly Thr Thr Ala Pro Gly Leu Pro Tyr Val Asp Glu
180 185 190
Ala Ile Thr Asn Ala Gly Asn Trp Leu Ile Gly Gly Asp Leu Glu Val
195 200 205
Leu Glu Pro Val Lys Tyr Asn Asp Gly Leu Asp Arg Phe Arg Leu Ser
210 215 220
Pro Ala Glu Leu Arg Lys Glu Leu Glu Lys Arg Asn Ala Asp Ala Val
225 230 235 240
Phe Ala Phe Gln Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu
245 250 255
Met Thr Asp Thr Arg Arg Arg Leu Leu Glu Met Gly Tyr Lys Asn Pro
260 265 270
Ile Leu Leu Leu His Pro Leu Gly Gly Phe Thr Lys Ala Asp Asp Val
275 280 285
Pro Leu Asp Trp Arg Met Lys Gln His Glu Lys Val Leu Glu Asp Gly

290	295	300
Val Leu Asp Pro Glu Thr Thr Val Val Ser Ile Phe Pro Ser Pro Met		
305	310	315
His Tyr Ala Gly Pro Thr Glu Val Gln Trp His Ala Lys Ala Arg Ile		
	325	330
Asn Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met		
	340	345
Gly His Pro Val Glu Lys Arg Asp Leu Tyr Asp Ala Asp His Gly Lys		
	355	360
Lys Val Leu Ser Met Ala Pro Gly Leu Glu Arg Leu Asn Ile Leu Pro		
	370	375
Phe Arg Val Ala Ala Tyr Asp Lys Thr Gln Gly Lys Met Ala Phe Phe		
385	390	395
Asp Pro Ser Arg Pro Gln Asp Phe Leu Phe Ile Ser Gly Thr Lys Met		
	405	410
Arg Thr Leu Ala Lys Asn Asn Glu Asn Pro Pro Asp Gly Phe Met Cys		
	420	425
Pro Gly Gly Trp Lys Val Leu Val Asp Tyr Tyr Glu Ser Leu Thr Pro		
	435	440
Ala Gly Asn Gly Arg Leu Pro Glu Val Val Pro Val		
450	455	460

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..373

(D) OTHER INFORMATION: / Ceres Seq. ID 1565813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met His Val Leu Ser Glu Gly Trp Thr Ser Pro Leu Gly Gly Phe Met		
1	5	10
Arg Glu Ser Glu Phe Leu Gln Thr Leu His Phe Asn Ser Leu Arg Leu		
	20	25
Asp Asp Gly Ser Val Val Asn Met Ser Val Pro Ile Val Leu Ala Ile		
	35	40
Asp Asp Glu Gln Lys Ala Arg Ile Gly Glu Ser Thr Arg Val Ala Leu		
	50	55
Phe Asn Ser Asp Gly Asn Pro Val Ser Ile Leu Ser Asp Ile Glu Ile		
65	70	75
Tyr Lys His Pro Lys Glu Glu Arg Ile Ala Arg Thr Trp Gly Thr Thr		
	85	90
Ala Pro Gly Leu Pro Tyr Val Asp Glu Ala Ile Thr Asn Ala Gly Asn		
	100	105
Trp Leu Ile Gly Gly Asp Leu Glu Val Leu Glu Pro Val Lys Tyr Asn		
	115	120
Asp Gly Leu Asp Arg Phe Arg Leu Ser Pro Ala Glu Leu Arg Lys Glu		
	130	135
Leu Glu Lys Arg Asn Ala Asp Ala Val Phe Ala Gln Leu Arg Asn		
145	150	155
Pro Val His Asn Gly His Ala Leu Leu Met Thr Asp Thr Arg Arg Arg		
	165	170
Leu Leu Glu Met Gly Tyr Lys Asn Pro Ile Leu Leu Leu His Pro Leu		
	180	185
Gly Gly Phe Thr Lys Ala Asp Asp Val Pro Leu Asp Trp Arg Met Lys		
	195	200
Gln His Glu Lys Val Leu Glu Asp Gly Val Leu Asp Pro Glu Thr Thr		
210	215	220

Val Val Ser Ile Phe Pro Ser Pro Met His Tyr Ala Gly Pro Thr Glu
225 230 235 240
Val Gln Trp His Ala Lys Ala Arg Ile Asn Ala Gly Ala Asn Phe Tyr
245 250 255
Ile Val Gly Arg Asp Pro Ala Gly Met Gly His Pro Val Glu Lys Arg
260 265 270
Asp Leu Tyr Asp Ala Asp His Gly Lys Lys Val Leu Ser Met Ala Pro
275 280 285
Gly Leu Glu Arg Leu Asn Ile Leu Pro Phe Arg Val Ala Ala Tyr Asp
290 295 300
Lys Thr Gln Gly Lys Met Ala Phe Phe Asp Pro Ser Arg Pro Gln Asp
305 310 315 320
Phe Leu Phe Ile Ser Gly Thr Lys Met Arg Thr Leu Ala Lys Asn Asn
325 330 335
Glu Asn Pro Pro Asp Gly Phe Met Cys Pro Gly Gly Trp Lys Val Leu
340 345 350
Val Asp Tyr Tyr Glu Ser Leu Thr Pro Ala Gly Asn Gly Arg Leu Pro
355 360 365
Glu Val Val Pro Val
370

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..747
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ctcttcatta	tcttcaaaat	cgctcgagag	tgagaactct	actcttcttc	ttcttctccc	60
goccatagcta	caatgcttag	tctctcaata	gctaagcgcg	ggacggCggc	gatttttctg	120
agaggaactg	cttcggcgac	ttcaacttct	tcttcattcc	atggtgtcag	aatccagcac	180
cagggtttctg	ctcgcgtccc	cgcgcgcgcg	acgatatcgt	cgctcgtctcc	taaaccgtcg	240
gtgggtgatga	tgtcgaaaaa	agagggcgaa	ttgaaagaga	taagatcgaa	gacgacggag	300
cagttacaag	aggagggttg	tgaccttaaa	ggtgagctct	ttatgcttcg	tctccagaaa	360
tcggcaagga	atgagttcaa	atctagcGac	ttctgctgta	tgaagaaaaca	agttgtctcg	420
atgttgacg	ttaaaagaga	gagggagatc	aaagaaggga	taaagaaaaa	gttgtcgag	480
aaacttgaca	gacaatggaa	gaacaagcata	gtaccaagac	cacctccgtc	tctgaagaaa	540
cttcaagaag	aagaagctgc	agaagaaGca	gctgaagctg	ctaaatctgc	ttgaaaaaac	600
ccgctattga	tttatggtct	cttctctgtt	gtttcctcga	gatgttgta	atctctgtta	660
tttgttgctg	aaccatctg	tattgttttt	tcttttggtg	taaacacttt	ccttatcaag	720
tagtttcat	gaatccctta	aagattg				

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..173
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Met	Leu	Ser	Leu	Ser	Ile	Ala	Thr	Pro	Gly	Thr	Ala	Ala	Ile	Phe	Arg
1		5						10					15		
Arg	Gly	Thr	Ala	Ser	Ala	Thr	Ser	Thr	Ser	Ser	Ser	Phe	His	Gly	Val
		20					25						30		

Arg	Ile	Gln	His	Gln	Val	Ser	Ala	Arg	Val	Pro	Ala	Ala	Ala	Thr	Ile
	35						40					45			
Ser	Ser	Ser	Ser	Pro	Lys	Pro	Ser	Val	Val	Met	Met	Ser	Lys	Arg	Glu
	50					55					60				
Ala	Glu	Leu	Lys	Glu	Ile	Arg	Ser	Lys	Thr	Thr	Glu	Gln	Leu	Gln	Glu
	65				70					75					80
Glu	Val	Val	Asp	Leu	Lys	Gly	Glu	Leu	Phe	Met	Leu	Arg	Leu	Gln	Lys
			85						90					95	
Ser	Ala	Arg	Asn	Glu	Phe	Lys	Ser	Ser	Asp	Phe	Arg	Arg	Met	Lys	Lys
			100						105				110		
Gln	Val	Ala	Arg	Met	Leu	Thr	Val	Lys	Arg	Glu	Arg	Glu	Ile	Lys	Glu
			115				120						125		
Gly	Ile	Lys	Lys	Arg	Leu	Ser	Arg	Lys	Leu	Asp	Arg	Gln	Trp	Lys	Lys
	130					135					140				
Ser	Ile	Val	Pro	Arg	Pro	Pro	Pro	Ser	Leu	Lys	Lys	Leu	Gln	Glu	Glu
	145				150					155					160
Glu	Ala	Ala	Glu	Glu	Ala	Ala	Glu	Ala	Ala	Lys	Ser	Ala			
			165						170						

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1565818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Met	Met	Ser	Lys	Arg	Glu	Ala	Glu	Leu	Lys	Glu	Ile	Arg	Ser	Lys	Thr
1			5						10					15	
Thr	Glu	Gln	Leu	Gln	Glu	Glu	Val	Val	Asp	Leu	Lys	Gly	Glu	Leu	Phe
			20					25					30		
Met	Leu	Arg	Leu	Gln	Lys	Ser	Ala	Arg	Asn	Glu	Phe	Lys	Ser	Ser	Asp
			35				40					45			
Phe	Arg	Arg	Met	Lys	Lys	Gln	Val	Ala	Arg	Met	Leu	Thr	Val	Lys	Arg
	50				55					60					
Glu	Arg	Glu	Ile	Lys	Glu	Gly	Ile	Lys	Lys	Arg	Leu	Ser	Arg	Lys	Leu
	65				70				75					80	
Asp	Arg	Gln	Trp	Lys	Lys	Ser	Ile	Val	Pro	Arg	Pro	Pro	Pro	Ser	Leu
			85					90					95		
Lys	Lys	Leu	Gln	Glu	Glu	Ala	Ala	Glu	Glu	Ala	Ala	Glu	Ala	Ala	
			100				105					110			
Lys	Ser	Ala													
			115												

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1565819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Met	Ser	Lys	Arg	Glu	Ala	Glu	Leu	Lys	Glu	Ile	Arg	Ser	Lys	Thr	Thr
1				5					10					15	
Glu	Gln	Leu	Gln	Glu	Glu	Val	Val	Asp	Leu	Lys	Gly	Glu	Leu	Phe	Met

	20		25		30
Leu Arg Leu Gln Lys Ser Ala	Arg Asn Glu Phe	Lys Ser Ser Asp Phe			
35	40	45			
Arg Arg Met Lys Lys Gln Val Ala Arg Met Leu Thr Val Lys Arg Glu					
50	55	60			
Arg Glu Ile Lys Glu Gly Ile Lys Lys Arg Leu Ser Arg Lys Leu Asp					
65	70	75		80	
Arg Gln Trp Lys Lys Ser Ile Val Pro Arg Pro Pro Ser Leu Lys					
85	90	95			
Lys Leu Gln Glu Glu Ala Ala Glu Glu Ala Ala Glu Ala Lys					
100	105	110			
Ser Ala					

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2216

(D) OTHER INFORMATION: / Ceres Seq. ID 1565820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ggtttttcgcg gacccatcga acctttcttc tctttctctt ctgactcctt agccgacgac	60
acagagaaga agaagacgaa gacgttgagg agtcacatca aagcttaaac ctttcgtgat	120
ttattctcct tttcccgagg ttcggattaa tttttcaaat tccgacgaaa ttcgctatct	180
ctctggtgctt gacgtgctta gctaaagtga gcagagagag tacaattgtt tatgttttgt	240
taaaattaag agattcttgg caaaattctg aagtagcagc agtagctgtg ttttgtgttc	300
atagagaagt ggagcagaag aatttccgag tgtttccgtt aactcaaatg caatggacaa	360
cgctgaatat accgacacag atttggtgtt tgccgttaga aaggcccttg caactgtcca	420
aaatggagat accgacgatt atagtgcagt taaaacagtg atgtgcctta cagaagacgc	480
tgatttcgat gcagtggcac agcttgagac agtcttgaaa agtctatcac tttccggttg	540
ttggatagat ttagtttcat ataaagatct tcttgaagct atttttaaga tgagcttgtg	600
gtatcatagt cacagaccta gtgtaattga tgcattgggt gacctaatca tatcactggc	660
cgctactagt ggaataatct tggatccttg ttggaatag ctcgtaagaa atttcagtca	720
acctactttt aagcataaag ttccacaacac ccagtttagt aaaaagatgc aggaagtcca	780
tcacacgggtg catgcagcctg ttccacaagt tctttattta attcctcttg ctccctggaa	840
tttagttgct atacttgcgc agaacatgcg taaaattgac aaaaaggacc ctctctatgt	900
gacataatgt gataacctct tgaggttgga gaatagctca atcggagaag ttgttggcag	960
cgtagtattct atgatgcaa tggagaggat gctagattta gatttggtaa gtgtagtgta	1020
tgactctaat ggaggcatct ttgatatgga acttgaagat cgagtggaaa gcaacttgaa	1080
tgaaggagac gagtttccag tgggggctct aaaaacaaat acttcagggt gaaatgtagt	1140
ctctggaactg ttggacaatt tgatggtcct attttttcat catctagaat cctgtcaaaa	1200
ctctgtatcgt ttgatgaga tccgtgaaat tgtggtgtga gatttgcag taagcttgtt	1260
gacataatct tctccagcaa cacatgtcga cttactagga tgagtgcagt ggcttatcta	1320
gctagtctatt tgtctcgttg aaggtttttg cctgcttctt ttgtggctag catgttgaaa	1380
agatttggttg acgagtgtgc ggaatatctg ggaacatgca atgatgatgt gaagccagaa	1440
gcacatcaag tgttctattc tggatgtcag gcaatctgtt atgtgctagt ctccgaaatg	1500
agatccatag tggagattct tgcctttcaa tgcagtttta gatcatatga gtccaattta	1560
tctcacaacac taaaccacac actgggtgtg tttccatctg tagtttccga gtccctttaa	1620
caagccaaag ctggtgtgtct gtccatttgt tcaRgaAtcc ttcatttttg atgacctaca	1680
cgagtctgag ctctctcgtgt cttttggttg ctttgaagg cttagacacat tcttcccggt	1740
tgaccctgtc ttgttgaaaa tgtctagcac ctacatctcc ccgaactcca acttcttggtc	1800
aaatgttgaaa acgacttatg gagaagatgg tgacgaagag ctttggtagt aggtcatagt	1860
gaatggagat gcagacagat cggaaggaacc tgacgatgac gtggaacttg atagtggagt	1920
gaacacagat tctacaactc cgaaacactc tttcatgcga gaacacagaa ggctcttgaa	1980
gatgccttca agaatcagac catccactag tctctctgaa tctctcttaa tctaatagtc	2040
atagagagag ggaatgcaat tttgcaatgt aggtttctta ttacaatctc ttagctagt	2100
cgtaaactct aaaaaaaga agttgacatg agttttgtgc gagtctgtgg tattatctga	2160

tcgcacgtgtg tttttagca aaattttgaa gaacatctat gaagtaatat ttatgtc

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..310

(D) OTHER INFORMATION: / Ceres Seq. ID 1565821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Met	Gly	Ala	Glu	Phe	Pro	Ser	Val	Pro	Phe	Asn	Ser	Asn	Ala	Met	
1			5				10						15		
Asp	Asn	Ala	Glu	Tyr	Thr	Asp	Thr	Asp	Leu	Val	Phe	Ala	Val	Arg	Lys
			20				25						30		
Ala	Leu	Ala	Ser	Val	Gln	Asn	Gly	Asp	Thr	Asp	Asp	Tyr	Ser	Gln	Leu
			35				40					45			
Lys	Thr	Val	Met	Cys	Leu	Thr	Glu	Asp	Ala	Asp	Phe	Asp	Ala	Val	Ala
			50				55				60				
Gln	Leu	Glu	Thr	Val	Leu	Lys	Ser	Leu	Ser	Val	Ser	Val	Ala	Trp	Ile
			65				70				75			80	
Asp	Leu	Val	His	His	Lys	Asp	Leu	Leu	Glu	Ala	Ile	Phe	Lys	Met	Ser
							85				90			95	
Leu	Trp	Tyr	His	Ser	His	Arg	Pro	Ser	Val	Met	Asp	Ala	Leu	Val	Asp
							100				105			110	
Leu	Ile	Ile	Ser	Leu	Ala	Ala	Thr	Ser	Gly	Lys	Tyr	Leu	Asp	Pro	Cys
							115				120			125	
Leu	Asn	Met	Leu	Val	Arg	Asn	Phe	Ser	Gln	Pro	Thr	Phe	Lys	His	Lys
							130				135			140	
Val	Ser	Gln	Thr	Gln	Leu	Val	Lys	Lys	Met	Gln	Glu	Val	His	Pro	Arg
							145				150			155	
Val	His	Ala	Ala	Leu	His	Lys	Ile	Ser	Tyr	Leu	Ile	Pro	Leu	Ala	Pro
							165				170			175	
Trp	Asn	Leu	Val	Ser	Ile	Leu	Ala	Gln	Asn	Met	Arg	Lys	Ile	Asp	Lys
							180				185			190	
Lys	Asp	Pro	Ser	Ile	Val	Thr	Tyr	Val	Asp	Asn	Leu	Leu	Arg	Leu	Glu
							195				200			205	
Asn	Ser	Ser	Ile	Gly	Glu	Val	Val	Gly	Ser	Val	Ile	Leu	Met	Met	Ala
							210				215			220	
Met	Glu	Arg	Met	Leu	Asp	Leu	Asp	Leu	Val	Ser	Gly	Cys	Asp	Asp	Ser
							225				230			235	
Asn	Gly	Gly	Met	Phe	Asp	Met	Glu	Leu	Glu	Asp	Ala	Val	Glu	Ser	Thr
							245				250			255	
Met	Asn	Glu	Gly	Asp	Glu	Phe	Pro	Val	Gly	Ala	Leu	Lys	Gln	Asn	Thr
							260				265			270	
Ser	Gly	Gly	Asn	Val	Val	Ser	Glu	Leu	Leu	Asp	Lys	Leu	Met	Val	Leu
							275				280			285	
Phe	Phe	His	His	Leu	Glu	Ser	Cys	Gln	Asn	Ser	Asp	Arg	Leu	Asp	Glu
							290				295			300	
Ile	Leu	Lys	Ile	Val	Val										
							305				310				

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..295

(D) OTHER INFORMATION: / Ceres Seq. ID 1565822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Met Asp Asn Ala Glu Tyr Thr Asp Thr Asp Leu Val Phe Ala Val Arg
1 5 10 15
Lys Ala Leu Ala Ser Val Gln Asn Gly Asp Thr Asp Asp Tyr Ser Gln
20 25 30
Leu Lys Thr Val Met Cys Leu Thr Glu Asp Ala Asp Phe Asp Ala Val
35 40 45
Ala Gln Leu Glu Thr Val Leu Lys Ser Leu Ser Val Ser Val Ala Trp
50 55 60
Ile Asp Leu Val His His Lys Asp Leu Leu Glu Ala Ile Phe Lys Met
65 70 75 80
Ser Leu Trp Tyr His Ser His Arg Pro Ser Val Met Asp Ala Leu Val
85 90 95
Asp Leu Ile Ile Ser Leu Ala Ala Thr Ser Gly Lys Tyr Leu Asp Pro
100 105 110
Cys Leu Asn Met Leu Val Arg Asn Phe Ser Gln Pro Thr Phe Lys His
115 120 125
Lys Val Ser Gln Thr Gln Leu Val Lys Lys Met Gln Glu Val His Pro
130 135 140
Arg Val His Ala Ala Leu His Lys Ile Ser Tyr Leu Ile Pro Leu Ala
145 150 155 160
Pro Trp Asn Leu Val Ser Ile Leu Ala Gln Asn Met Arg Lys Ile Asp
165 170 175
Lys Lys Asp Pro Ser Ile Val Thr Tyr Val Asp Asn Leu Leu Arg Leu
180 185 190
Glu Asn Ser Ser Ile Gly Glu Val Val Gly Ser Val Ile Leu Met Met
195 200 205
Ala Met Glu Arg Met Leu Asp Leu Asp Leu Val Ser Gly Cys Asp Asp
210 215 220
Ser Asn Gly Gly Met Phe Asp Met Glu Leu Glu Asp Ala Val Glu Ser
225 230 235 240
Thr Met Asn Glu Gly Asp Glu Phe Pro Val Gly Ala Leu Lys Gln Asn
245 250 255
Thr Ser Gly Gly Asn Val Val Ser Glu Leu Leu Asp Lys Leu Met Val
260 265 270
Leu Phe Phe His His Leu Glu Ser Cys Gln Asn Ser Asp Arg Leu Asp
275 280 285
Glu Ile Leu Lys Ile Val Val
290 295

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..259

(D) OTHER INFORMATION: / Ceres Seq. ID 1565823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met Cys Leu Thr Glu Asp Ala Asp Phe Asp Ala Val Ala Gln Leu Glu
1 5 10 15
Thr Val Leu Lys Ser Leu Ser Val Ser Val Ala Trp Ile Asp Leu Val
20 25 30
His His Lys Asp Leu Leu Glu Ala Ile Phe Lys Met Ser Leu Trp Tyr
35 40 45
His Ser His Arg Pro Ser Val Met Asp Ala Leu Val Asp Leu Ile Ile

(1) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
FEATURES:

(A) NAME/KEY: -

(D) OTHER INFORMATION

ccactctcgt tgctgattcc atttatcggt cttattgacc c

caccatc aacattgtgg tcattggcca cgtcgaattct c

gacctgtgac	tacaagttgt	gtgtgtattga	caagctgtgc	attgtagagc	tccgaagaag	240
gcttgcattg	atgaacaaga	gtgtctctca	taoagctatg	ttgttggaac	aactaagaag	300
tgagctgtga	ctgtgtatca	ctctgtgcat	tgctctctgg	aatgttcgaa	accacaagt	360
ctaactgaac	cgattgtatg	ctccttgtaa	tcgtgtattc	atgcaaac	tgatcactg	420
taactccaa	gctgattgtg	ctgtctctat	cattgactcc	acctactgtg	gttttgagc	480
tggtatctcc	aaggtatgtc	agaccctgtc	gaagctctc	cttctgttca	cccttggtg	540
acaagcagat	atctcgtgtt	gtacaagaat	ggatgccact	acccccaagt	actccaaagc	600
caggtacgat	gaatcatca	aggagttgtc	ttctcactg	aagaagatgt	gttcaacacc	660
gcacaaactc	ccatttgtgc	ccatctctgc	atttgagggt	gacacatga	ttgagaagtc	720
caccacaact	gactgtgata	agggacaac	ctctcttgag	gcctctgacc	agatcaacga	780
gcccaagaag	cgctcagaca	agccctcttc	ttctccaact	caggaatgat	acaagaatgg	840
tggtatttga	acggtgcga	tgggaactgt	tgagactgtg	atgatcaacg	ctggtgatgt	900
ttgtagacctt	gtcccacag	tgtagcacac	tgaggctca	ttctgttgga	tgcaacacga	960
gtctcttctt	gaggcacttc	caggtgcaca	cgttgggttc	aatgttaaga	attgttctgt	1020
caaggaattc	aagagagagg	actcgtcatc	caactccaag	tgagaccttc	ccaaggggtc	1080
tgctaatctc	actcccgaag	tcacatctca	gaaccaccc	ggctcagatt	tgaacggtta	1140
gcgcccaagc	cttgattgtc	caactctcca	cattgcagtc	aagtctctct	agatcctgtac	1200
caagattgac	agagctgtgt	gtaaggagat	tgaagaagg	cttaaatctc	tgagaatgtg	1260
taatctgtat	atgtcaaga	gaactccaac	acagccatga	ccttgtagaa	cctctctga	1320

gtacccacca	cttgagcgtt	tgcgtgtgag	ggacatgagg	cagactgttg	cagtcggtgt	1380
tatcaagagt	gttgacaaga	aggacccaac	tgagccaag	gttaccaagg	ctgcagtcac	1440
gaagggtgcc	aagtgaactc	tgaacatcaa	aactctttcc	gctgatgaaa	tgaaggacta	1500
ttttatgttc	tttactttag	tagtttggt	tttggttggt	tgtttgtgtt	accgcttcgt	1560
ttattctcgc	toggagctca	attctcgga	ttgggttcct	gacggaggt	gpcgaggtg	1620
cttgccactc	gagcttccgt	tttatttctt	ttgttttggt	ttatgatttt	gaaccttttt	1680
ggatattcgg	ttatattgata	tttctgtcat	tcctgcc			

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 449 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..449

(D) OTHER INFORMATION: / Ceres Seq. ID 1565829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Met	Gly	Lys	Lys	Lys	Phe	His	Ile	Asn	Ile	Val	Val	Ile	Gly	His	Val
1			5					10					15		
Asp	Ser	Gly	Lys	Ser	Thr	Thr	Thr	Gly	His	Leu	Ile	Tyr	Lys	Leu	Gly
			20					25					30		
Gly	Ile	Asp	Lys	Arg	Val	Ile	Glu	Arg	Phe	Glu	Lys	Glu	Ala	Ala	Glu
			35					40				45			
Met	Asn	Lys	Arg	Ser	Phe	Lys	Tyr	Ala	Trp	Val	Leu	Asp	Lys	Leu	Lys
			50					55				60			
Ala	Glu	Arg	Glu	Arg	Gly	Ile	Thr	Ile	Asp	Ile	Ala	Leu	Trp	Lys	Phe
			65					70				75			80
Glu	Thr	Thr	Lys	Tyr	Tyr	Cys	Thr	Val	Ile	Asp	Ala	Pro	Gly	His	Arg
			85					90					95		
Asp	Phe	Ile	Lys	Asn	Met	Ile	Thr	Gly	Thr	Ser	Gln	Ala	Asp	Cys	Ala
			100					105					110		
Val	Leu	Ile	Asp	Ser	Thr	Thr	Gly	Gly	Phe	Glu	Ala	Gly	Ile	Ser	
			115					120				125			
Lys	Asp	Gly	Gln	Thr	Arg	Glu	His	Ala	Leu	Leu	Ala	Phe	Thr	Leu	Gly
			130					135				140			
Val	Lys	Gln	Met	Ile	Cys	Cys	Cys	Asn	Lys	Met	Asp	Ala	Thr	Thr	Pro
			145					150				155			160
Lys	Tyr	Ser	Lys	Ala	Arg	Tyr	Asp	Glu	Ile	Ile	Lys	Glu	Val	Ser	Ser
			165					170					175		
Tyr	Leu	Lys	Lys	Val	Gly	Tyr	Asn	Pro	Asp	Lys	Ile	Pro	Phe	Val	Pro
			180					185					190		
Ile	Ser	Gly	Phe	Glu	Gly	Asp	Asn	Met	Ile	Glu	Arg	Ser	Thr	Asn	Leu
			195					200				205			
Asp	Trp	Tyr	Lys	Gly	Pro	Thr	Leu	Leu	Glu	Ala	Leu	Asp	Gln	Ile	Asn
			210					215				220			
Glu	Pro	Lys	Arg	Pro	Ser	Asp	Lys	Pro	Leu	Arg	Leu	Pro	Leu	Gln	Asp
			225					230				235			240
Val	Tyr	Lys	Ile	Gly	Gly	Ile	Gly	Thr	Val	Pro	Val	Gly	Arg	Val	Glu
			245					250					255		
Thr	Gly	Met	Ile	Lys	Pro	Gly	Met	Val	Val	Thr	Phe	Ala	Pro	Thr	Gly
			260					265					270		
Leu	Thr	Thr	Glu	Val	Lys	Ser	Val	Glu	Met	His	His	Glu	Ser	Leu	Leu
			275					280				285			
Glu	Ala	Leu	Pro	Gly	Asp	Asn	Val	Gly	Phe	Asn	Val	Lys	Asn	Val	Ala
			290					295				300			
Val	Lys	Asp	Leu	Lys	Arg	Gly	Tyr	Val	Ala	Ser	Asn	Ser	Lys	Asp	Asp
			305					310				315			320
Pro	Ala	Lys	Gly	Ala	Ala	Asn	Phe	Thr	Ser	Gln	Val	Ile	Ile	Met	Asn
			325					330					335		

His	Pro	Gly	Gln	Ile	Gly	Asn	Gly	Tyr	Ala	Pro	Val	Leu	Asp	Cys	His	
			340					345					350			
Thr	Ser	His	Ile	Ala	Val	Lys	Phe	Ser	Glu	Ile	Leu	Thr	Lys	Ile	Asp	
		355					360					365				
Arg	Arg	Ser	Gly	Lys	Glu	Ile	Glu	Lys	Glu	Pro	Lys	Phe	Leu	Lys	Asn	
		370				375					380					
Gly	Asp	Ala	Gly	Met	Val	Lys	Met	Thr	Pro	Thr	Lys	Pro	Met	Val	Val	
	385				390				395					400		
Glu	Thr	Phe	Ser	Glu	Tyr	Pro	Pro	Leu	Gly	Arg	Phe	Ala	Val	Arg	Asp	
			405					410					415			
Met	Arg	Gln	Thr	Val	Ala	Val	Gly	Val	Ile	Lys	Ser	Val	Asp	Lys	Lys	
		420					425					430				
Asp	Pro	Thr	Gly	Ala	Lys	Val	Thr	Lys	Ala	Ala	Val	Lys	Lys	Gly	Ala	
		435					440					445				
Lys																

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..401

(D) OTHER INFORMATION: / Ceres Seq. ID 1565830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Met	Asn	Lys	Arg	Ser	Phe	Lys	Tyr	Ala	Trp	Val	Leu	Asp	Lys	Leu	Lys	
1			5				10				15					
Ala	Glu	Arg	Glu	Arg	Gly	Ile	Thr	Ile	Asp	Ile	Ala	Leu	Trp	Lys	Phe	
		20					25				30					
Glu	Thr	Thr	Lys	Tyr	Tyr	Cys	Thr	Val	Ile	Asp	Ala	Pro	Gly	His	Arg	
		35				40					45					
Asp	Phe	Ile	Lys	Asn	Met	Ile	Thr	Gly	Thr	Ser	Gln	Ala	Asp	Cys	Ala	
	50				55					60						
Val	Leu	Ile	Ile	Asp	Ser	Thr	Thr	Gly	Gly	Phe	Glu	Ala	Gly	Ile	Ser	
	65			70				75					80			
Lys	Asp	Gly	Gln	Thr	Arg	Glu	His	Ala	Leu	Leu	Ala	Phe	Thr	Leu	Gly	
			85					90					95			
Val	Lys	Gln	Met	Ile	Cys	Cys	Cys	Asn	Lys	Met	Asp	Ala	Thr	Thr	Pro	
		100					105					110				
Lys	Tyr	Ser	Lys	Ala	Arg	Tyr	Asp	Glu	Ile	Ile	Lys	Glu	Val	Ser	Ser	
	115					120					125					
Tyr	Leu	Lys	Lys	Val	Gly	Tyr	Asn	Pro	Asp	Lys	Ile	Pro	Phe	Val	Pro	
	130				135						140					
Ile	Ser	Gly	Phe	Glu	Gly	Asp	Asn	Met	Ile	Glu	Arg	Ser	Thr	Asn	Leu	
	145			150					155					160		
Asp	Trp	Tyr	Lys	Gly	Pro	Thr	Leu	Leu	Glu	Ala	Leu	Asp	Gln	Ile	Asn	
			165					170					175			
Glu	Pro	Lys	Arg	Pro	Ser	Asp	Lys	Pro	Leu	Arg	Leu	Pro	Leu	Gln	Asp	
		180					185					190				
Val	Tyr	Lys	Ile	Gly	Gly	Ile	Gly	Thr	Val	Pro	Val	Gly	Arg	Val	Glu	
		195				200						205				
Thr	Gly	Met	Ile	Lys	Pro	Gly	Met	Val	Val	Thr	Phe	Ala	Pro	Thr	Gly	
		210			215						220					
Leu	Thr	Thr	Glu	Val	Lys	Ser	Val	Glu	Met	His	His	Glu	Ser	Leu	Leu	
	225				230				235					240		
Glu	Ala	Leu	Pro	Gly	Asp	Asn	Val	Gly	Phe	Asn	Val	Lys	Asn	Val	Ala	
			245					250				255				
Val	Lys	Asp	Leu	Lys	Arg	Gly	Tyr	Val	Ala	Ser	Asn	Ser	Lys	Asp	Asp	

(2) INFORMATION FOR SEO ID NO:104:

(A) LENGTH: 348 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1565831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met	Ile	Thr	Gly	5	Thr	Ser	Gln	Ala	Asp	Cys	10	Ala	Val	Leu	Ile	Ile	Asp
1	Ser	Thr	Thr	Gly	Gly	Phe	Glu	Ala	Gly	Ile	25	Ser	Lys	Asp	Gly	Gln	Thr
			20												30		
Arg	Glu	His	Ala	Leu	Leu	Ala	Phe	Thr	Leu	Gly	Val	Lys	Gln	Met	Ile		
		35						40					45				
Cys	Cys	Cys	Asn	Lys	Met	Asp	Ala	Thr	Thr	Pro	Lys	Tyr	Ser	Lys	Ala		
		50				55					60						
Arg	Tyr	Asp	Glu	Ile	Ile	Lys	Glu	Val	Ser	Ser	Tyr	Leu	Lys	Lys	Val		
65					70					75					80		
Gly	Tyr	Asn	Pro	Asp	Lys	Ile	Pro	Phe	Val	Pro	Ile	Ser	Gly	Phe	Glu		
				85					90					95			
Gly	Asp	Asn	Met	Ile	Glu	Arg	Ser	Thr	Asn	Leu	Asp	Trp	Tyr	Lys	Gly		
			100					105					110				
Pro	Thr	Leu	Leu	Glu	Ala	Leu	Asp	Gln	Ile	Asn	Glu	Pro	Lys	Arg	Pro		
		115				120						125					
Ser	Asp	Lys	Pro	Leu	Arg	Leu	Pro	Leu	Gln	Asp	Val	Tyr	Lys	Ile	Gly		
						135					140						
Gly	Ile	Gly	Thr	Val	Pro	Val	Gly	Arg	Val	Glu	Thr	Gly	Met	Ile	Lys		
145					150					155					160		
Pro	Gly	Met	Val	Val	Thr	Phe	Ala	Pro	Thr	Lys	Leu	Thr	Thr	Glu	Val		
				165					170					175			
Lys	Ser	Val	Glu	Met	His	His	Glu	Ser	Leu	Leu	Glu	Ala	Leu	Pro	Gly		
			180					185					190				
Asp	Asn	Val	Gly	Phe	Asn	Val	Lys	Asn	Val	Ala	Val	Lys	Asp	Leu	Lys		
		195				200					205						
Arg	Gly	Tyr	Val	Ala	Ser	Asn	Ser	Lys	Asp	Asp	Pro	Ala	Lys	Gly	Ala		
						215					220						
Ala	Asn	Phe	Thr	Ser	Gln	Val	Ile	Ile	Met	Asn	His	Pro	Gly	Gln	Ile		
225					230					235					240		

Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His Thr Ser His Ile Ala
245 250 255
Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp Arg Arg Ser Gly Lys
260 265 270
Glu Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn Gly Asp Ala Gly Met
275 280 285
Val Lys Met Thr Pro Thr Lys Pro Met Val Val Glu Thr Phe Ser Glu
290 295 300
Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr Val
305 310 315 320
Ala Val Gly Val Ile Lys Ser Val Asp Lys Lys Asp Pro Thr Gly Ala
325 330 335
Lys Val Thr Lys Ala Ala Val Lys Lys Gly Ala Lys
340 345

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..635
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

tctctctaca	acaaaatcag	cgacaGctca	aacgtcgata	ttttctccg	gctttcttag	60
ggttttaatt	ttctttccga	tcagagatta	atggcgactc	tagactccga	cgttaccatg	120
attctcgcgc	gagaagcctc	cagcagcgta	gccgcgtcgt	cttccaaaca	gaaagctaaag	180
cgattcgaaa	ttaagaagtg	gagcgccgtt	gctctctggg	cttgggatat	cgttgttgac	240
aactgtgcga	tctgcagaaa	ccacatcatg	gatotttgta	tcgagtgtoa	ggctaatacg	300
gccagtgcga	caagtgaaga	gtgcactgta	gcttgggggg	tttgcaatca	cgctttccac	360
tttcaactgca	tcagcagatg	gctaaagact	cgtcaagttt	gtccattgga	taacagttag	420
tgggagtttc	agaaatatgg	tcactaaatc	aacaaatggg	tccagcaagc	atgtgtctaa	480
tcgtgaagac	atcagggttc	tttggttacc	accgcgatg	ataactaaag	attgttcaag	540
tttttgcctt	tttttttgta	ctgtatttta	caatttggtg	aaacagagat	ttactgttca	600

gtgttcaacta aacctattat ggtgtgtgctt tgggt

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met Ala Thr Leu Asp Ser Asp Val Thr Met Ile Pro Ala Gly Glu Ala	
1 5 10 15	
Ser Ser Ser Val Ala Ala Ser Ser Ser Asn Lys Lys Ala Lys Arg Phe	
20 25 30	
Glu Ile Lys Lys Trp Ser Ala Val Ala Leu Trp Ala Trp Asp Ile Val	
35 40 45	
Val Asp Asn Cys Ala Ile Cys Arg Asn His Ile Met Asp Leu Cys Ile	
50 55 60	
Glu Cys Gln Ala Asn Gln Ala Ser Ala Thr Ser Glu Glu Cys Thr Val	
65 70 75 80	
Ala Trp Gly Val Cys Asn His Ala Phe His Phe His Cys Ile Ser Arg	
85 90 95	

Trp Leu Lys Thr Arg Gln Val Cys Pro Leu Asp Asn Ser Glu Trp Glu
100 105 110
Phe Gln Lys Tyr Gly His
115

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met Ile Pro Ala Gly Glu Ala Ser Ser Ser Val Ala Ala Ser Ser Ser
1 5 10 15
Asn Lys Lys Ala Lys Arg Phe Glu Ile Lys Lys Trp Ser Ala Val Ala
20 25 30
Leu Trp Ala Trp Asp Ile Val Val Asp Asn Cys Ala Ile Cys Arg Asn
35 40 45
His Ile Met Asp Leu Cys Ile Glu Cys Gln Ala Asn Gln Ala Ser Ala
50 55 60
Thr Ser Glu Glu Cys Thr Val Ala Trp Gly Val Cys Asn His Ala Phe
65 70 75 80
His Phe His Cys Ile Ser Arg Trp Leu Lys Thr Arg Gln Val Cys Pro
85 90 95
Leu Asp Asn Ser Glu Trp Glu Phe Gln Lys Tyr Gly His
100 105

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met Val Thr Lys Ser Thr Asn Gly Ser Ser Lys His Val Ser Asn Arg
1 5 10 15
Glu Asp Ile Arg Phe Ile Trp Leu Pro His Met Ile Thr Lys Asp
20 25 30
Cys Ser Ser Phe Cys Pro Phe Phe Gly Thr Val Phe Tyr Asn Leu Trp
35 40 45
Lys Gln Arg Phe Thr Val Gln Cys Ser Leu Asn Leu Leu Trp Leu Cys
50 55 60
Phe Gly
65

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..1618

(D) OTHER INFORMATION: / Ceres Seq. ID 1565840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

aatagattag	ttttgtactt	ctgttacgtg	gtgattatta	aaacttgtaa	taacagtata	60
atctggtttt	gttgggtgag	attgatgatt	tcaacattgc	aaagaaggaa	gaggacattg	120
ggttctaagc	tggatttggt	gggtgtctct	tcatgtctcg	acgagctttt	acatctgtgg	180
catggggagt	tgttctgcat	cggttatgta	gaaaacctgt	aatcctcata	ggaaccgctt	240
cagtggttgt	ttttaatact	ctgttttgcc	taagtttaaa	ttcttggatg	gctattatca	300
caagattttg	ccctcggtagt	tccaacgggt	tacttgggtc	tatcaaggct	tacgcaatgg	360
aaatattccg	tgatgagtat	caagggtttg	cactctcagc	agtttagtaca	gcttggggaa	420
ttggactccg	cattggccct	gctataggag	gttttcttgc	tcagcctgca	aagcaataatc	480
caagtttatt	cttcacaggac	tccatttttg	gcaaattttc	ctcttttttg	ccatgtctag	540
caatatccgt	ttttgcattc	ttggtagacca	tagtttcatc	aaggattccg	gaaacattgc	600
acaatcacaa	gttttaatga	gatgagtctt	atgatgctct	caaagatttg	ctctgatgacc	660
ctgaatctaa	taaaagtggca	gagagaaagt	gaaaaagttc	tctcttgacc	aactggccat	720
taatttcaat	tatcatogta	tactgcgtct	tttcaactaca	tgatattggt	tacacagaga	780
tccttttcat	gtgggcaaac	agtcaggaga	aatatggagg	tttgggtatc	tcactgtcag	840
atgttggttt	tgttcttgcc	ttttcaggct	ttgtgtctct	tatctttcag	ctttcgctct	900
actcttacgc	agagaggctt	ttaggaccta	tcatagtttac	acgtatatct	gggagcctag	960
caatggctgt	cttatcatgt	taocccactaa	tagcaaaagt	atctgggtta	gtccttaccg	1020
tgaactgtaac	ttctgcacgc	gtagcaaaaga	gtgttttagg	tactttctgt	ataactggat	1080
tattcatcct	tcaaaaacag	gctgtgagac	aagaccaWag	aggagcagct	aatggaattg	1140
ccatgacagc	gatgtctctt	ttcaaaagcca	taggtccagc	agcagcagga	atcatttttt	1200
cgtggagcga	gaaacgtcag	gggtgtctct	ttctcctcgt	caoccaaagt	gtattcttta	1260
tactgaatgt	gggttttgcca	cttggagttg	tattgacatt	caaacatttt	ctagctgaaa	1320
cacaagaatg	gaaaatgatg	aagattttga	tgttatttcaa	attacataat	cagaaatgat	1380
tgtataatat	atagatYtgt	atgtctgac	caaaagttaga	ttagaaaaat	ggcaagagaa	1440
aaagaaaaaa	aacttgtttg	aattgttgtc	atcatccttt	gtatgtttta	ggacaagtgt	1500
ttcacaataa	tttgtcta	gtgtcagaac	cattgtaaga	aggatttcaat	aatgtttttt	1560
gtacatgatg	tttgcggaat	aatattgaca	agtcgtcaaa	tcctatcctg	agattccct	

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..392

(D) OTHER INFORMATION: / Ceres Seq. ID 1565841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met	Leu	Gly	Arg	Ala	Phe	Thr	Ser	Val	Ala	Trp	Gly	Leu	Val	Ala	Asp
1			5						10					15	
Arg	Tyr	Gly	Arg	Lys	Pro	Val	Ile	Leu	Ile	Gly	Thr	Ala	Ser	Val	Val
			20					25					30		
Val	Phe	Asn	Thr	Leu	Phe	Gly	Leu	Ser	Leu	Asn	Phe	Trp	Met	Ala	Ile
			35					40				45			
Ile	Thr	Arg	Phe	Cys	Leu	Gly	Ser	Phe	Asn	Gly	Leu	Leu	Gly	Pro	Ile
			50				55					60			
Lys	Ala	Tyr	Ala	Met	Glu	Ile	Phe	Arg	Asp	Glu	Tyr	Gln	Gly	Leu	Ala
65					70				75					80	
Leu	Ser	Ala	Val	Ser	Thr	Ala	Trp	Gly	Ile	Gly	Leu	Ile	Ile	Gly	Pro
					85				90					95	
Ala	Ile	Gly	Gly	Phe	Leu	Ala	Gln	Pro	Ala	Lys	Gln	Tyr	Pro	Ser	Leu
			100					105					110		
Phe	Ser	Gln	Asp	Ser	Ile	Phe	Gly	Lys	Phe	Pro	Phe	Phe	Leu	Pro	Cys
			115				120					125			
Leu	Ala	Ile	Ser	Val	Phe	Ala	Phe	Leu	Val	Thr	Ile	Val	Ser	Ser	Arg
			130				135					140			
Ile	Pro	Glu	Thr	Leu	His	Asn	His	Lys	Phe	Asn	Asp	Glu	Ser	Tyr	

145	150	155	160
Asp Ala Leu Lys Asp	Leu Ser Asp Asp	Pro Glu Ser Asn Lys	Val Ala
165	170	175	
Glu Arg Asn Gly Lys	Ser Ser Leu Leu	Asn Asn Trp Pro	Leu Ile Ser
180	185	190	
Ser Ile Ile Val Tyr	Cys Val Phe Ser	Leu His Asp Met	Ala Tyr Thr
195	200	205	
Glu Ile Phe Ser Leu	Trp Ala Asn Ser	Pro Arg Lys Tyr	Gly Gly Leu
210	215	220	
Gly Tyr Ser Thr Ala	Asp Val Gly Ser	Val Leu Ala Phe	Ser Gly Phe
225	230	235	240
Gly Leu Leu Ile Phe	Gln Leu Ser Leu	Tyr Ser Tyr Ala	Glu Arg Leu
245	250	255	
Leu Gly Pro Ile Val	Thr Arg Ile Ser	Gly Ser Leu Ala	Met Val
260	265	270	
Val Leu Ser Cys Tyr	Pro Leu Ile Ala	Lys Leu Ser Gly	Leu Val Leu
275	280	285	
Thr Val Thr Val Thr	Ser Ala Ser Val	Ala Lys Ser Val	Leu Gly Thr
290	295	300	
Ser Ala Ile Thr Gly	Leu Phe Ile Leu	Gln Asn Lys Ala	Val Arg Gln
305	310	315	320
Asp Xaa Arg Gly Ala	Ala Asn Gly Ile	Ala Met Thr Ala	Met Ser Leu
325	330	335	
Phe Lys Ala Ile Gly	Pro Ala Ala Ala	Gly Ile Ile Phe	Ser Trp Ser
340	345	350	
Glu Lys Arg Gln Gly	Ala Ala Phe Leu	Pro Gly Thr Gln	Met Val Phe
355	360	365	
Phe Ile Leu Asn Val	Val Leu Ala Leu	Gly Val Val Leu	Thr Phe Lys
370	375	380	
Pro Phe Leu Ala Glu	Thr Gln Gln		
385	390		

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..347
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Met Ala Ile Ile Thr	Arg Phe Cys Leu	Gly Ser Phe Asn	Gly Leu Leu
1	5	10	15
Gly Pro Ile Lys Ala	Tyr Ala Met Glu	Ile Phe Arg Asp	Glu Tyr Gln
20	25	30	
Gly Leu Ala Leu Ser	Ala Val Ser Thr	Ala Trp Gly Ile	Gly Leu Ile
35	40	45	
Ile Gly Pro Ala Ile	Gly Gly Phe Leu	Ala Gln Pro Ala	Lys Gln Tyr
50	55	60	
Pro Ser Leu Phe Ser	Gln Asp Ser Ile	Phe Gly Lys Phe	Pro Phe Phe
65	70	75	80
Leu Pro Cys Leu Ala	Ile Ser Val Phe	Ala Phe Leu Val	Thr Ile Val
85	90	95	
Ser Ser Arg Ile Pro	Glu Thr Leu His	Asn His Lys Phe	Asn Asp Asp
100	105	110	
Glu Ser Tyr Asp Ala	Leu Lys Asp Leu	Ser Asp Asp Pro	Glu Ser Asn
115	120	125	
Lys Val Ala Glu Arg	Asn Gly Lys Ser	Ser Ser Leu Leu	Asn Asn Trp Pro
130	135	140	

Leu Ile Ser Ser Ile Ile Val Tyr Cys Val Phe Ser Leu His Asp Met
145 150 155 160
Ala Tyr Thr Glu Ile Phe Ser Leu Trp Ala Asn Ser Pro Arg Lys Tyr
165 170 175
Gly Gly Leu Gly Tyr Ser Thr Ala Asp Val Gly Ser Val Leu Ala Phe
180 185 190
Ser Gly Phe Gly Leu Leu Ile Phe Gln Leu Ser Leu Tyr Ser Tyr Ala
195 200 205
Glu Arg Leu Leu Gly Pro Ile Ile Val Thr Arg Ile Ser Gly Ser Leu
210 215 220
Ala Met Val Val Leu Ser Cys Tyr Pro Leu Ile Ala Lys Leu Ser Gly
225 230 235 240
Leu Val Leu Thr Val Thr Val Thr Ser Ala Ser Val Ala Lys Ser Val
245 250 255
Leu Gly Thr Ser Ala Ile Thr Gly Leu Phe Ile Leu Gln Asn Lys Ala
260 265 270
Val Arg Gln Asp Xaa Arg Gly Ala Ala Asn Gly Ile Ala Met Thr Ala
275 280 285
Met Ser Leu Phe Lys Ala Ile Gly Pro Ala Ala Ala Gly Ile Ile Phe
290 295 300
Ser Trp Ser Glu Lys Arg Gln Gly Ala Ala Phe Leu Pro Gly Thr Gln
305 310 315 320
Met Val Phe Phe Ile Leu Asn Val Val Leu Ala Leu Gly Val Val Leu
325 330 335
Thr Phe Lys Pro Phe Leu Ala Glu Thr Gln Gln
340 345

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..324

(D) OTHER INFORMATION: / Ceres Seq. ID 1565843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Glu Ile Phe Arg Asp Glu Tyr Gln Gly Leu Ala Leu Ser Ala Val
1 5 10 15
Ser Thr Ala Trp Gly Ile Gly Leu Ile Ile Gly Pro Ala Ile Gly Gly
20 25 30
Phe Leu Ala Gln Pro Ala Lys Gln Tyr Pro Ser Leu Phe Ser Gln Asp
35 40 45
Ser Ile Phe Gly Lys Phe Pro Phe Phe Leu Pro Cys Leu Ala Ile Ser
50 55 60
Val Phe Ala Phe Leu Val Thr Ile Val Ser Arg Ile Pro Glu Thr
65 70 75 80
Leu His Asn His Lys Phe Asn Asp Asp Glu Ser Tyr Asp Ala Leu Lys
85 90 95
Asp Leu Ser Asp Asp Pro Glu Ser Asn Lys Val Ala Glu Arg Asn Gly
100 105 110
Lys Ser Ser Leu Leu Asn Asn Trp Pro Leu Ile Ser Ser Ile Ile Val
115 120 125
Tyr Cys Val Phe Ser Leu His Asp Met Ala Tyr Thr Glu Ile Phe Ser
130 135 140
Leu Trp Ala Asn Ser Pro Arg Lys Tyr Gly Gly Leu Gly Tyr Ser Thr
145 150 155 160
Ala Asp Val Gly Ser Val Leu Ala Phe Ser Gly Phe Gly Leu Leu Ile
165 170 175
Phe Gln Leu Ser Leu Tyr Ser Tyr Ala Glu Arg Leu Leu Gly Pro Ile

180	185	190
Ile Val Thr Arg Ile Ser Gly Ser Leu Ala Met Val Val Leu Ser Cys		
195	200	205
Tyr Pro Leu Ile Ala Lys Leu Ser Gly Leu Val Leu Thr Val Thr Val		
210	215	220
Thr Ser Ala Ser Val Ala Lys Ser Val Leu Gly Thr Ser Ala Ile Thr		
225	230	235
Gly Leu Phe Ile Leu Gln Asn Lys Ala Val Arg Gln Asp Xaa Arg Gly		
245	250	255
Ala Ala Asn Gly Ile Ala Met Thr Ala Met Ser Leu Phe Lys Ala Ile		
260	265	270
Gly Pro Ala Ala Gly Ile Ile Phe Ser Trp Ser Glu Lys Arg Gln		
275	280	285
Gly Ala Ala Phe Leu Pro Gly Thr Gln Met Val Phe Phe Ile Leu Asn		
290	295	300
Val Val Leu Ala Leu Gly Val Val Leu Thr Phe Lys Pro Phe Leu Ala		
305	310	315
Glu Thr Gln Gln		320

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1108

(D) OTHER INFORMATION: / Ceres Seq. ID 1565863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

agattcaagc atcacacaat cgagttttta gggtttttagc ggttgctctc tcggaagcca	60
gagagaagag ggaagaggaa gtctaattcc tctgcgtttt ttgcaattag ggtttttctca	120
attggaatcg aaaaatggtga cagacaagag caagaaggcg aaaaccgaag aagaaaaacgt	180
cgagcaaatc gatgcagagc ttgtcctctc aatcgaaaaa ctccaagaga tccaagacga	240
ctctgagaag ataaaatgaaa aggctagtga tgaagtgttg gaagtggagc agaaaataaa	300
ttgtataaag aaacctgttt atgacaagcg taacgagatc atcaaaaacca tccctgattt	360
ctgggttaact gottttcttga gtcacctcgc ttttagtgaa cttttgactg aagaagacca	420
aaagattttc aaatatctta gctctcttga tgttgaggat gccaaagatg tgaatctctgg	480
atactctatc actttttctc tcaatcccaa tccatttttt gaagatggaa aactgacaaa	540
gactttttac tttctcgaag aagggaacac caaaatcaac gccacgccta tcaaatggaa	600
agaggggcaa ggcctggcga atggagttaa tcatgagaag aatggaaaca aacgtgcact	660
acctgaagag agctctcttta ctctggttag tgatgctcaa cacaaggagg atgttgagga	720
tgagatgcaa gacgagcagg ttgcagatat catcaaggaa gattttgtgc ccaacctctc	780
cacctacttc aacaatgacg ctgatgaaga ggactttgat ggagacgatg atggagatga	840
agaggagaaa gaaggtgact ctgatgaaga tgatgacgaa gaagacgaag ttggtgagga	900
atgatggcag ggatacccgag aaaccacaty tgcttacatg tcttctctat aacagagtgt	960
gtaaagtgtt gtgtgttgaa aggtKtttta attYttaagc aaaaagtggat tatgacNgac	1020
aacagacaag ctttttaatt ttatttCaCc gtaaatgta tatctgtgtg taagaaacca	1080
ttttcagcct tttgttgaaa aaactctgc	

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1565864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met	Val	Thr	Asp	Lys	Ser	Lys	Lys	Ala	Lys	Thr	Glu	Glu	Glu	Asn	Val
1			5						10					15	
Glu	Gln	Ile	Asp	Ala	Glu	Leu	Val	Leu	Ser	Ile	Glu	Lys	Leu	Gln	Glu
			20					25					30		
Ile	Gln	Asp	Asp	Leu	Glu	Lys	Ile	Asn	Glu	Lys	Ala	Ser	Asp	Glu	Val
			35				40				45				
Leu	Glu	Val	Glu	Gln	Lys	Tyr	Asn	Val	Ile	Arg	Lys	Pro	Val	Tyr	Asp
			50			55					60				
Lys	Arg	Asn	Glu	Ile	Ile	Lys	Thr	Ile	Pro	Asp	Phe	Thr	Leu	Thr	Ala
			65		70				75				80		
Phe	Leu	Ser	His	Pro	Ala	Leu	Gly	Glu	Leu	Thr	Glu	Glu	Asp	Gln	
			85					90					95		
Lys	Ile	Phe	Lys	Tyr	Leu	Ser	Ser	Leu	Asp	Val	Glu	Asp	Ala	Lys	Asp
			100					105					110		
Val	Lys	Ser	Gly	Tyr	Ser	Ile	Thr	Phe	Ser	Phe	Asn	Pro	Asn	Pro	Phe
			115				120						125		
Phe	Glu	Asp	Gly	Lys	Leu	Thr	Lys	Thr	Phe	Thr	Phe	Leu	Glu	Glu	Gly
			130			135					140				
Thr	Thr	Lys	Ile	Thr	Ala	Thr	Pro	Ile	Lys	Trp	Lys	Glu	Gly	Lys	Gly
			145			150					155			160	
Leu	Ala	Asn	Gly	Val	Asn	His	Glu	Lys	Asn	Gly	Asn	Lys	Arg	Ala	Leu
			165					170					175		
Pro	Glu	Glu	Ser	Phe	Phe	Thr	Trp	Phe	Ser	Asp	Ala	Gln	His	Lys	Glu
			180					185					190		
Asp	Val	Glu	Asp	Glu	Met	Gln	Asp	Glu	Gln	Val	Ala	Asp	Ile	Ile	Lys
			195				200					205			
Glu	Asp	Leu	Trp	Pro	Asn	Pro	Leu	Thr	Tyr	Phe	Asn	Asn	Asp	Ala	Asp
			210			215					220				
Glu	Glu	Asp	Phe	Asp	Gly	Asp	Asp	Asp	Gly	Asp	Glu	Glu	Glu	Lys	Glu
			225			230				235				240	
Gly	Asp	Ser	Asp	Glu	Asp	Asp	Asp	Glu	Glu	Asp	Glu	Val	Gly	Glu	Glu
			245					250					255		

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1710 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1710

(D) OTHER INFORMATION: / Ceres Seq. ID 1565871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

atgcaacatt	ataaaatatt	Ttattttcat	aaccacCccc	gatatggctg	ctccacaaaa	60
gaaaccaggc	ctaagtaacg	tggagctact	ttgtaattat	aaagatttat	tgtttcccat	120
aaactcggtta	aatgatttta	gaaactaaaag	taaaatgagc	ttgacactag	agtttctgct	180
tcttctgatt	gtacttatct	tgagtcacca	tgctcattct	ggctctattg	tcaaatctct	240
tcctggtttt	gaaggccccc	ttccttttga	actcgaaacc	gggtacattg	gtattgggtga	300
ggaagaggaa	gtgcaattat	tctactattt	catcaaatct	gagaagaatc	cagaagaaga	360
ccctctcttt	ctatggttaa	gtggaggacc	tggatgttcc	tctcttactg	gcctctcttt	420
tgagaatgga	coggtggcct	tgaagtgcga	ggttttacaat	ggaagtgttc	catcttttgt	480
ctctactaca	tattcatgga	caaagatggc	gaacataata	tctcttgatc	agccagttgg	540
atctggcttc	tcctattcaa	gaactccact	tggtgataaa	attagtgaca	ctgggtgaagt	600
taagaggatt	tatgagtttc	ttcaaaagtg	gttaagcaaa	catcaacaat	ttttttccaa	660
ccctttttac	gttgggtggag	attcttatto	aggtatgatt	gttccacccc	tagttcaaga	720
aatcggaaaa	ggtagttctg	ttaattcata	tcaatcaatc	cccatcacct	tttcttgtaa	780
tattgtttta	ttgtctgtct	ctcaataatt	aacaatatat	acaatgatgc	aggaaattat	840

```
caaaaaaatc tacaggttgt agatatattat ttgttttotta ttttttgtaa tttaaaaaaa    900
tattgaagat taatagtaaat atgttctttac gaaaataggg ttatatcttc ggaaccgga    960
taacagatcac tgaactctgaa caaaactatc agattccata tgctcatgga atggcattaa    1020
tctctgatga actatacaag tcaatggaga gaactctgcaa aggaaattat gtgaaagtgg    1080
attcacttaa cacaanaatgc tataaactaa tcaaagatta tcaaaagtgt attcataaac    1140
tgaataagta tcatatatta ttacctgact gcgataatac atctcctgat tgctttgtaa    1200
ttatataaggt atactctcat aaccttttgg gccacaaca agagcgctcg cgaagctctg    1260
caagtcaata agtggtgacc atgatatgat ggtgccttcc cttgcaactc aagcctggat    1320
aagatctctc aattattcca tcaactgatga ttggaagcct tggatgataa acgatcaaat    1380
tgctggatac acgagaagtt attccaataa gatgacattt gctactatca aagcaagtct    1440
tctgtgtcca acttaataatt tgtattgtcc ttagactgca ataaaaaaga ctttgtttta    1500
attgttttga gttttgttta tttatttttt tgttaaaggg aagtgggaac acagcagagt    1560
ataaaccaaa agagacctct atcatgttca aaagatggat cagtggccag cctttgtaaa    1620
agaggatgat ggtctttggc tatgtagaat aaaactatgt aacataaaaa atgttttgtat    1680
acaatataat catctacttg gtaattaaat
```

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..211

(D) OTHER INFORMATION: / Ceres Seq. ID 1565872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

```
Met Ser Leu Thr Leu Glu Phe Leu Leu Leu Ile Val Leu Ile Leu
1 5 10 15
Ser His His Ala His Ser Gly Ser Ile Val Lys Phe Leu Pro Gly Phe
20 25 30
Glu Gly Pro Leu Pro Phe Glu Leu Glu Thr Gly Tyr Ile Gly Ile Gly
35 40 45
Glu Glu Glu Glu Val Gln Leu Phe Tyr Tyr Phe Ile Lys Ser Glu Lys
50 55 60
Asn Pro Glu Glu Asp Pro Leu Leu Leu Trp Leu Ser Gly Gly Pro Gly
65 70 75 80
Cys Ser Ser Leu Thr Gly Leu Leu Phe Glu Asn Gly Pro Val Ala Leu
85 90 95
Lys Phe Glu Val Tyr Asn Gly Ser Val Pro Ser Leu Val Ser Thr Thr
100 105 110
Tyr Ser Trp Thr Lys Met Ala Asn Ile Ile Phe Leu Asp Gln Pro Val
115 120 125
Gly Ser Gly Phe Ser Tyr Ser Arg Thr Pro Leu Val Asp Lys Ile Ser
130 135 140
Asp Thr Gly Glu Val Lys Arg Ile Tyr Glu Phe Leu Gln Lys Trp Leu
145 150 155 160
Ser Lys His Gln Gln Phe Phe Ser Asn Pro Phe Tyr Val Gly Gly Asp
165 170 175
Ser Tyr Ser Gly Met Ile Val Pro Pro Leu Val Gln Glu Ile Gly Lys
180 185 190
Gly Met Phe Val Asn Ser Tyr Gln Ser Ile Pro Ile His Phe Ser Trp
195 200 205
Asn Ile Val
210
```

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1673 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1673

(D) OTHER INFORMATION: / Ceres Seq. ID 1565880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

```
aatattaatt tcttcaatta accttgataa gagtataaaa agtataaaac ctcgagaaga      60
gtgtgagctg tgggtcaacac ttgagagcca gcacgatgag ctccatatgg gacgttgcaa      120
tgttgatggt agcttttggtg gttgtgagga tcagccactg gctttaccga ttggtcaaac      180
ctaagtgcgc ttggcaagtta ccacctggat cgatgggttt tccaatcatt ggagagactc      240
tcgattttct taagccttgt ggagtcgaag gtatcccaac ctttgtcaag aagaggatga      300
taagtgatgt gcggttgttt gcaacaacaa tttttggttc caaaacccgt gtttcgacag      360
atccggatgt gatccaccag attttccggc aagagaacac gtcttttgag ctaggctatc      420
cagacatatt tgtgaaagta ttggaaaag ataatttgtt ctggaaggaa gtgttctatc      480
acaagtacct ccaaaaaact actatgcaaa ttcttggtct cgaggggttg aagcaaacaa      540
tgttaggaaa catggacaaa gcaacccgcg accatattag gtccattgct agccagggga      600
gcttcaatgt tcgtaagaaa gttgaaaact ttgtagttag gtacatgaca ccaaagctga      660
taagtaacct taacaccagag acgcaatcaa agcttataga taatctcaac gccttcaatc      720
ttgatttggt taagtctctt ttaagactct ctacttgcaa agctgtccac aaagccctca      780
agtcacgtga agaagctatc caggtgatga aagacgttct catgatgaga aaagagacgc      840
gagagaagca agaagacttc tttaaacacg ttctagaaga actggagaaa gacggtagct      900
ttttcgacca aggatcggtc ataaatctca tcttctcttc ggcgtttgcc ttgagagaag      960
gtacctctag ttgtactgtt ttggccgtga agttcatatc caaagaccgc aaagtgtctg      1020
cagagctcaa gcgtgagcat aaggcaattg tagacaacag aaaagataag gaagctggag      1080
ttagctggga agaatataga cacacaatga ctttcaccaa gttggttagc aatgaggtGc      1140
ttgccttagc aaacacgacc cctttgttgt ttcgaaagcg ggtgcaagat gtggaagata      1200
aaggataatc aattccggct ggttggaatt ttggtgttgc accttcagcg gttaattttg      1260
atccgtcaat ctactgagaac ccatttgagt ttaatccgat gagatgggag gggaaagaaa      1320
tgattttggg atctaaaaac ttcatggcgt ttggatatgg agttagactt tgtgtaggtg      1380
cagagttttc gcggttctca atggcaatct tctccatcat tcttggtcca tattacgatt      1440
ttcctaatgt ccaagactcc gagatcattc gttccacatt ccatcaatc accaagatc      1500
tgcttataaa catctctcag tctctacca agtgaaccaa gcatgagctt tccaatatt      1560
aataatcaga tcattatatg caataatctc atttctGct tccgcaaaat ctctggagtc      1620
tttttatgtg taatatgca tctctataat ttttaaaag tatctattt gcc
```

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 479 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..479

(D) OTHER INFORMATION: / Ceres Seq. ID 1565881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

```
Met Ser Ser Ile Trp Asp Val Ala Met Leu Met Val Ala Leu Val Val
1      5      10      15
Val Arg Ile Ser His Trp Leu Tyr Arg Trp Ser Asn Pro Lys Cys Pro
20     25     30
Gly Lys Leu Pro Pro Gly Ser Met Gly Phe Pro Ile Ile Gly Glu Thr
35     40     45
Leu Asp Phe Phe Lys Pro Cys Gly Val Glu Gly Ile Pro Thr Phe Val
50     55     60     65
Lys Lys Arg Met Ile Arg Tyr Gly Pro Leu Phe Arg Thr Asn Ile Phe
70     75     80
Gly Ser Lys Thr Val Val Val Ser Thr Asp Pro Asp Val Ile His Gin Ile
85     90     95
Phe Arg Gln Glu Asn Thr Ser Phe Glu Leu Gly Tyr Pro Asp Ile Phe
100    105    110
Val Lys Val Phe Gly Lys Asp Asn Leu Phe Leu Lys Glu Val Phe Ile
```

[illegible]

(2) INFORMATION FOR SEO ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..471
(D) OTHER INFORMATION: / Ceres Seq. ID 1565882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Met	Leu	Met	Val	Ala	Leu	Val	Val	Val	Arg	Ile	Ser	His	Trp	Leu	Tyr
1				5					10					15	
Arg	Trp	Ser	Asn	Pro	Lys	Cys	Pro	Gly	Lys	Leu	Pro	Pro	Gly	Ser	Met
			20					25					30		

Gly Phe Pro Ile Ile Gly Glu Thr Leu Asp Phe Phe Lys Pro Cys Gly
35 40 45
Val Glu Gly Ile Pro Thr Phe Val Lys Lys Arg Met Ile Arg Tyr Gly
50 55 60
Pro Leu Phe Arg Thr Asn Ile Phe Gly Ser Lys Thr Val Val Ser Thr
65 70 75
Asp Pro Asp Val Ile His Gln Ile Phe Arg Gln Glu Asn Thr Ser Phe
85 90 95
Glu Leu Gly Tyr Pro Asp Ile Phe Val Lys Val Phe Gly Lys Asp Asn
100 105 110
Leu Phe Leu Lys Glu Val Phe Ile His Lys Tyr Leu Gln Lys Ile Thr
115 120 125
Met Gln Ile Leu Gly Ser Glu Gly Leu Lys Gln Thr Met Leu Gly Asn
130 135 140
Met Asp Lys Ala Thr Arg Asp His Ile Arg Ser Ile Ala Ser Gln Gly
145 150 155
Ser Phe Asn Val Arg Lys Glu Val Glu Asn Leu Val Val Ala Tyr Met
165 170 175
Thr Pro Lys Leu Ile Ser Asn Leu Lys Pro Glu Thr Gln Ser Lys Leu
180 185 190
Ile Asp Asn Leu Asn Ala Phe Asn Leu Asp Trp Phe Lys Ser Phe Leu
195 200 205
Arg Leu Ser Thr Trp Lys Ala Val Thr Lys Ala Leu Lys Ser Arg Glu
210 215 220
Glu Ala Ile Gln Val Met Lys Asp Val Leu Met Met Arg Lys Glu Thr
225 230 235
Arg Glu Lys Gln Glu Asp Phe Leu Asn Thr Leu Leu Glu Glu Leu Glu
245 250 255
Lys Asp Gly Ser Phe Phe Asp Gln Gly Ser Ala Ile Asn Leu Ile Phe
260 265 270
Leu Leu Ala Phe Ala Leu Arg Glu Gly Thr Ser Ser Cys Thr Ala Leu
275 280 285
Ala Val Lys Phe Ile Ser Lys Asp Pro Lys Val Leu Ala Glu Leu Lys
290 295 300
Arg Glu His Lys Ala Ile Val Asp Asn Arg Lys Asp Lys Glu Ala Gly
305 310 315
Val Ser Trp Glu Glu Tyr Arg His Asn Met Thr Phe Thr Asn Met Val
325 330 335
Ser Asn Glu Val Leu Arg Leu Ala Asn Thr Thr Pro Leu Leu Phe Arg
340 345 350
Lys Ala Val Gln Asp Val Glu Ile Lys Gly Tyr Thr Ile Pro Ala Gly
355 360 365
Trp Ile Val Ala Val Ala Pro Ser Ala Val His Phe Asp Pro Ala Ile
370 375 380
Tyr Glu Asn Pro Phe Glu Phe Asn Pro Trp Arg Trp Glu Gly Lys Glu
385 390 395
Met Ile Trp Gly Ser Lys Thr Phe Met Ala Phe Gly Tyr Gly Val Arg
405 410 415
Leu Cys Val Gly Ala Glu Phe Ser Arg Leu Gln Met Ala Ile Phe Leu
420 425 430
His His Leu Val Ala Tyr Tyr Asp Phe Ser Met Val Gln Asp Ser Glu
435 440 445
Ile Ile Arg Ser Pro Phe His Gln Tyr Thr Lys Asp Leu Leu Ile Asn
450 455 460
Ile Ser Gln Ser Pro Thr Lys
465 470

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..469
 (D) OTHER INFORMATION: / Ceres Seq. ID 1565883
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Met	Val	Ala	Leu	Val	Val	Val	Arg	Ile	Ser	His	Trp	Leu	Tyr	Arg	Trp
1			5					10					15		
Ser	Asn	Pro	Lys	Cys	Pro	Gly	Lys	Leu	Pro	Gly	Ser	Met	Gly	Phe	
			20					25				30			
Pro	Ile	Ile	Gly	Glu	Thr	Leu	Asp	Phe	Phe	Lys	Pro	Cys	Gly	Val	Glu
			35				40					45			
Gly	Ile	Pro	Thr	Phe	Val	Lys	Arg	Met	Ile	Arg	Tyr	Gly	Pro	Leu	
			50			55				60					
Phe	Arg	Thr	Asn	Ile	Phe	Gly	Ser	Lys	Thr	Val	Ser	Thr	Asp	Pro	
65				70				75					80		
Asp	Val	Ile	His	Gln	Ile	Phe	Arg	Gln	Glu	Asn	Thr	Ser	Phe	Glu	Leu
			85					90					95		
Gly	Tyr	Pro	Asp	Ile	Phe	Val	Lys	Val	Phe	Gly	Lys	Asp	Asn	Leu	Phe
			100					105					110		
Leu	Lys	Glu	Val	Phe	Ile	His	Lys	Tyr	Leu	Gln	Lys	Ile	Thr	Met	Gln
			115				120					125			
Ile	Leu	Gly	Ser	Glu	Gly	Leu	Lys	Gln	Thr	Met	Leu	Gly	Asn	Met	Asp
			130			135				140					
Lys	Ala	Thr	Arg	Asp	His	Ile	Arg	Ser	Ile	Ala	Ser	Gln	Gly	Ser	Phe
145				150				155					160		
Asn	Val	Arg	Lys	Glu	Val	Glu	Asn	Leu	Val	Val	Ala	Tyr	Met	Thr	Pro
			165					170					175		
Lys	Leu	Ile	Ser	Asn	Leu	Lys	Pro	Glu	Thr	Gln	Ser	Lys	Leu	Ile	Asp
			180				185					190			
Asn	Leu	Asn	Ala	Phe	Asn	Leu	Asp	Trp	Phe	Lys	Ser	Phe	Leu	Arg	Leu
			195				200					205			
Ser	Thr	Trp	Lys	Ala	Val	Thr	Lys	Ala	Leu	Lys	Ser	Arg	Glu	Glu	Ala
			210			215						220			
Ile	Gln	Val	Met	Lys	Asp	Val	Leu	Met	Met	Arg	Lys	Glu	Thr	Arg	Glu
225				230				235					240		
Lys	Gln	Glu	Asp	Phe	Leu	Asn	Thr	Leu	Leu	Glu	Glu	Leu	Glu	Lys	Asp
			245					250					255		
Gly	Ser	Phe	Phe	Asp	Gln	Gly	Ser	Ala	Ile	Asn	Leu	Ile	Phe	Leu	Leu
			260			265							270		
Ala	Phe	Ala	Ileu	Arg	Glu	Gly	Thr	Ser	Ser	Cys	Thr	Ala	Leu	Ala	Val
			275				280					285			
Lys	Phe	Ile	Ser	Lys	Asp	Pro	Lys	Val	Leu	Ala	Glu	Leu	Lys	Arg	Glu
			290			295					300				
His	Lys	Ala	Ile	Val	Asp	Asn	Arg	Lys	Asp	Lys	Glu	Ala	Gly	Val	Ser
305				310				315					320		
Trp	Glu	Glu	Tyr	Arg	His	Asn	Met	Thr	Phe	Thr	Asn	Met	Val	Ser	Asn
			325					330					335		
Glu	Val	Leu	Arg	Leu	Ala	Asn	Thr	Thr	Pro	Leu	Leu	Phe	Arg	Lys	Ala
			340				345					350			
Val	Gln	Asp	Val	Glu	Ile	Lys	Gly	Tyr	Thr	Ile	Pro	Ala	Gly	Trp	Ile
			355			360					365				
Val	Ala	Val	Ala	Pro	Ser	Ala	Val	His	Phe	Asp	Pro	Ala	Ile	Tyr	Glu
			370			375				380					
Asn	Pro	Phe	Glu	Phe	Asn	Pro	Trp	Arg	Trp	Glu	Lys	Glu	Met	Ile	
385				390				395					400		
Trp	Gly	Ser	Lys	Thr	Phe	Met	Ala	Phe	Gly	Tyr	Gly	Val	Arg	Leu	Cys
			405					410					415		
Val	Gly	Ala	Glu	Phe	Ser	Arg	Leu	Gln	Met	Ala	Ile	Phe	Leu	His	His
			420				425					430			

Leu Val Ala Tyr Tyr Asp Phe Ser Met Val Gln Asp Ser Glu Ile Ile
435 440 445
Arg Ser Pro Phe His Gln Tyr Thr Lys Asp Leu Leu Ile Asn Ile Ser
450 455 460
Gln Ser Pro Thr Lys
465

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2253

(D) OTHER INFORMATION: / Ceres Seq. ID 1565898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

attgggttct	ttctctcttt	ctccagatt	catcaatccc	tctcgtacc	gcgagagagt	60
aacaactcac	cggacgtttc	aaatccatcc	tccgataaact	atattcgttt	cgttagatct	120
agatctgagc	gtcggtgaga	gattttctgg	atctgtgata	cgttccaggga	aacatggcgga	180
cgatgaaaag	tttgataggt	ctgataaaca	aaatccagag	ggcgtgtact	gtcctcggag	240
atcatggcgg	tgaaggaatg	tcgctttggg	aagctctccc	aaccgtcgct	gtcgttggtg	300
gcagagtgct	gcgaaaatct	tcagttctag	aaagtgttgt	gggaagagat	ttctgcctc	360
gtggatctgg	tatcgttaca	aggaggccat	tggtgttgca	acttcataag	actgaagacg	420
ggacaactga	tgacgtctgag	ttcttctcat	ctcctaagaa	gagatttgtct	gattttgctg	480
ctgtgcggaa	agaaattgag	gatgaaactg	atcgtattac	tggaagatca	aaacaactct	540
caaacatctc	aattcagctg	agcataatct	ctcctaattg	gtttaatctg	acgctcatag	600
attctccggg	tttgaccaag	gtcgcgtgag	atggacaacc	ggaagattat	gtccaagaca	660
ttgaaacatt	ggctccgtct	tatgttgtaa	agccaaattg	catcatattg	gctattttct	720
cagcaaatca	agatattgct	acctcagatg	ctataaaact	tgttagagaa	gttagaccta	780
caggcgaaa	gacttttggg	gttgcaacca	agcttgatat	catggataaa	ggaacagatt	840
gtctagatgt	tcttgaggga	aggtcatacc	gtttgcaaca	tccttgggtt	ggaattgtga	900
atcgttcaca	agctgatatt	aataagagag	tcgatatgat	tgctgcacgt	agaaaagagc	960
aagaatatct	tgaacaagc	ccggaatacg	ggcaacttag	cagtagaatg	ggatcagaat	1020
atctagcaaa	actcttgtct	cagcaacttag	agactgttat	caggcgaaaa	atccccagta	1080
tgtgtgcttt	gatacaacaa	agcatcgtat	agataaatgc	agaacttgat	aggattggga	1140
gaccacttgc	agtatagtca	ggagcccaac	tttacaacat	tttgaaactc	tgccgggcat	1200
ttgatctgtg	ctttaaggag	catttgatg	gaggacgacc	tggtggagac	cgaaatttat	1260
gagtttttgc	ccatcaatta	ccagcagcct	taaaagaaat	tcctcttgat	cgacattctg	1320
ctaccaaaaa	tgttcagaag	gtgttttcag	aagcagatgg	ttatcagcgc	gctattttat	1380
ctctctgaaca	aggatagaca	aggctcattg	atggatccat	aagctatttc	aaaggaccag	1440
ctgaagccac	tgctgatgca	gtgcatttgc	tattgaagga	gctggtcaga	aagcacaatt	1500
cagaaaacaga	ggaactgaag	cggtttcccg	ctctagcaag	cgatatagca	gctgctgcac	1560
atgaagctct	tgaagaagtc	agagacgaaa	gcaggaaaaa	ggttttgggt	ctgggtgata	1620
tggaactctg	ctacctcagc	gttgagtctc	tcaggaaact	ccatctgaa	cccgagaaa	1680
agaaaacaaa	cccaaggaat	gccccagcac	caaacgcaga	ccctactctc	gataatcact	1740
tcagaagaat	cggatccaac	gBgagtgcat	acataaacat	ggtctgcgac	acatttgagaa	1800
actctctctc	caaaagctgtc	gtttactgcc	aagttagaga	agctaaagaa	tcgcttctca	1860
actctctctc	cgctcaagtt	ggcaggaaga	agaagagaaa	gtcgggtgct	atgttggaac	1920
aagaccacaga	cgctgatggaa	cgaagaggaa	ccttagotaa	acgggttagag	ctttacaaac	1980
aagcttagaga	gcacatcgat	cgagtggctt	ggaagtaagg	gggttttgcta	agacataattc	2040
ttttatattg	taattttctt	gttctgtgtg	gcacactgca	ttataaatga	tatgtttgta	2100
gttctaaact	ccagctacata	caaacataca	cgcgactact	catgtttttc	tggttgcgta	2160
attttatcca	accatttccc	actttttttt	gggtgtgtatc	ttcgattctt	gaatactgggt	2220
ttttagaaca	gttaagacat	attttgaagt	cgc			

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) OTHER INFORMATION: / Ceres Seq. ID 1565899

1	Met	Ala	Thr	Met	5	Ser	Leu	Ile	Gly	Leu	Ile	Asn	Lys	Ile	Gln	Arg
Ala	Cys	Thr	Val	20	Leu	Gly	Asp	His	Gly	Gly	Glu	Gly	Met	Ser	Leu	Trp
Glu	Ala	Leu	Pro	35	Thr	Val	Ala	Val	Val	Gly	Gly	Gln	Ser	Ser	Gly	Lys
Ser	Ser	Val	Leu	50	Glu	Ser	Val	55	Val	Arg	Asp	Phe	Leu	Pro	Arg	Gly
Ser	Gly	Ile	Val	65	Thr	Arg	Arg	Pro	Leu	Val	Leu	Gln	Leu	His	Lys	Thr
Glu	Asp	Gly	Thr	85	Thr	Glu	Tyr	Ala	Glu	Phe	Leu	His	Ala	Pro	Lys	Lys
Arg	Phe	Ala	Asp	100	Phe	Ala	Ala	Val	Arg	Lys	Glu	Ile	Glu	Asp	Glu	Thr
Asp	Arg	Ile	Thr	115	Gly	Lys	Ser	Lys	Gln	Ile	Ser	Asn	Ile	Pro	Ile	Gln
Leu	Ser	Ile	Tyr	130	Ser	Pro	Asn	Val	Val	Asn	Leu	Thr	Leu	Ile	Asp	Leu
Pro	Gly	Leu	Thr	145	Lys	Val	Ala	Val	Asp	Gly	Gln	Pro	Glu	Ser	Ile	Val
Gln	Asp	Ile	Glu	165	Asn	Met	Val	Arg	Ser	Tyr	Val	Glu	Lys	Pro	Asn	Cys
Ile	Ile	Leu	Ala	180	Ile	Ser	Pro	Ala	Asn	Gln	Asp	Ile	Ala	Thr	Ser	Asp
Ala	Ile	Lys	Leu	195	Ala	Arg	Glu	Val	Asp	Pro	Thr	Gly	Glu	Arg	Thr	Phe
Gly	Val	Ala	Thr	210	Lys	Leu	Asp	Ile	Met	Asp	Lys	Gly	Thr	Asp	Cys	Leu
Asp	Val	Leu	Glu	225	Gly	Arg	Ser	Tyr	Arg	Leu	Gln	His	Pro	Trp	Val	Gly
Ile	Val	Asn	Arg	245	Ser	Gln	Ala	Asp	Ile	Asn	Lys	Arg	Val	Asp	Met	Ile
Ala	Ala	Arg	Arg	260	Lys	Glu	Gln	Glu	Tyr	Phe	Glu	Thr	Ser	Pro	Glu	Tyr
Gly	His	Leu	Ala	275	Ser	Arg	Met	Gly	Ser	Glu	Tyr	Leu	Ala	Lys	Leu	Leu
Ser	Gln	His	Leu	290	Glu	Thr	Val	Ile	Arg	Gln	Lys	Ile	Pro	Ser	Ile	Val
Ala	Leu	Ile	Asn	305	Lys	Ser	Ile	Asp	Glu	Ile	Asn	Ala	Glu	Leu	Asp	Arg
Ile	Gly	Arg	Pro	325	Ile	Ala	Val	Asp	Ser	Gly	Ala	Gln	Leu	Tyr	Thr	Ile
Leu	Glu	Leu	Cys	340	Arg	Ala	Phe	Asp	Arg	Val	Phe	Lys	Glu	His	Leu	Asp
Gly	Gly	Arg	Pro	355	Gly	Gly	Asp	Arg	Ile	Tyr	Gly	Val	Phe	Asp	His	Gln
Leu	Pro	Ala	Ala	370	Leu	Lys	Leu	Pro	Phe	Asp	Arg	His	Leu	Ser	Thr	His
Lys	Asn	Val	Gln	385	Lys	Val	Val	Ser	Glu	Ala	Asp	Gly	Tyr	Gln	Pro	His
Leu	Ile	Ala	Pro	405	Glu	Gln	Gly	Tyr	Arg	Arg	Leu	Ile	Asp	Gly	Ser	Ile
Ser	Tyr	Phe	Lys	420	Gly	Pro	Ala	Glu	Ala	Thr	Val	Asp	Ala	Val	His	Phe

Val Leu Lys Glu Leu Val Arg Lys Ser Ile Ser Glu Thr Glu Glu Leu
435 440 445
Lys Arg Phe Pro Thr Leu Ala Ser Asp Ile Ala Ala Ala Asn Glu
450 455 460
Ala Leu Glu Arg Phe Arg Asp Glu Ser Arg Lys Thr Val Leu Arg Leu
465 470 475 480
Val Asp Met Glu Ser Ser Tyr Leu Thr Val Glu Phe Phe Arg Lys Leu
485 490 495
His Leu Glu Pro Glu Lys Glu Lys Pro Asn Pro Arg Asn Ala Pro Ala
500 505 510
Pro Asn Ala Asp Pro Tyr Ser Asp Asn His Phe Arg Lys Ile Gly Ser
515 520 525
Asn Xaa Ser Ala Tyr Ile Asn Met Val Cys Asp Thr Leu Arg Asn Ser
530 535 540
Leu Pro Lys Ala Val Val Tyr Cys Gln Val Arg Glu Ala Lys Arg Ser
545 550 555 560
Leu Leu Asn Phe Phe Tyr Ala Gln Val Gly Arg Lys Glu Lys Glu Lys
565 570 575
Leu Gly Ala Met Leu Asp Glu Asp Pro Gln Leu Met Glu Arg Arg Gly
580 585 590
Thr Leu Ala Lys Arg Leu Glu Leu Tyr Lys Gln Ala Arg Asp Asp Ile
595 600 605
Asp Ala Val Ala Trp Lys
610

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 611 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..611

(D) OTHER INFORMATION: / Ceres Seq. ID 1565900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Met Lys Ser Leu Ile Gly Leu Ile Asn Lys Ile Gln Arg Ala Cys Thr
1 5 10 15
Val Leu Gly Asp His Gly Gly Glu Gly Met Ser Leu Trp Glu Ala Leu
20 25 30
Pro Thr Val Ala Val Val Gly Gly Gln Ser Ser Gly Lys Ser Ser Val
35 40 45
Leu Glu Ser Val Val Gly Arg Asp Phe Leu Pro Arg Gly Ser Gly Ile
50 55 60
Val Thr Arg Arg Pro Leu Val Leu Gln Leu His Lys Thr Glu Asp Gly
65 70 75 80
Thr Thr Glu Tyr Ala Glu Phe Leu His Ala Pro Lys Lys Arg Phe Ala
85 90 95
Asp Phe Ala Ala Val Arg Lys Glu Ile Glu Asp Glu Thr Asp Arg Ile
100 105 110
Thr Gly Lys Ser Lys Gln Ile Ser Asn Ile Pro Ile Gln Leu Ser Ile
115 120 125
Tyr Ser Pro Asn Val Val Asn Leu Thr Leu Ile Asp Leu Pro Gly Leu
130 135 140
Thr Lys Val Ala Val Asp Gly Gln Pro Glu Ser Ile Val Gln Asp Ile
145 150 155 160
Glu Asn Met Val Arg Ser Tyr Val Glu Lys Pro Asn Cys Ile Ile Leu
165 170 175
Ala Ile Ser Pro Ala Asn Gln Asp Ile Ala Thr Ser Asp Ala Ile Lys
180 185 190
Leu Ala Arg Glu Val Asp Pro Thr Gly Glu Arg Thr Phe Val Ala

195	200	205
Thr Lys Leu Asp Ile Met Asp Lys Gly Thr Asp Cys Leu Asp Val Leu		
210	215	220
Glu Gly Arg Ser Tyr Arg Leu Gln His Pro Trp Val Gly Ile Val Asn		
225	230	235
Arg Ser Gln Ala Asp Ile Asn Lys Arg Val Asp Met Ile Ala Ala Arg		
245	250	255
Arg Lys Glu Gln Glu Tyr Phe Glu Thr Ser Pro Glu Tyr Gly His Leu		
260	265	270
Ala Ser Arg Met Gly Ser Glu Tyr Leu Ala Lys Leu Leu Ser Gln His		
275	280	285
Leu Glu Thr Val Ile Arg Gln Lys Ile Pro Ser Ile Val Ala Leu Ile		
290	295	300
Asn Lys Ser Ile Asp Glu Ile Asn Ala Glu Leu Asp Arg Ile Gly Arg		
305	310	315
Pro Ile Ala Val Asp Ser Gly Ala Gln Leu Tyr Thr Ile Leu Glu Leu		
325	330	335
Cys Arg Ala Phe Asp Arg Val Phe Lys Glu His Leu Asp Gly Gly Arg		
340	345	350
Pro Gly Gly Asp Arg Ile Tyr Gly Val Phe Asp His Gln Leu Pro Ala		
355	360	365
Ala Leu Lys Lys Leu Pro Phe Asp Arg His Leu Ser Thr Lys Asn Val		
370	375	380
Gln Lys Val Val Ser Glu Ala Asp Gly Tyr Gln Pro His Leu Ile Ala		
385	390	395
Pro Glu Gln Gly Tyr Arg Arg Leu Ile Asp Gly Ser Ile Ser Tyr Phe		
405	410	415
Lys Gly Pro Ala Glu Ala Thr Val Asp Ala Val His Phe Val Leu Lys		
420	425	430
Glu Leu Val Arg Lys Ser Ile Ser Glu Thr Glu Glu Leu Lys Arg Phe		
435	440	445
Pro Thr Leu Ala Ser Asp Ile Ala Ala Ala Asn Glu Ala Leu Glu		
450	455	460
Arg Phe Arg Asp Glu Ser Arg Lys Thr Val Leu Arg Leu Val Asp Met		
465	470	475
Glu Ser Ser Tyr Leu Thr Val Glu Phe Phe Arg Lys Leu His Leu Glu		
485	490	495
Pro Glu Lys Glu Lys Pro Asn Pro Arg Asn Ala Pro Ala Pro Asn Ala		
500	505	510
Asp Pro Tyr Ser Asp Asn His Phe Arg Lys Ile Gly Ser Asn Xaa Ser		
515	520	525
Ala Tyr Ile Asn Met Val Cys Asp Thr Leu Arg Asn Ser Leu Pro Lys		
530	535	540
Ala Val Val Tyr Cys Gln Val Arg Glu Ala Lys Arg Ser Leu Leu Asn		
545	550	555
Phe Phe Tyr Ala Gln Val Gly Arg Lys Glu Lys Glu Lys Leu Gly Ala		
565	570	575
Met Leu Asp Glu Asp Pro Gln Leu Met Glu Arg Arg Gly Thr Leu Ala		
580	585	590
Lys Arg Leu Glu Leu Tyr Lys Gln Ala Arg Asp Asp Ile Asp Ala Val		
595	600	605
Ala Trp Lys		
610		

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 586 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..586

(D) OTHER INFORMATION: / Ceres Seq. ID 1565901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

1	Ser	Leu	Trp	5	Glu	Ala	Leu	Pro	Thr	Val	Ala	Val	Val	Gly	Gly	Gln
1	Ser	Ser	Gly	20	Ser	Ser	Val	Leu	Glu	Ser	Val	Val	Gly	Arg	Asp	Phe
Leu	Pro	Arg	Gly	35	Ser	Gly	Ile	Val	Thr	Arg	Arg	Pro	Leu	Val	Leu	Gln
Leu	His	Lys	Thr	50	Glu	Asp	Gly	Thr	Thr	Glu	Tyr	Ala	Glu	Phe	Leu	His
Ala	Pro	Lys	Lys	65	Arg	Phe	Ala	Asp	Phe	Ala	Ala	Val	Arg	Lys	Glu	Ile
Glu	Asp	Glu	Thr	85	Asp	Arg	Ile	Thr	Gly	Lys	Ser	Lys	Gln	Ile	Ser	Asn
Ile	Pro	Ile	Gln	100	Leu	Ser	Ile	Tyr	Ser	Pro	Asn	Val	Val	Asn	Leu	Thr
Leu	Ile	Asp	Leu	115	Pro	Gly	Leu	Thr	Lys	Val	Ala	Val	Asp	Gly	Gln	Pro
Glu	Ser	Ile	Val	130	Gln	Asp	Ile	Glu	Asn	Met	Val	Arg	Ser	Tyr	Val	Glu
Lys	Pro	Asn	Cys	145	Ile	Ile	Leu	Ala	Ile	Ser	Pro	Ala	Asn	Gln	Asp	Ile
Ala	Thr	Ser	Asp	165	Ala	Ile	Lys	Leu	Ala	Arg	Glu	Val	Asp	Pro	Thr	Gly
Glu	Arg	Thr	Phe	180	Gly	Val	Ala	Thr	Lys	Leu	Asp	Ile	Met	Asp	Lys	Gly
Thr	Asp	Cys	Leu	195	Asp	Val	Leu	Glu	Gly	Arg	Ser	Tyr	Arg	Leu	Gln	His
Pro	Trp	Val	Gly	210	Ile	Val	Asn	Arg	Ser	Gln	Ala	Asp	Ile	Asn	Lys	Arg
Val	Asp	Met	Ile	225	Ala	Ala	Arg	Arg	Lys	Glu	Gln	Glu	Tyr	Phe	Glu	Thr
Ser	Pro	Glu	Tyr	245	Gly	His	Leu	Ala	Ser	Arg	Met	Gly	Ser	Glu	Tyr	Leu
Ala	Lys	Leu	Leu	260	Ser	Gln	His	Leu	Glu	Thr	Val	Ile	Arg	Gln	Lys	Ile
Pro	Ser	Ile	Val	275	Ala	Leu	Ile	Asn	Lys	Ser	Ile	Asp	Glu	Ile	Asn	Ala
Glu	Leu	Asp	Arg	290	Ile	Gly	Arg	Pro	Ile	Ala	Val	Asp	Ser	Gly	Ala	Gln
Leu	Tyr	Thr	Ile	305	Leu	Glu	Leu	Cys	Arg	Ala	Phe	Asp	Arg	Val	Phe	Lys
Glu	His	Leu	Asp	320	Gly	Gly	Arg	Pro	Gly	Gly	Asp	Arg	Ile	Tyr	Gly	Val
Phe	Asp	His	Gln	335	Leu	Pro	Ala	Ala	Leu	Lys	Lys	Leu	Pro	Phe	Asp	Arg
His	Leu	Ser	Thr	350	Lys	Asn	Val	Gln	Lys	Val	Val	Ser	Glu	Ala	Asp	Gly
Tyr	Gln	Pro	His	365	Leu	Ile	Ala	Pro	Glu	Gln	Gly	Tyr	Arg	Arg	Leu	Ile
Asp	Gly	Ser	Ile	380	Ser	Tyr	Phe	Lys	Gly	Pro	Ala	Glu	Ala	Thr	Val	Asp
Ala	Val	His	Phe	395	Val	Leu	Lys	Glu	Leu	Val	Arg	Lys	Ser	Ile	Ser	Glu
Thr	Glu	Glu	Leu	410	Lys	Arg	Phe	Pro	Thr	Leu	Ala	Ser	Asp	Ile	Ala	Ala
Ala	Ala	Asn	Glu	425	Ala	Leu	Glu	Arg	Phe	Arg	Asp	Glu	Ser	Arg	Lys	Thr
Val	Leu	Arg	Leu	440	Val	Asp	Met	Glu	Ser	Ser	Tyr	Leu	Thr	Val	Glu	Phe

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Met Ala Gln Ser Cys Leu Lys Ile Val Arg Ile Asn Asn Leu Arg Asn
1 5 10 15
Arg Val Asn Arg Arg Ile Leu Ile Leu Arg Arg Phe Thr Arg Leu Leu
20 25 30
Trp Ser Arg Ile Val Ala Cys Thr Pro Gly Lys Ser Arg Arg Tyr Leu
35 40 45
Leu Leu Ser Arg Ala Leu Pro Ser Pro Thr Val Ser Arg Pro Ser Pro
50 55 60
Ser Pro Ile Pro Ala Val Asp Val Val Val Gly Gly Gly Gly Gly
65 70 75 80
Gly Glu Phe Val Arg Arg Ser Ser Val Val Tyr Asp Asn Asp Asn Ser
85 90 95
His Arg Arg Ser Asp Ser Asp Leu Val Ser Leu Lys Ile Ser Leu Leu
100 105 110
Gly Asp Pro Glu Ile Gly Lys Thr Ser Phe Leu Ala Lys Tyr Val Gly
115 120 125
Glu Glu Lys Glu Val Glu Met Arg Glu Leu Glu Lys Gly Ile Asn Cys
130 135 140
Thr Asp Lys Thr Leu Tyr Met Gly Gly Ala Arg Ile Ser Tyr Ser Ile
145 150 155 160
Trp Glu Leu Glu Ala Glu Arg Ser Arg Asp Gln Ile Pro Val Ala Cys
165 170 175
Lys Asp Ser Val Ala Ile Leu Phe Met Phe Asp Leu Thr Ser Arg Cys
180 185 190
Thr Leu Asn Ser Val Ile Ser Trp Tyr Gln Gln Ala Arg Lys Ser Asn
195 200 205
Gln Thr Ala Ile Pro Val Met Val Gly Thr Lys Phe Asp Glu Phe Ile
210 215 220
Gln Leu Pro Ile Asp Leu Gln Trp Thr Ile Ala Ser Gln Ala Arg Thr
225 230 235 240
Tyr Ala Lys Ala Leu Asn Ala Thr Leu Phe Phe Ser Ser Ala Ser Tyr
245 250 255
Asn Ile Asn Val Asn Lys Ile Phe Lys Phe Cys Asp Gly Glu Ala Leu
260 265 270
Arg Leu Thr Met Asp Gly Gly Thr Gln Ser His Asn Arg Arg Thr Asn
275 280 285
His Arg Leu Leu Glu Tyr Val Phe Val Tyr Asn Ile Lys Glu Ala Asn
290 295 300
Pro Glu Glu Cys Val Phe Phe Phe Phe Phe Phe Asn Ser Ala Ala Lys
305 310 315 320
Ala Cys Arg Arg Gly Thr Asp Arg Thr Ser Arg Ile
325 330

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..198
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Met Arg Glu Leu Glu Lys Gly Ile Asn Cys Thr Asp Lys Thr Leu Tyr
1 5 10 15
Met Gly Gly Ala Arg Ile Ser Tyr Ser Ile Trp Glu Leu Glu Ala Glu
20 25 30
Arg Ser Arg Asp Gln Ile Pro Val Ala Cys Lys Asp Ser Val Ala Ile
35 40 45
Leu Phe Met Phe Asp Leu Thr Ser Arg Cys Thr Leu Asn Ser Val Ile

50	55	60	
Ser Trp Tyr Gln Gln	Ala Arg Lys Ser Asn Gln Thr Ala Ile Pro Val		
65	70	75	80
Met Val Gly Thr Lys Phe Asp Glu Phe Ile Gln Leu Pro Ile Asp Leu			
	85	90	95
Gln Trp Thr Thr Ile Ala Ser Gln Ala Arg Thr Tyr Ala Lys Ala Leu Asn			
	100	105	110
Ala Thr Leu Phe Phe Ser Ser Ala Ser Tyr Asn Ile Asn Val Asn Lys			
	115	120	125
Ile Phe Lys Phe Cys Asp Gly Glu Ala Leu Arg Leu Thr Met Asp Gly			
	130	135	140
Gly Thr Gln Ser His Asn Arg Arg Thr Asn His Arg Leu Leu Glu Tyr			
145	150	155	160
Val Phe Val Tyr Asn Ile Lys Glu Ala Asn Pro Glu Glu Cys Val Phe			
	165	170	175
Phe Phe Phe Phe Phe Asn Ser Ala Ala Lys Ala Cys Arg Arg Gly Thr			
	180	185	190
Asp Arg Thr Ser Arg Ile			
	195		

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 182 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Met Gly Gly Ala Arg Ile Ser Tyr Ser Ile Trp Glu Leu Glu Ala Glu	
1	5
Arg Ser Arg Asp Gln Ile Pro Val Ala Cys Lys Asp Ser Val Ala Ile	
	20
Leu Phe Met Phe Asp Leu Thr Ser Arg Cys Thr Leu Asn Ser Val Ile	
	35
Ser Trp Tyr Gln Gln Ala Arg Lys Ser Asn Gln Thr Ala Ile Pro Val	
50	55
Met Val Gly Thr Lys Phe Asp Glu Phe Ile Gln Leu Pro Ile Asp Leu	
65	70
Gln Trp Thr Thr Ile Ala Ser Gln Ala Arg Thr Tyr Ala Lys Ala Leu Asn	
	85
Ala Thr Leu Phe Phe Ser Ser Ala Ser Tyr Asn Ile Asn Val Asn Lys	
	100
Ile Phe Lys Phe Cys Asp Gly Glu Ala Leu Arg Leu Thr Met Asp Gly	
	115
Gly Thr Gln Ser His Asn Arg Arg Thr Asn His Arg Leu Leu Glu Tyr	
	130
Val Phe Val Tyr Asn Ile Lys Glu Ala Asn Pro Glu Glu Cys Val Phe	
145	150
Phe Phe Phe Phe Phe Asn Ser Ala Ala Lys Ala Cys Arg Arg Gly Thr	
	165
Asp Arg Thr Ser Arg Ile	
	180

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1599 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

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(2) INFORMATION FOR SEQ ID NO:130:
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 368 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: peptide
  (ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..368
      (D) OTHER INFORMATION: / Ceres Seq. ID 1565927

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:																
Met	Asn	Ser	Thr	Ser	Thr	His	Phe	Val	Pro	Pro	Arg	Arg	Val	Gly	Ile	
1				5					10					15		
Tyr	Glu	Pro	Val	His	Gln	Phe	Gly	Met	Trp	Gly	Glu	Ser	Phe	Lys	Ser	
			20					25					30			
Asn	Ile	Ser	Asn	Gly	Thr	Met	Asn	Thr	Pro	Asn	His	Ile	Ile	Ile	Pro	
		35					40					45				
Asn	Asn	Gln	Lys	Leu	Asp	Asn	Asn	Val	Ser	Glu	Asp	Thr	Ser	His	Gly	
		50				55					60					
Thr	Ala	Gly	Thr	Pro	His	Met	Phe	Asp	Gln	Glu	Ala	Ser	Thr	Ser	Arg	
65				70						75				80		
His	Pro	Asp	Lys	Ile	Gln	Arg	Arg	Leu	Ala	Gln	Asn	Arg	Glu	Ala	Ala	
			85					90						95		
Arg	Lys	Ser	Arg	Leu	Arg	Lys	Lys	Ala	Tyr	Val	Gln	Gln	Leu	Glu	Thr	
		100						105					110			
Ser	Arg	Leu	Lys	Leu	Ile	Gln	Leu	Glu	Gln	Glu	Leu	Asp	Arg	Ala	Arg	
		115					120					125				

Met	Trp	Gly	Glu	Ser	Phe	Lys	Ser	Asn	Ile	Ser	Asn	Gly	Thr	Met	Asn
1				5				10						15	
Thr	Pro	Asn	His	Ile	Ile	Ile	Pro	Asn	Asn	Gln	Lys	Leu	Asp	Asn	Asn
		20						25					30		
Val	Ser	Glu	Asp	Thr	Ser	His	Gly	Thr	Ala	Gly	Thr	Pro	His	Met	Phe
		35					40					45			
Asp	Gln	Glu	Ala	Ser	Thr	Ser	Arg	His	Pro	Asp	Lys	Ile	Gln	Arg	Arg
	50					55					60				
Leu	Ala	Gln	Asn	Arg	Glu	Ala	Ala	Arg	Lys	Ser	Arg	Leu	Arg	Lys	Lys
65					70					75				80	
Ala	Tyr	Val	Gln	Gln	Leu	Glu	Thr	Ser	Arg	Leu	Lys	Leu	Ile	Gln	Leu
				85					90					95	
Glu	Gln	Glu	Leu	Asp	Arg	Ala	Arg	Gln	Gln	Gly	Phe	Tyr	Val	Gly	Asn
			100					105					110		
Gly	Ile	Asp	Thr	Asn	Ser	Leu	Gly	Phe	Ser	Glu	Thr	Met	Asn	Pro	Gly
		115					120					125			
Ile	Ala	Ala	Phe	Glu	Met	Glu	Tyr	Gly	His	Trp	Val	Glu	Glu	Gln	Asn


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      130              135              140
Arg  Gln  Ile  Cys  Glu  Leu  Arg  Thr  Val  Leu  His  Gly  His  Ile  Asn  Asp
145              150              155              160
Ile  Glu  Leu  Arg  Ser  Leu  Val  Glu  Asn  Ala  Met  Lys  His  Tyr  Phe  Glu
      165              170
Leu  Phe  Arg  Met  Lys  Ser  Ser  Ala  Ala  Lys  Ala  Asp  Val  Phe  Phe  Val
      180              185
Met  Ser  Gly  Met  Trp  Arg  Thr  Ser  Ala  Glu  Arg  Phe  Phe  Leu  Trp  Ile
      195              200              205
Gly  Gly  Phe  Arg  Pro  Ser  Asp  Leu  Leu  Lys  Val  Leu  Leu  Pro  His  Phe
      210              215              220
Asp  Val  Leu  Thr  Asp  Gln  Gln  Leu  Leu  Asp  Val  Cys  Asn  Leu  Lys  Gln
225              230              235              240
Ser  Cys  Gln  Gln  Ala  Glu  Asp  Ala  Leu  Thr  Gln  Gly  Met  Glu  Lys  Leu
      245              250              255
Gln  His  Thr  Leu  Ala  Asp  Cys  Val  Ala  Ala  Gly  Gln  Leu  Gly  Glu  Gly
      260              265              270
Ser  Tyr  Ile  Pro  Gln  Val  Asn  Ser  Ala  Met  Asp  Arg  Leu  Glu  Ala  Leu
      275              280              285
Val  Ser  Phe  Val  Asn  Gln  Ala  Asp  His  Leu  Arg  His  Glu  Thr  Leu  Gln
      290              295              300
Gln  Met  Tyr  Arg  Ile  Leu  Thr  Thr  Arg  Gln  Ala  Ala  Arg  Gly  Leu  Leu
305              310              315              320
Ala  Leu  Gly  Glu  Tyr  Phe  Gln  Arg  Leu  Arg  Ala  Leu  Ser  Ser  Ser  Trp
      325              330              335
Ala  Thr  Arg  His  Arg  Glu  Pro  Thr
      340

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(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..330
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```

Met  Asn  Thr  Pro  Asn  His  Ile  Ile  Ile  Pro  Asn  Asn  Gln  Lys  Leu  Asp
1              5              10              15
Asn  Asn  Val  Ser  Glu  Asp  Thr  Ser  His  Gly  Thr  Ala  Gly  Thr  Pro  His
      20              25              30
Met  Phe  Asp  Gln  Glu  Ala  Ser  Thr  Ser  Arg  His  Pro  Asp  Lys  Ile  Gln
      35              40              45
Arg  Arg  Leu  Ala  Gln  Asn  Arg  Glu  Ala  Ala  Arg  Lys  Ser  Arg  Leu  Arg
      50              55              60
Lys  Lys  Ala  Tyr  Val  Gln  Gln  Leu  Glu  Thr  Ser  Arg  Leu  Lys  Leu  Ile
      65              70              75
Gln  Leu  Glu  Gln  Glu  Leu  Asp  Arg  Ala  Arg  Gln  Gln  Gly  Phe  Tyr  Val
      85              90              95
Gly  Asn  Gly  Ile  Asp  Thr  Asn  Ser  Leu  Gly  Phe  Ser  Glu  Thr  Met  Asn
      100              105              110
Pro  Gly  Ile  Ala  Ala  Phe  Glu  Met  Glu  Tyr  Gly  His  Trp  Val  Glu  Glu
      115              120              125
Gln  Asn  Arg  Gln  Ile  Cys  Glu  Leu  Arg  Thr  Val  Leu  His  Gly  His  Ile
      130              135              140
Asn  Asp  Ile  Glu  Leu  Arg  Ser  Leu  Val  Glu  Asn  Ala  Met  Lys  His  Tyr
145              150              155              160
Phe  Glu  Leu  Phe  Arg  Met  Lys  Ser  Ser  Ala  Ala  Lys  Ala  Asp  Val  Phe
      165              170              175

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Phe Val Met Ser Gly Met Trp Arg Thr Ser Ala Glu Arg Phe Phe Leu
180 185 190
Trp Ile Gly Gly Phe Arg Pro Ser Asp Leu Leu Lys Val Leu Leu Pro
195 200 205
His Phe Asp Val Leu Thr Asp Gln Gln Leu Leu Asp Val Cys Asn Leu
210 215 220
Lys Gln Ser Cys Gln Gln Ala Glu Asp Ala Leu Thr Gln Gly Met Glu
225 230 235 240
Lys Leu Gln His Thr Leu Ala Asp Cys Val Ala Ala Gly Gln Leu Gly
245 250 255
Glu Gly Ser Tyr Ile Pro Gln Val Asn Ser Ala Met Asp Arg Leu Glu
260 265 270
Ala Leu Val Ser Phe Val Asn Gln Ala Asp His Leu Arg His Glu Thr
275 280 285
Leu Gln Gln Met Tyr Arg Ile Leu Thr Thr Arg Gln Ala Ala Arg Gly
290 295 300
Leu Leu Ala Leu Gly Glu Tyr Phe Gln Arg Leu Arg Ala Leu Ser Ser
305 310 315 320
Ser Trp Ala Thr Arg His Arg Glu Pro Thr
325 330

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1477
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

tagttctgctc	ctccgtcaat	ctctctcgcc	gctttatcct	tggtacaaat	cccatcgatc	60
ttttcggaat	cttccctcat	tatgctcagc	caccattaac	agagctccat	tggttcagtt	120
ctccgttcaa	cgattatcgg	aattattcac	aacactatta	gtatcacctg	cgccaacoga	180
ttttgattac	caagcttttgt	gacgacagtc	gtgattaagg	aggtttttgt	aaatttcttc	240
gttccgtgtt	gttttcaaa	atggctgctt	tgaaagggtta	tggtttgtgt	tctatggact	300
ctgctcttcc	attccctcgt	cctaagctat	tcaatggcta	taagagaagg	agctcgaaat	360
gggtctctcc	caaacgagct	gttgtaaccca	atttccatct	cccaatgcgc	agcttggagg	420
ttaaaacagc	gacaaacaca	gacgacatta	aagctctcac	tgatgatcac	gctatcaaaa	480
cacgctatct	acctgatgga	agattcgacc	ttgaagccta	cgatgactta	gtcaacattc	540
agatacaaaa	cggtgctgaa	ggtgtcatgt	ttggtgttac	aactgtgaag	gacaaactgat	600
gagctgggag	gaacacatta	tgcctatagg	ccataccggt	aactgttttg	gtcgaagcat	660
caaagtcatt	ggaacacgtg	gaagcaattc	gactagagaa	gcaatccacg	cgactgaaca	720
aggattcgcg	gttggaatgc	atgctgctct	tcatataaac	ccttactact	gcaagacttc	780
tattgaggga	ctgattgcac	atttccagtc	tggtcttcat	atggggacoga	cgattatata	840
caatgtgcct	ggctgaacag	ggcaagatat	acgcctcgtt	gccatcttca	aaactttctca	900
gaatcgcgaat	ttagctgtgt	tgaaggaaatg	ttgtgggaac	aagcgagctg	aagagtacac	960
tgagaatggg	gttggttgtg	ggagtgaggaa	tgatgatgag	tgctcatgatt	ccagatggga	1020
ttatggagca	acaggagatta	tatcagttac	tactaattta	gttccggggt	tgatgaggaa	1080
gtgtgatgtt	gaaggttaga	attcatcttt	gaactcaaa	cttctacctt	tgatggcttg	1140
gctgttccac	gaagcaaac	cgattggaat	caacaactgt	ttggtctcag	ttggagtttc	1200
gagggcggtt	tttaggttac	catatgtacc	attgccactg	tctaagaggg	ttgagtttgt	1260
gaaactggtg	aaggagattg	gacgagagca	ttttgtgggt	gagaaagatg	tccaggtctc	1320
tgatgatgat	gattttatcc	ttatcggtgc	atattagcat	actttttttt	ttgaattttt	1380
ggttctcttt	tggttgggtg	taatgaagaa	gagatggttc	tatcatttgg	ttttatgtag	1440
ctgatgaatg	aatgaaaaact	caaggaaatga	tttcatc			

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..252
(D) OTHER INFORMATION: / Ceres Seq. ID 1565939
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met	Ser	Trp	Asp	Glu	His	Ile	Met	Leu	Ile	Gly	His	Thr	Val	Asn	Cys
1			5					10					15		
Phe	Gly	Gly	Ser	Ile	Lys	Val	Ile	Gly	Asn	Thr	Gly	Ser	Asn	Ser	Thr
			20					25					30		
Arg	Glu	Ala	Ile	His	Ala	Thr	Glu	Gln	Gly	Phe	Ala	Val	Gly	Met	His
		35					40					45			
Ala	Ala	Leu	His	Ile	Asn	Pro	Tyr	Tyr	Gly	Lys	Thr	Ser	Ile	Glu	Gly
		50				55					60				
Leu	Ile	Ala	His	Phe	Gln	Ser	Val	Leu	His	Met	Gly	Pro	Thr	Ile	Ile
65					70					75				80	
Tyr	Asn	Val	Pro	Gly	Arg	Thr	Gly	Gln	Asp	Ile	Pro	Pro	Arg	Ala	Ile
			85						90					95	
Phe	Lys	Leu	Ser	Gln	Asn	Pro	Asn	Leu	Ala	Gly	Val	Lys	Glu	Cys	Val
			100					105					110		
Gly	Asn	Lys	Arg	Val	Glu	Glu	Tyr	Thr	Glu	Asn	Gly	Val	Val	Val	Trp
			115				120					125			
Ser	Gly	Asn	Asp	Asp	Glu	Cys	His	Asp	Ser	Arg	Trp	Asp	Tyr	Gly	Ala
		130				135					140				
Thr	Gly	Val	Ile	Ser	Val	Thr	Ser	Asn	Leu	Val	Pro	Gly	Leu	Met	Arg
145					150					155				160	
Lys	Leu	Met	Phe	Glu	Gly	Arg	Asn	Ser	Ser	Leu	Asn	Ser	Lys	Leu	Leu
			165							170				175	
Pro	Leu	Met	Ala	Trp	Leu	Phe	His	Glu	Pro	Asn	Pro	Ile	Gly	Ile	Asn
			180					185					190		
Thr	Ala	Leu	Ala	Gln	Leu	Gly	Val	Ser	Arg	Pro	Val	Phe	Arg	Leu	Pro
		195						200					205		
Tyr	Val	Pro	Leu	Pro	Leu	Ser	Lys	Arg	Leu	Glu	Phe	Val	Lys	Leu	Val
		210					215					220			
Lys	Glu	Ile	Gly	Arg	Glu	His	Phe	Val	Gly	Glu	Lys	Asp	Val	Gln	Ala
225					230					235				240	
Leu	Asp	Asp	Asp	Asp	Phe	Ile	Leu	Ile	Gly	Arg	Tyr				
			245						250						

(2) INFORMATION FOR SEQ ID NO:135:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..245
(D) OTHER INFORMATION: / Ceres Seq. ID 1565940
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met	Leu	Ile	Gly	His	Thr	Val	Asn	Cys	Phe	Gly	Gly	Ser	Ile	Lys	Val
1			5						10				15		
Ile	Gly	Asn	Thr	Gly	Ser	Asn	Ser	Thr	Arg	Glu	Ala	Ile	His	Ala	Thr
			20					25					30		
Glu	Gln	Gly	Phe	Ala	Val	Gly	Met	His	Ala	Ala	Leu	His	Ile	Asn	Pro
		35					40					45			
Tyr	Tyr	Gly	Lys	Thr	Ser	Ile	Glu	Gly	Leu	Ile	Ala	His	Phe	Gln	Ser
		50				55					60				
Val	Leu	His	Met	Gly	Pro	Thr	Ile	Ile	Tyr	Asn	Val	Pro	Gly	Arg	Thr

65	70	75	80
Gly Gln Asp Ile	Pro Pro Arg Ala Ile	Phe Lys Leu Ser Gln	Asn Pro
	85	90	95
Asn Leu Ala Gly	Val Lys Glu Cys Val	Gly Asn Lys Arg Val	Glu Glu
	100	105	110
Tyr Thr Glu Asn	Gly Val Val Val Trp Ser	Gly Asn Asp Asp	Glu Cys
	115	120	125
His Asp Ser Arg	Trp Asp Tyr Gly Ala Thr	Gly Val Ile Ser	Val Thr
	130	135	140
Ser Asn Leu Val	Pro Gly Leu Met Arg Lys	Leu Met Phe Glu	Gly Arg
	145	150	155
Asn Ser Ser Leu	Asn Ser Lys Leu Leu Pro	Leu Met Ala Trp	Leu Phe
	165	170	175
His Glu Pro Asn	Pro Ile Gly Ile Asn Thr	Ala Leu Ala Gln	Leu Gly
	180	185	190
Val Ser Arg Pro	Val Phe Arg Leu Pro	Tyr Val Pro Leu	Pro Leu Ser
	195	200	205
Lys Arg Leu Glu	Phe Val Lys Leu Val Lys	Glu Ile Gly Arg	Glu His
	210	215	220
Phe Val Gly Glu	Lys Asp Val Gln Ala Leu	Asp Asp Asp Asp	Phe Ile
	225	230	235
Leu Ile Gly Arg	Tyr		240
	245		

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..206
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met His Ala Ala	Leu His Ile Asn Pro Tyr Gly Lys Thr Ser Ile
1	5 10 15
Glu Gly Leu Ile	Ala His Phe Gln Ser Val Leu His Met Gly Pro Thr
	20 25 30
Ile Ile Tyr Asn	Val Pro Gly Arg Thr Gly Gln Asp Ile Pro Pro Arg
	35 40 45
Ala Ile Phe Lys	Leu Ser Gln Asn Pro Asn Leu Ala Gly Val Lys Glu
	50 55 60
Cys Val Gly Asn	Lys Arg Val Glu Glu Tyr Thr Glu Asn Gly Val Val
	65 70 75
Val Trp Ser Gly	Asn Asp Asp Glu Cys His Asp Ser Arg Trp Asp Tyr
	85 90 95
Gly Ala Thr Gly	Val Ile Ser Val Thr Ser Asn Leu Val Pro Gly Leu
	100 105 110
Met Arg Lys Leu	Met Phe Glu Gly Arg Asn Ser Ser Leu Asn Ser Lys
	115 120 125
Leu Leu Pro Leu	Met Ala Trp Leu Phe His Glu Pro Asn Pro Ile Gly
	130 135 140
Ile Asn Thr Ala	Leu Ala Gln Leu Gly Val Ser Arg Pro Val Phe Arg
	145 150 155
Leu Pro Tyr Val	Pro Leu Pro Leu Ser Lys Arg Leu Glu Phe Val Lys
	165 170 175
Leu Val Lys Glu	Ile Gly Arg Glu His Phe Val Gly Glu Lys Asp Val
	180 185 190
Gln Ala Leu Asp	Asp Asp Asp Phe Ile Leu Ile Gly Arg Tyr
	195 200 205

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..858
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

attgaatacc	atatatatat	agatacacag	acataataac	acacaaatat	tcgtgttttt	60
ttcaaaactgt	gagagaaaaa	gaaagagaga	aagagatggg	agagattggg	tttacagaga	120
agcaagaagc	tttgggtgaag	gaatcgtggg	agatactgaa	acaagacatc	cccaaataca	180
gccttctact	cttctcacag	atactggaga	tagcaccagc	agcaaaaaggc	ttgttctctt	240
tcctaagaga	ctcagatgaa	gtccctcaca	acaatcctaa	actcaaaagt	catgctgtta	300
aagtcttoaa	gatgacatgt	gaaacagcta	tacagctgag	ggaggaaagg	aagggtgtag	360
tggctgacac	aaccctccaa	tatttaggct	caattcatct	caaaaagcgc	gttattgacc	420
ctcacttcga	ggtggtgaaa	gaagctttgc	taaggacatt	gaaagagggg	ttgggggaga	480
aatacaatga	agaagtgga	ggtgcttggt	ctcaagctta	tgatcacttg	gctttagcca	540
tcaagaccga	gatgaaacaa	gaagagtcac	aaaacccctat	tgatcatttg	ggatcgcact	600
acatgaatct	attccacata	catgatacac	atatactgtg	tctgtgtgtg	gtactatggt	660
gcctcttaac	tttctacagt	tcactatttt	aattataaag	aaggatcttg	tgctatcatt	720
agggagatag	gtgatactgt	agttcttctt	gaaattgtta	ttcgtgagaa	atatcatggt	780
ttgaagtatt	tattttcaca	agatggatgt	taacgtgggg	atcattttac	aatcattcta	840
caataatatt	tacttctc					

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met	Gly	Glu	Ile	Gly	Phe	Thr	Glu	Lys	Gln	Glu	Ala	Leu	Val	Lys	Glu
1			5						10					15	
Ser	Trp	Glu	Ile	Leu	Lys	Gln	Asp	Ile	Pro	Lys	Tyr	Ser	Leu	His	Phe
			20					25					30		
Phe	Ser	Gln	Ile	Leu	Glu	Ile	Ala	Pro	Ala	Ala	Lys	Gly	Leu	Phe	Ser
			35					40					45		
Phe	Leu	Arg	Asp	Ser	Asp	Glu	Val	Pro	His	Asn	Asn	Pro	Lys	Leu	Lys
			50					55					60		
Ala	His	Ala	Val	Lys	Val	Phe	Lys	Met	Thr	Cys	Glu	Thr	Ala	Ile	Gln
			65					70					75		80
Leu	Arg	Glu	Glu	Gly	Lys	Val	Val	Val	Val	Ala	Asp	Thr	Thr	Leu	Gln
			85					90					95		
Leu	Gly	Ser	Ile	His	Leu	Lys	Ser	Gly	Val	Ile	Asp	Pro	His	Phe	Glu
			100					105					110		
Val	Val	Lys	Glu	Ala	Leu	Leu	Arg	Thr	Leu	Lys	Glu	Gly	Leu	Gly	Glu
			115					120					125		
Lys	Tyr	Asn	Glu	Glu	Val	Glu	Gly	Ala	Trp	Ser	Gln	Ala	Tyr	Asp	His
			130					135					140		
Leu	Ala	Leu	Ala	Ile	Lys	Thr	Glu	Met	Lys	Gln	Glu	Glu	Ser		
			145					150					155		

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..86
(D) OTHER INFORMATION: / Ceres Seq. ID 1565948
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:
Met Thr Cys Glu Thr Ala Ile Gln Leu Arg Glu Glu Gly Lys Val Val
1 5 10 15
Val Ala Asp Thr Thr Leu Gln Tyr Leu Gly Ser Ile His Leu Lys Ser
20 25 30
Gly Val Ile Asp Pro His Phe Glu Val Val Lys Glu Ala Leu Leu Arg
35 40 45
Thr Leu Lys Glu Gly Leu Gly Glu Lys Tyr Asn Glu Glu Val Glu Gly
50 55 60
Ala Trp Ser Gln Ala Tyr Asp His Leu Ala Leu Ala Ile Lys Thr Glu
65 70 75 80
Met Lys Gln Glu Glu Ser
85

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1262
(D) OTHER INFORMATION: / Ceres Seq. ID 1565957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

aaagcaacaa aaacttaacc cattctctct tctttttttg ttctctctctc acaaacacaa 60
caaatatgga atacagctgt gtacagcaga gtagtactac gtcagaatct ctctccatct 120
ctactactcc aaagccgaca acgacaacgg agaagaaact ctcttctcca ccggcgactt 180
cgatcgctct ctacagaatg ggaagcgcgc gaagcagcgt tgttttgat tcagagaaacg 240
cgctcgagac cgagtcacga aagcttccgt cgtcgaaata caaaggcggt gtgcctcagc 300
ctaacggaag atggggagct cagatttacg agaagcatca gcgagtttgg ctccggtactt 360
tcaacgagga agaagaagct cgctctctct acgacatcgc cgtgaggagg ttccgaggcc 420
gcgcgcgcgt cactaaactc aaatctcaag ttgatggaaa cgacgcggaa tcgggttttc 480
ttgacgctca ttctaaagct gagatcgctg atatgttgag gaaacacact tacgcgatg 540
agtttgagca gagtagacgg aagtttgtta accgcgacgg aaaacgctct ggtttggaga 600
cggcgacgta cggaaacgac gctgttttga gagcgcgtga ggttttgttc gagaagactg 660
ttacgcgagc cgagctcggg aagctgaacc gtttagtgat accgaaacaa cacgcggaga 720
agcattttcc gttatcggcg atgcagacgg cgtatgggat gaatccGtct ccgacgaaag 780
gcgttttgat taactttgaa gatagaacag ggaaagtgtg ccggttcctg tacagttaact 840
ggaacagcag tcaaaagttac gtgttgacca agggctggag ccggttcctg aaagagaaga 900
atcttcgacg cgggtgatgtg gtttgttctc agagatcaac ccgaccagac ccgcaattgt 960
atatccactg gaaagtcggc tctagtcggc ttcagactgt ggttaggcta ttccgagtc 1020
acattttcaa tgttgagtaac gagaacccaa acgacgtcgc agtagagtgt gttggcaaga 1080
agagatctcg ggaagatgat ttgttttcgt taggggtgtc caagaagcag gcgattatca 1140
acatcttggt acaaatcttt ttttttgggt ttttttctt caattttgtt ctccgttttt 1200
aatattttgt attgaaatg caagttgtta attaggacaa tacaagaaaa aatgacaact 1260

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..382
 (D) OTHER INFORMATION: / Ceres Seq. ID 1565958
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Ser	Asn	Lys	Asn	Leu	Thr	His	Phe	Phe	Phe	Phe	Cys	Phe	Ser	Leu
1				5					10				15	
Thr	Asn	Thr	Thr	Asn	Met	Glu	Tyr	Ser	Cys	Val	Asp	Asp	Ser	Thr
			20					25					30	
Thr	Ser	Glu	Ser	Leu	Ser	Ile	Ser	Thr	Thr	Pro	Lys	Pro	Thr	Thr
		35					40					45		
Thr	Glu	Lys	Lys	Leu	Ser	Ser	Pro	Pro	Ala	Thr	Ser	Met	Arg	Leu
	50				55					60				
Arg	Met	Gly	Ser	Gly	Gly	Ser	Ser	Val	Val	Leu	Asp	Ser	Glu	Asn
65				70					75					80
Val	Glu	Thr	Glu	Ser	Arg	Lys	Leu	Pro	Ser	Ser	Lys	Tyr	Lys	Gly
			85					90					95	
Val	Pro	Gln	Pro	Asn	Gly	Arg	Trp	Gly	Ala	Gln	Ile	Tyr	Glu	Lys
		100						105					110	
Gln	Arg	Val	Trp	Leu	Gly	Thr	Phe	Asn	Glu	Glu	Glu	Glu	Ala	Ser
		115						120				125		
Ser	Tyr	Asp	Ile	Ala	Val	Arg	Arg	Phe	Arg	Gly	Arg	Asp	Ala	Val
	130				135						140			
Asn	Phe	Lys	Ser	Gln	Val	Asp	Gly	Asn	Asp	Ala	Glu	Ser	Ala	Phe
145				150					155					160
Asp	Ala	His	Ser	Lys	Ala	Glu	Ile	Val	Asp	Met	Leu	Arg	Lys	His
			165					170					175	
Tyr	Ala	Asp	Glu	Phe	Glu	Gln	Ser	Arg	Arg	Lys	Phe	Val	Asn	Gly
		180					185						190	
Gly	Lys	Arg	Ser	Gly	Leu	Glu	Thr	Ala	Thr	Tyr	Gly	Asn	Asp	Ala
		195				200						205		
Leu	Arg	Ala	Arg	Glu	Val	Leu	Phe	Glu	Lys	Thr	Val	Thr	Pro	Ser
	210				215						220			
Val	Gly	Lys	Leu	Asn	Arg	Leu	Val	Ile	Pro	Lys	Gln	His	Ala	Glu
225				230						235				240
His	Phe	Pro	Leu	Ser	Ala	Met	Thr	Thr	Ala	Met	Gly	Met	Asn	Pro
			245						250				255	
Pro	Thr	Lys	Gly	Val	Leu	Ile	Asn	Leu	Glu	Asp	Arg	Thr	Gly	Lys
		260					265						270	
Trp	Arg	Phe	Arg	Tyr	Ser	Tyr	Trp	Asn	Ser	Ser	Gln	Ser	Tyr	Val
	275						280					285		
Thr	Lys	Gly	Trp	Ser	Arg	Phe	Val	Lys	Glu	Lys	Asn	Leu	Arg	Ala
	290					295					300			
Asp	Val	Val	Cys	Phe	Glu	Arg	Ser	Thr	Gly	Pro	Asp	Arg	Gln	Leu
	305				310					315				320
Ile	His	Trp	Lys	Val	Arg	Ser	Ser	Pro	Val	Gln	Thr	Val	Val	Arg
			325						330				335	
Phe	Gly	Val	Asn	Ile	Phe	Asn	Val	Ser	Asn	Glu	Lys	Pro	Asn	Asp
		340					345						350	
Ala	Val	Glu	Cys	Val	Gly	Lys	Lys	Arg	Ser	Arg	Glu	Asp	Asp	Leu
		355				360						365		
Ser	Leu	Gly	Cys	Ser	Lys	Lys	Gln	Ala	Ile	Ile	Asn	Ile	Leu	
	370					375					380			

- (2) INFORMATION FOR SEQ ID NO:142:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..361

(D) OTHER INFORMATION: / Ceres Seq. ID 1565959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met	Glu	Tyr	Ser	Cys	Val	Asp	Asp	Ser	Ser	Thr	Thr	Ser	Glu	Ser	Leu
1			5					10					15		
Ser	Ile	Ser	Thr	Thr	Pro	Lys	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Lys	Leu
			20					25					30		
Ser	Ser	Pro	Pro	Ala	Thr	Ser	Met	Arg	Leu	Tyr	Arg	Met	Gly	Ser	Gly
		35					40					45			
Gly	Ser	Ser	Val	Val	Leu	Asp	Ser	Glu	Asn	Gly	Val	Glu	Thr	Glu	Ser
	50					55					60				
Arg	Lys	Leu	Pro	Ser	Ser	Lys	Tyr	Lys	Gly	Val	Val	Pro	Gln	Pro	Asn
	65				70					75				80	
Gly	Arg	Trp	Gly	Ala	Gln	Ile	Tyr	Glu	Lys	His	Gln	Arg	Val	Trp	Leu
			85						90				95		
Gly	Thr	Phe	Asn	Glu	Glu	Glu	Ala	Ala	Ser	Ser	Tyr	Asp	Ile	Ala	
		100					105					110			
Val	Arg	Arg	Phe	Arg	Gly	Arg	Asp	Ala	Val	Thr	Asn	Phe	Lys	Ser	Gln
	115						120					125			
Val	Asp	Gly	Asn	Asp	Ala	Glu	Ser	Ala	Phe	Leu	Asp	Ala	His	Ser	Lys
	130					135					140				
Ala	Glu	Ile	Val	Asp	Met	Leu	Arg	Lys	His	Thr	Tyr	Ala	Asp	Glu	Phe
	145				150					155				160	
Glu	Gln	Ser	Arg	Arg	Lys	Phe	Val	Asn	Gly	Asp	Gly	Lys	Arg	Ser	Gly
			165						170				175		
Leu	Glu	Thr	Ala	Thr	Tyr	Gly	Asn	Asp	Ala	Val	Leu	Arg	Ala	Arg	Glu
	180						185						190		
Val	Leu	Phe	Glu	Lys	Thr	Val	Thr	Pro	Ser	Asp	Val	Gly	Lys	Leu	Asn
	195						200					205			
Arg	Leu	Val	Ile	Pro	Lys	Gln	His	Ala	Glu	Lys	His	Phe	Pro	Leu	Ser
	210					215					220				
Ala	Met	Thr	Thr	Ala	Met	Gly	Met	Asn	Pro	Ser	Pro	Thr	Lys	Gly	Val
	225				230					235				240	
Leu	Ile	Asn	Leu	Glu	Asp	Arg	Thr	Gly	Lys	Val	Trp	Arg	Phe	Arg	Tyr
			245						250				255		
Ser	Tyr	Trp	Asn	Ser	Ser	Gln	Ser	Tyr	Val	Leu	Thr	Lys	Gly	Trp	Ser
		260						265					270		
Arg	Phe	Val	Lys	Glu	Lys	Asn	Leu	Arg	Ala	Gly	Asp	Val	Val	Cys	Phe
	275					280						285			
Glu	Arg	Ser	Thr	Gly	Pro	Asp	Arg	Gln	Leu	Tyr	Ile	His	Trp	Lys	Val
	290					295					300				
Arg	Ser	Ser	Pro	Val	Gln	Thr	Val	Val	Arg	Leu	Phe	Gly	Val	Asn	Ile
	305				310				315					320	
Phe	Asn	Val	Ser	Asn	Glu	Lys	Pro	Asn	Asp	Val	Ala	Val	Glu	Cys	Val
			325						330					335	
Gly	Lys	Lys	Arg	Ser	Arg	Glu	Asp	Asp	Leu	Phe	Ser	Leu	Gly	Cys	Ser
			340				345						350		
Lys	Lys	Gln	Ala	Ile	Ile	Asn	Ile	Leu							
		355				360									

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 322 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..322

(D) OTHER INFORMATION: / Ceres Seq. ID 1565960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```

Met Arg Leu Tyr Arg Met Gly Ser Gly Gly Ser Ser Val Val Leu Asp
1      5      10      15
Ser Glu Asn Gly Val Glu Thr Glu Ser Arg Lys Leu Pro Ser Ser Lys
20      25      30
Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile
35      40      45
Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Glu
50      55      60
Glu Ala Ala Ser Ser Tyr Asp Ile Ala Val Arg Arg Phe Arg Gly Arg
65      70      75      80
Asp Ala Val Thr Asn Phe Lys Ser Gln Val Asp Gly Asn Asp Ala Glu
85      90      95
Ser Ala Phe Leu Asp Ala His Ser Lys Ala Glu Ile Val Asp Met Leu
100      105      110
Arg Lys His Thr Tyr Ala Asp Glu Phe Glu Gln Ser Arg Arg Lys Phe
115      120      125
Val Asn Gly Asp Gly Lys Arg Ser Gly Leu Glu Thr Ala Thr Tyr Gly
130      135      140
Asn Asp Ala Val Leu Arg Ala Arg Glu Val Leu Phe Glu Lys Thr Val
145      150      155      160
Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln
165      170      175
His Ala Glu Lys His Phe Pro Leu Ser Ala Met Thr Thr Ala Met Gly
180      185      190
Met Asn Pro Ser Pro Thr Lys Gly Val Leu Ile Asn Leu Glu Asp Arg
195      200      205
Thr Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln
210      215      220
Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Asn
225      230      235      240
Leu Arg Ala Gly Asp Val Val Cys Phe Glu Arg Ser Thr Gly Pro Asp
245      250      255
Arg Gln Leu Tyr Ile His Trp Lys Val Arg Ser Ser Pro Val Gln Thr
260      265      270
Val Val Arg Leu Phe Gly Val Asn Ile Phe Asn Val Ser Asn Glu Lys
275      280      285
Pro Asn Asp Val Ala Val Glu Cys Val Gly Lys Lys Arg Ser Arg Glu
290      295      300
Asp Asp Leu Phe Ser Leu Gly Cys Ser Lys Lys Gln Ala Ile Ile Asn
305      310      315      320
Ile Leu

```

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1351 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1351

(D) OTHER INFORMATION: / Ceres Seq. ID 1565965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```

aactggtaaa ccctaagaat cctccgcaat ttgcgaattt tgtgaaggag ccgccggcta      60
aatttgatgg cagaccacaag ttccggagatc gtcaatgctc tgtcgtcgga gatggaagct      120
gtttccggtt catcaactca ggcattctct tcgtccgatg gattccagat gattggaagaa      180
gttgagaaga gatacaaaat tgtaggagat atcggtaggg aatgtatata agaggaagag      240

```

```
ctaagaatc ttcttgcata gaagctgct cagatttgc acgacggct tgaaccatca 300
ggaagaatgc acattgctca gggagtgatg aaagtcatca atgtgaacaa aatgacttca 360
ctgggtttcca gagtgaagat ttggattTgc tgatttggtt gctcagttga acaacaaaaat 420
gggtggtgac ttgaagaaaa tcagagtgggt tggagaatac tttcaagaga tatggaaggc 480
tgctgggatg gataatgaca aagtagagtt tttgtggtcg tccgaagaaa ttaattctaa 540
ggcagataag tattggcctc ttgtgatgga cattgctcgc aaaaaacaag cccttagaat 600
cttaaggtgt gtgcagatta tgggacgtag tgagactgat gaactgagtg ctgccagact 660
cctttaccoca tgcattgcaat gtgcagatat ttttttctt gaggtgata ttgccaagct 720
tgggatggat caaagaaaaa taaCatgtgc tagcgagaga atactgtgat gacataaaga 780
ggaaaaacaa accgataatc ttgtcacacc atatgcttcc tggctctocaa caaggacaag 840
aaaaagatgc caaaagtgtat ccaattctct ctatctttat ggaagatgaa gaggtcgaag 900
ttaatgtgaa gatcaagaaa gcttactgoc ctccaaaagt cgtgaagggc aatccatgcc 960
tcgaatacat caaatcacat aaatacatca ttctaccatg gtttgatgag ttccacagttg 1020
agagaaatga agaataatgac ggttaacaaga cctacaaaag ctttgaagac attgctgctg 1080
actatgagag cggcgagttg caccctggcg atctaaagaa aggcctgatg aacgcgttga 1140
ataagatttt gcaacctgtt cgtgatcatt tcaaaacaga cgcacgcgcg aagaattctac 1200
tcaaacagat caaggcttac agagtcacca gataaaaata gagagccaga atgtgtcatt 1260
gaaagctttc tctcacttta tgaacttat tattacaaa aacacactgt aaaactcctg 1320
gattttgttt atttgggtat atcagatgct c
```

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1565966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```
Met Leu Pro Gly Leu Gln Gln Gly Gln Lys Met Ser Lys Ser Asp
1 5 10 15
Pro Leu Ser Ala Ile Phe Met Glu Asp Glu Glu Ala Glu Val Asn Val
20 25 30
Lys Ile Lys Lys Ala Tyr Cys Pro Pro Lys Val Val Lys Gly Asn Pro
35 40 45
Cys Leu Glu Tyr Ile Lys Tyr Ile Lys Tyr Ile Ile Leu Pro Trp Phe
50 55 60
Asp Glu Phe Thr Val Glu Arg Asn Glu Glu Tyr Gly Gly Asn Lys Thr
65 70 75 80
Tyr Lys Ser Phe Glu Asp Ile Ala Ala Asp Tyr Glu Ser Gly Glu Leu
85 90 95
His Pro Gly Asp Leu Lys Lys Gly Leu Met Asn Ala Leu Asn Lys Ile
100 105 110
Leu Gln Pro Val Arg Asp His Phe Lys Thr Asp Ala Arg Ala Lys Asn
115 120 125
Leu Leu Lys Gln Ile Lys Ala Tyr Arg Val Thr Arg
130 135 140
```

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1565967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```

Met Ser Lys Ser Asp Pro Leu Ser Ala Ile Phe Met Glu Asp Glu Glu
1          5          10          15
Ala Glu Val Asn Val Lys Ile Lys Lys Ala Tyr Cys Pro Pro Lys Val
20          25          30
Val Lys Gly Asn Pro Cys Leu Glu Tyr Ile Lys Tyr Ile
35          40          45
Ile Leu Pro Trp Phe Asp Glu Phe Thr Val Glu Arg Asn Glu Glu Tyr
50          55          60
Gly Gly Asn Lys Thr Tyr Lys Ser Phe Glu Asp Ile Ala Ala Asp Tyr
65          70          75          80
Glu Ser Gly Glu Leu His Pro Gly Asp Leu Lys Lys Gly Leu Met Asn
85          90          95
Ala Leu Asn Lys Ile Leu Gln Pro Val Arg Asp His Phe Lys Thr Asp
100         105         110
Ala Arg Ala Lys Asn Leu Leu Lys Gln Ile Lys Ala Tyr Arg Val Thr
115         120         125
Arg

```

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

```

Met Glu Asp Glu Glu Ala Glu Val Asn Val Lys Ile Lys Lys Ala Tyr
1          5          10          15
Cys Pro Pro Lys Val Val Lys Gly Asn Pro Cys Leu Glu Tyr Ile Lys
20          25          30
Tyr Ile Lys Tyr Ile Ile Leu Pro Trp Phe Asp Glu Phe Thr Val Glu
35          40          45
Arg Asn Glu Glu Tyr Gly Gly Asn Lys Thr Tyr Lys Ser Phe Glu Asp
50          55          60
Ile Ala Ala Asp Tyr Glu Ser Gly Glu Leu His Pro Gly Asp Leu Lys
65          70          75          80
Lys Gly Leu Met Asn Ala Leu Asn Lys Ile Leu Gln Pro Val Arg Asp
85          90          95
His Phe Lys Thr Asp Ala Arg Ala Lys Asn Leu Leu Lys Gln Ile Lys
100         105         110
Ala Tyr Arg Val Thr Arg
115

```

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

```

aattagctca aggagaatca aaAgcgtogt ctcttggtcC ttccgctgcc aacaaaatgg      60
agctgtcgtc tgcgtccgcc atattaagcc actcctcctc cgccgctcag ctctctcagac      120
ctaagctcgg gtttattgat tgcgttcctc gtcgagcgat gatggtttct tctccttctt      180

```

ctctgcttcc	tcgatttttt	cggatggaat	ctcaatctca	gcttcgccaa	tctatctctt	240
gcctcgtctc	ttctctctct	ttctatggcat	taggtagaat	tgagagaagta	aagagagtaa	300
caaaaggaac	gaatgttttc	gtgaagatta	atttgatgg	tactggagtt	gcagatagtt	360
ctagtggaa	tcctttccct	gaccatattg	tagatcaact	tgcttcgcgt	ggcttgtttg	420
atgtgcacgt	tagagctact	gggtgatgtt	acattgatga	tcatacact	aatgaagata	480
tagctcttgc	cattggaaat	gctctattaa	aggctcttgg	tgagcgtaaa	gggattaacc	540
ggtttggtga	cttcacagct	cctctagatg	aagcgcttat	acatgtttcc	ttggacttgt	600
ctggctgacc	atatcttgg	tacaacttgg	agataccaa	tcagagagtt	ggaacatagt	660
atactcagtt	gggtgagcac	tttttccagt	cattggtgaa	tactcttggt	atgactcttc	720
acatccggca	gctcgtctgt	gaaaactctc	atcacataat	agagggcagc	tttaaggcgt	780
ttgcacagc	tctacagcaa	gcaacagaga	ctgacCacg	cgtgtgtggg	acaataccaa	840
gttcaaaagg	agctcttatca	cgtctcttga	agctaataca	acacacaaga	cagttccocag	900
attcacactt	catcgtcgag	ttcatgagcc	atcgtcaatt	ctcttatggt	accaaatgcc	960
aagcctgttg	gatcttctgt	ttccattcca	ttacagaagc	acaaaagcga	aaatgtgaaa	1020
atagattaga	gatcacacag	ttcagaagat	cataggctca	tctttatatt	aactcgttgt	1080
tgacagtggt	attaaacctc	ttaccattgc	tgtatcatca	tcaactgaga	acttactgtg	1140
agttgaagtg	actgttaatt	gctc				

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..288

(D) OTHER INFORMATION: / Ceres Seq. ID 1565974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Leu	Ala	Gln	Gly	Glu	Ser	Lys	Ala	Ser	Ser	Leu	Val	Pro	Ser	Ala	Ala
1		5		10		15		20		25		30		35	
Asn	Lys	Met	Glu	Ser	Ser	Ala	Ser	Ala	Ile	Leu	Ser	His	Ser	Ser	
		20		25		30		35		40		45		50	
Ser	Ala	Ala	Gln	Leu	Leu	Arg	Pro	Lys	Leu	Gly	Phe	Ile	Asp	Leu	Leu
		35		40		45		50		55		60		65	
Pro	Arg	Arg	Ala	Met	Ile	Val	Ser	Ser	Pro	Ser	Ser	Ser	Leu	Pro	Arg
		50		55		60		65		70		75		80	
Phe	Leu	Arg	Met	Glu	Ser	Gln	Ser	Gln	Leu	Arg	Gln	Ser	Ile	Ser	Cys
65		70		75		80		85		90		95		100	
Ser	Ala	Ser	Ser	Ser	Ser	Met	Ala	Leu	Gly	Arg	Ile	Gly	Glu	Val	
		85		90		95		100		105		110		115	
Lys	Arg	Val	Thr	Lys	Glu	Thr	Asn	Val	Ser	Val	Lys	Ile	Asn	Leu	Asp
		100		105		110		115		120		125		130	
Gly	Thr	Gly	Val	Ala	Asp	Ser	Ser	Ser	Gly	Ile	Pro	Phe	Leu	Asp	His
		115		120		125		130		135		140		145	
Met	Leu	Asp	Gln	Leu	Ala	Ser	His	Gly	Leu	Phe	Asp	Val	His	Val	Arg
		130		135		140		145		150		155		160	
Ala	Thr	Gly	Asp	Val	His	Ile	Asp	Asp	His	His	Thr	Asn	Glu	Asp	Ile
145		150		155		160		165		170		175		180	
Ala	Leu	Ala	Ile	Gly	Thr	Ala	Leu	Leu	Lys	Ala	Leu	Gly	Glu	Arg	Lys
		165		170		175		180		185		190		195	
Gly	Ile	Asn	Arg	Phe	Gly	Asp	Phe	Thr	Ala	Pro	Leu	Asp	Glu	Ala	Leu
		180		185		190		195		200		205		210	
Ile	His	Val	Ser	Leu	Asp	Leu	Ser	Gly	Arg	Pro	Tyr	Leu	Gly	Tyr	Asn
		195		200		205		210		215		220		225	
Leu	Glu	Ile	Pro	Thr	Gln	Arg	Val	Gly	Thr	Tyr	Asp	Thr	Gln	Leu	Val
		210		215		220		225		230		235		240	
Glu	His	Phe	Phe	Gln	Ser	Leu	Val	Asn	Thr	Ser	Gly	Met	Thr	Leu	His
225		230		235		240		245		250		255		260	
Ile	Arg	Gln	Leu	Ala	Gly	Glu	Asn	Ser	His	His	Ile	Ile	Glu	Ala	Thr
		245		250		255		260		265		270		275	

Phe	Lys	Ala	Phe	Ala	Arg	Ala	Leu	Arg	Gln	Ala	Thr	Glu	Thr	Asp	Pro	
		260						265					270			
Arg	Arg	Gly	Gly	Thr	Ile	Pro	Ser	Ser	Lys	Gly	Val	Leu	Ser	Arg	Ser	
		275					280					285				

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..270

(D) OTHER INFORMATION: / Ceres Seq. ID 1565975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Met	Glu	Leu	Ser	Ser	Ala	Ser	Ala	Ile	Leu	Ser	His	Ser	Ser	Ser	Ala	
1			5					10						15		
Ala	Gln	Leu	Leu	Arg	Pro	Lys	Leu	Gly	Phe	Ile	Asp	Leu	Leu	Pro	Arg	
		20					25						30			
Arg	Ala	Met	Ile	Val	Ser	Ser	Pro	Ser	Ser	Ser	Leu	Pro	Arg	Phe	Leu	
		35					40				45					
Arg	Met	Glu	Ser	Gln	Ser	Gln	Leu	Arg	Gln	Ser	Ile	Ser	Cys	Ser	Ala	
		50				55					60					
Ser	Ser	Ser	Ser	Ser	Met	Ala	Leu	Gly	Arg	Ile	Gly	Glu	Val	Lys	Arg	
65					70				75					80		
Val	Thr	Lys	Glu	Thr	Asn	Val	Ser	Val	Lys	Ile	Asn	Leu	Asp	Gly	Thr	
			85					90					95			
Gly	Val	Ala	Asp	Ser	Ser	Ser	Gly	Ile	Pro	Phe	Leu	Asp	His	Met	Leu	
		100						105					110			
Asp	Gln	Leu	Ala	Ser	His	Gly	Leu	Phe	Asp	Val	His	Val	Arg	Ala	Thr	
		115					120					125				
Gly	Asp	Val	His	Ile	Asp	Asp	His	His	Thr	Asn	Glu	Asp	Ile	Ala	Leu	
		130				135					140					
Ala	Ile	Gly	Thr	Ala	Leu	Leu	Lys	Ala	Leu	Gly	Glu	Arg	Lys	Gly	Ile	
145					150				155					160		
Asn	Arg	Phe	Gly	Asp	Phe	Thr	Ala	Pro	Leu	Asp	Glu	Ala	Leu	Ile	His	
			165					170					175			
Val	Ser	Leu	Asp	Leu	Ser	Gly	Arg	Pro	Tyr	Leu	Gly	Tyr	Asn	Leu	Glu	
		180					185						190			
Ile	Pro	Thr	Gln	Arg	Val	Gly	Thr	Tyr	Asp	Thr	Gln	Leu	Val	Glu	His	
		195					200					205				
Phe	Phe	Gln	Ser	Leu	Val	Asn	Thr	Ser	Gly	Met	Thr	Leu	His	Ile	Arg	
		210				215					220					
Gln	Leu	Ala	Gly	Glu	Asn	Ser	His	His	Ile	Ile	Glu	Ala	Thr	Phe	Lys	
225					230					235					240	
Ala	Phe	Ala	Arg	Ala	Leu	Arg	Gln	Ala	Thr	Glu	Thr	Asp	Pro	Arg	Arg	
			245					250					255			
Gly	Gly	Thr	Ile	Pro	Ser	Ser	Lys	Gly	Val	Leu	Ser	Arg	Ser			
		260					265						270			

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1565976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Met	Ile	Val	Ser	Ser	Pro	Ser	Ser	Ser	Leu	Pro	Arg	Phe	Leu	Arg	Met
1			5					10					15		
Glu	Ser	Gln	Ser	Gln	Leu	Arg	Gln	Ser	Ile	Ser	Cys	Ser	Ala	Ser	Ser
			20					25					30		
Ser	Ser	Ser	Met	Ala	Leu	Gly	Arg	Ile	Gly	Glu	Val	Lys	Arg	Val	Thr
			35				40					45			
Lys	Glu	Thr	Asn	Val	Ser	Val	Lys	Ile	Asn	Leu	Asp	Gly	Thr	Gly	Val
			50				55				60				
Ala	Asp	Ser	Ser	Ser	Gly	Ile	Pro	Phe	Leu	Asp	His	Met	Leu	Asp	Gln
65					70					75				80	
Leu	Ala	Ser	His	Gly	Leu	Phe	Asp	Val	His	Val	Arg	Ala	Thr	Gly	Asp
			85					90						95	
Val	His	Ile	Asp	Asp	His	His	Thr	Asn	Glu	Asp	Ile	Ala	Leu	Ala	Ile
			100					105						110	
Gly	Thr	Ala	Leu	Leu	Lys	Ala	Leu	Gly	Glu	Arg	Lys	Gly	Ile	Asn	Arg
			115				120						125		
Phe	Gly	Asp	Phe	Thr	Ala	Pro	Leu	Asp	Glu	Ala	Leu	Ile	His	Val	Ser
			130				135				140				
Leu	Asp	Leu	Ser	Gly	Arg	Pro	Tyr	Leu	Gly	Tyr	Asn	Leu	Glu	Ile	Pro
145					150					155					160
Thr	Gln	Arg	Val	Gly	Thr	Tyr	Asp	Thr	Gln	Leu	Val	Glu	His	Phe	Phe
			165					170						175	
Gln	Ser	Leu	Val	Asn	Thr	Ser	Gly	Met	Thr	Leu	His	Ile	Arg	Gln	Leu
			180					185					190		
Ala	Gly	Glu	Asn	Ser	His	His	Ile	Ile	Glu	Ala	Thr	Phe	Lys	Ala	Phe
			195				200					205			
Ala	Arg	Ala	Leu	Arg	Gln	Ala	Thr	Glu	Thr	Asp	Pro	Arg	Arg	Gly	Gly
			210				215				220				
Thr	Ile	Pro	Ser	Ser	Lys	Gly	Val	Leu	Ser	Arg	Ser				
225					230					235					

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1820 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1820

(D) OTHER INFORMATION: / Ceres Seq. ID 1565981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

acaatcattt	gattatttcc	tctctccgt	atctgtgtct	ctctctctct	gatcttttag	60
tggtcttgct	ttgtcgcttc	aacgcttaag	tttggaattg	tgtagctctg	cataatcatg	120
gcgaggaaga	tgcttgttga	tggtgagatt	gataaggttg	cgctgatgat	agcccaacgcg	180
acgcactatg	attttgattt	gtttgtcatc	ggtgccggga	gtggcgtggt	tcgtgctgct	240
agggttttcg	gttaatcatg	cgctaaggtt	ggtaattgtg	agcttcattt	tcacctatt	300
agcgtctagg	agattggagg	cgttggtgga	acctgtgtta	tcctgtggtt	gtttcctaaa	360
aagattctcg	tctatggagc	tacttacggt	ggtagaactg	aggatgctaa	aaattatggg	420
tggaataata	atgagaagat	cgacttcaca	tggaaagaagc	ttttgcaaaa	gaagactgat	480
gagataactga	gactgaataa	tatctacaag	cggttatgtg	caaatgctgc	ggtgaatttg	540
tatgaagctg	aaggaagagt	agttggtccc	aacgaagtgg	aggtagagca	atagatggc	600
acaaaaataa	gtttataccg	aaagcacata	ttgattgcca	ctggcagctg	ggcgcaaaa	660
cctaattatc	ctggacatga	ggtggctatt	acatctgatg	aagctttgag	cttggaagaa	720
tttcccaagc	gtgctatagt	gcttggagga	gggtatatgt	ctgtggagtt	tgcatcaata	780
tggtgtggaa	tggtgtctac	tgtagattta	ttcttcagga	aggaacttcc	cgtaaggggt	840
ttttagtacg	aaatgagggc	actagttgct	agaaatcttg	aaggaagggg	cgttaatctg	900
catccacaaa	caagtttgac	tcagtttgaca	aaaacagacc	aggggatcaa	atgcatatcg	960

tcccatgggg	aggaattcgt	ggcagatgtc	gtccatattg	ctactggcag	aagtccta	1020
acccaaaagt	tgaatttaga	agctgtgtgt	gttgaaactg	atcaggctgg	agctgtgaag	1080
gttgacgagt	attcacgaac	taataatact	agcatatggg	ctgtaggaga	tgcacaaaac	1140
cgaattaacc	ttacacactg	tgcgttaaat	gaggccacct	gttttgcgaa	cactgctttt	1200
gggtgaaagc	ctactaaagc	agaatacagc	aagtgtgcct	gtgctgtatt	ttgcatacca	1260
ccactagctg	tagtgggtct	cagcgaagaa	gaagcagtag	aacaagcaac	cggtgataatt	1320
ctgggtcttca	cctcaggctt	taatccaatg	aagaacacca	ttcttggacg	ccaggaaaaag	1380
acattgatga	agctaaatag	tgatgagaag	agtgataaag	ttattggagc	atccatgtgc	1440
ggctctgatg	cagctgagat	catgcagggg	attgcaattg	cgctcaagtg	tggagcaaac	1500
aaagcacaa	ttgatagcac	ggbtsggatG	CGCacatcca	tcttctgcag	aggaattttg	1560
gacaattgcgc	agtgtgacca	gacgcattgc	ccacaaaccc	aaaccttaaga	caaattctatg	1620
aaocccaaaa	tataaagagc	tatatagcat	gaaaactcgg	tacacttagt	ttgatcaaaag	1680
agtcagacaa	cgatgagttt	aatcatactc	gtgtcccaat	aaaggatttg	taatttttgt	1740
ttgtttgtat	gatgtcttct	tcttacttta	cttgagaaaa	catcaagggt	tcttctctta	1800
ttgcttagtg	gaactttatt					

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 496 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..496

(D) OTHER INFORMATION: / Ceres Seq. ID 1565982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Met	Ala	Arg	Lys	Met	Leu	Val	Asp	Gly	Glu	Ile	Asp	Lys	Val	Ala	Ala
1				5					10					15	
Asp	Glu	Ala	Asn	Ala	Thr	His	Tyr	Asp	Phe	Asp	Leu	Phe	Val	Ile	Gly
			20					25					30		
Ala	Gly	Ser	Gly	Gly	Val	Arg	Ala	Ala	Arg	Phe	Ser	Ala	Asn	His	Gly
			35					40					45		
Ala	Lys	Val	Gly	Ile	Cys	Glu	Leu	Pro	Phe	His	Pro	Ile	Ser	Ser	Glu
			50					55					60		
Glu	Ile	Gly	Gly	Val	Gly	Gly	Thr	Cys	Val	Ile	Arg	Gly	Cys	Val	Pro
65				70					75					80	
Lys	Lys	Ile	Leu	Val	Tyr	Gly	Ala	Thr	Tyr	Gly	Gly	Glu	Leu	Glu	Asp
			85						90					95	
Ala	Lys	Asn	Tyr	Gly	Trp	Glu	Ile	Asn	Glu	Lys	Val	Asp	Phe	Thr	Trp
			100					105						110	
Lys	Lys	Leu	Leu	Gln	Lys	Lys	Thr	Asp	Glu	Ile	Leu	Arg	Leu	Asn	Asn
			115					120					125		
Ile	Tyr	Lys	Arg	Leu	Leu	Ala	Asn	Ala	Ala	Val	Lys	Leu	Tyr	Glu	Gly
			130					135						140	
Glu	Gly	Arg	Val	Val	Gly	Pro	Asn	Glu	Val	Glu	Val	Arg	Gln	Ile	Asp
145				150					155					160	
Gly	Thr	Lys	Ile	Ser	Tyr	Thr	Ala	Lys	His	Ile	Leu	Ile	Ala	Thr	Gly
			165					170						175	
Ser	Arg	Ala	Gln	Lys	Pro	Asn	Ile	Pro	Gly	His	Glu	Leu	Ala	Ile	Thr
			180					185						190	
Ser	Asp	Glu	Ala	Leu	Ser	Leu	Glu	Glu	Phe	Pro	Lys	Arg	Ala	Ile	Val
			195					200					205		
Leu	Gly	Gly	Gly	Tyr	Ile	Ala	Val	Glu	Phe	Ala	Ser	Ile	Trp	Arg	Gly
			210					215						220	
Met	Gly	Ala	Thr	Val	Asp	Leu	Phe	Phe	Arg	Lys	Glu	Leu	Pro	Leu	Arg
225				230					235					240	
Gly	Phe	Asp	Asp	Glu	Met	Arg	Ala	Leu	Val	Ala	Arg	Asn	Leu	Glu	Gly
			245						250					255	
Arg	Gly	Val	Asn	Leu	His	Pro	Gln	Thr	Ser	Leu	Thr	Gln	Leu	Thr	Lys
			260					265						270	

Thr	Asp	Gln	Gly	Ile	Lys	Val	Ile	Ser	Ser	His	Gly	Glu	Glu	Phe	Val
	275						280					285			
Ala	Asp	Val	Val	Leu	Phe	Ala	Thr	Gly	Arg	Ser	Pro	Asn	Thr	Lys	Arg
	290					295					300				
Leu	Asn	Leu	Glu	Ala	Val	Gly	Val	Glu	Leu	Asp	Gln	Ala	Gly	Ala	Val
	305				310					315				320	
Lys	Val	Asp	Glu	Tyr	Ser	Arg	Thr	Asn	Ile	Pro	Ser	Ile	Trp	Ala	Val
			325					330					335		
Gly	Asp	Ala	Thr	Asn	Arg	Ile	Asn	Leu	Thr	Pro	Val	Ala	Leu	Met	Glu
		340					345					350			
Ala	Thr	Cys	Phe	Ala	Asn	Thr	Ala	Phe	Gly	Gly	Lys	Pro	Thr	Lys	Ala
		355				360					365				
Glu	Tyr	Ser	Asn	Val	Ala	Cys	Ala	Val	Phe	Cys	Ile	Pro	Pro	Leu	Ala
	370				375					380					
Val	Val	Gly	Leu	Ser	Glu	Glu	Glu	Ala	Val	Glu	Gln	Ala	Thr	Gly	Asp
	385				390					395				400	
Ile	Leu	Val	Phe	Thr	Ser	Gly	Phe	Asn	Pro	Met	Lys	Asn	Thr	Ile	Ser
			405					410					415		
Gly	Arg	Gln	Glu	Lys	Thr	Leu	Met	Lys	Leu	Ile	Val	Asp	Glu	Lys	Ser
		420					425					430			
Asp	Lys	Val	Ile	Gly	Ala	Ser	Met	Cys	Gly	Pro	Asp	Ala	Ala	Glu	Ile
		435				440					445				
Met	Gln	Gly	Ile	Ala	Ile	Ala	Leu	Lys	Cys	Gly	Ala	Thr	Lys	Ala	Gln
	450				455					460					
Phe	Asp	Ser	Thr	Xaa	Xaa	Met	Arg	Thr	Ser	Ile	Phe	Cys	Arg	Gly	Ile
	465				470				475					480	
Cys	Asp	Asn	Ala	Gln	Cys	Asp	Gln	Thr	His	Cys	Pro	Gln	Thr	Gln	Thr
			485					490					495		

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..492
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Met	Leu	Val	Asp	Gly	Glu	Ile	Asp	Lys	Val	Ala	Ala	Asp	Glu	Ala	Asn
1			5					10					15		
Ala	Thr	His	Tyr	Asp	Phe	Asp	Leu	Phe	Val	Ile	Gly	Ala	Gly	Ser	Gly
		20					25					30			
Gly	Val	Arg	Ala	Ala	Arg	Phe	Ser	Ala	Asn	His	Gly	Ala	Lys	Val	Gly
		35				40					45				
Ile	Cys	Glu	Leu	Pro	Phe	His	Pro	Ile	Ser	Ser	Glu	Glu	Ile	Gly	Gly
	50				55					60					
Val	Gly	Gly	Thr	Cys	Val	Ile	Arg	Gly	Cys	Val	Pro	Lys	Lys	Ile	Leu
	65			70				75					80		
Val	Tyr	Gly	Ala	Thr	Tyr	Gly	Gly	Glu	Leu	Glu	Asp	Ala	Lys	Asn	Tyr
			85					90					95		
Gly	Trp	Glu	Ile	Asn	Glu	Lys	Val	Asp	Phe	Thr	Trp	Lys	Lys	Leu	Leu
		100					105					110			
Gln	Lys	Lys	Thr	Asp	Glu	Ile	Leu	Arg	Leu	Asn	Asn	Ile	Tyr	Lys	Arg
		115				120					125				
Leu	Leu	Ala	Asn	Ala	Ala	Val	Lys	Leu	Tyr	Glu	Gly	Glu	Gly	Arg	Val
	130				135					140					
Val	Gly	Pro	Asn	Glu	Val	Glu	Val	Arg	Gln	Ile	Asp	Gly	Thr	Lys	Ile

145 150 155 160
Ser Tyr Thr Ala Lys His Ile Leu Ile Ala Thr Gly Ser Arg Ala Gln
165 170 175
Lys Pro Asn Ile Pro Gly His Glu Leu Ala Ile Thr Ser Asp Glu Ala
180 185 190
Leu Ser Leu Glu Glu Phe Pro Lys Arg Ala Ile Val Leu Gly Gly Gly
195 200 205
Tyr Ile Ala Val Glu Phe Ala Ser Ile Trp Arg Gly Met Gly Ala Thr
210 215 220
Val Asp Leu Phe Phe Arg Lys Glu Leu Pro Leu Arg Gly Phe Asp Asp
225 230 235 240
Glu Met Arg Ala Leu Val Ala Arg Asn Leu Glu Gly Arg Gly Val Asn
245 250 255
Leu His Pro Gln Thr Ser Leu Thr Gln Leu Thr Lys Thr Asp Gln Gly
260 265 270
Ile Lys Val Ile Ser Ser His Gly Glu Glu Phe Val Ala Asp Val Val
275 280 285
Leu Phe Ala Thr Gly Arg Ser Pro Asn Thr Lys Arg Leu Asn Leu Glu
290 295 300
Ala Val Gly Val Glu Leu Asp Gln Ala Gly Ala Val Lys Val Asp Glu
305 310 315 320
Tyr Ser Arg Thr Asn Ile Pro Ser Ile Trp Ala Val Gly Asp Ala Thr
325 330 335
Asn Arg Ile Asn Leu Thr Pro Val Ala Leu Met Glu Ala Thr Cys Phe
340 345 350
Ala Asn Thr Ala Phe Gly Gly Lys Pro Thr Lys Ala Glu Tyr Ser Asn
355 360 365
Val Ala Cys Ala Val Phe Cys Ile Pro Pro Leu Ala Val Val Gly Leu
370 375 380
Ser Glu Glu Glu Ala Val Glu Gln Ala Thr Gly Asp Ile Leu Val Phe
385 390 395 400
Thr Ser Gly Phe Asn Pro Met Lys Asn Thr Ile Ser Gly Arg Gln Glu
405 410 415
Lys Thr Leu Met Lys Leu Ile Val Asp Glu Lys Ser Asp Lys Val Ile
420 425 430
Gly Ala Ser Met Cys Gly Pro Asp Ala Ala Glu Ile Met Gln Gly Ile
435 440 445
Ala Ile Ala Leu Lys Cys Gly Ala Thr Lys Ala Gln Phe Asp Ser Thr
450 455 460
Xaa Xaa Met Arg Thr Ser Ile Phe Cys Arg Gly Ile Cys Asp Asn Ala
465 470 475 480
Gln Cys Asp Gln Thr His Cys Pro Gln Thr Gln Thr
485 490

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..272

(D) OTHER INFORMATION: / Ceres Seq. ID 1565984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Met Gly Ala Thr Val Asp Leu Phe Phe Arg Lys Glu Leu Pro Leu Arg
1 5 10 15
Gly Phe Asp Asp Glu Met Arg Ala Leu Val Ala Arg Asn Leu Glu Gly
20 25 30
Arg Gly Val Asn Leu His Pro Gln Thr Ser Leu Thr Gln Leu Thr Lys
35 40 45

Thr	Asp	Gln	Gly	Ile	Lys	Val	Ile	Ser	Ser	His	Gly	Glu	Glu	Phe	Val
50					55						60				
Ala	Asp	Val	Val	Leu	Phe	Ala	Thr	Gly	Arg	Ser	Pro	Asn	Thr	Lys	Arg
65					70				75					80	
Leu	Asn	Leu	Glu	Ala	Val	Gly	Val	Glu	Leu	Asp	Gln	Ala	Gly	Ala	Val
				85					90					95	
Lys	Val	Asp	Glu	Tyr	Ser	Arg	Thr	Asn	Ile	Pro	Ser	Ile	Trp	Ala	Val
				100				105					110		
Gly	Asp	Ala	Thr	Asn	Arg	Ile	Asn	Leu	Thr	Pro	Val	Ala	Leu	Met	Glu
		115					120					125			
Ala	Thr	Cys	Phe	Ala	Asn	Thr	Ala	Phe	Gly	Gly	Lys	Pro	Thr	Lys	Ala
		130				135					140				
Glu	Tyr	Ser	Asn	Val	Ala	Cys	Ala	Val	Phe	Cys	Ile	Pro	Pro	Leu	Ala
145					150				155					160	
Val	Val	Gly	Leu	Ser	Glu	Glu	Glu	Ala	Val	Glu	Gln	Ala	Thr	Gly	Asp
			165						170					175	
Ile	Leu	Val	Phe	Thr	Ser	Gly	Phe	Asn	Pro	Met	Lys	Asn	Thr	Ile	Ser
			180					185					190		
Gly	Arg	Gln	Glu	Lys	Thr	Leu	Met	Lys	Leu	Ile	Val	Asp	Glu	Lys	Ser
		195					200					205			
Asp	Lys	Val	Ile	Gly	Ala	Ser	Met	Cys	Gly	Pro	Asp	Ala	Ala	Glu	Ile
		210				215					220				
Met	Gln	Gly	Ile	Ala	Ile	Ala	Leu	Lys	Cys	Gly	Ala	Thr	Lys	Ala	Gln
225				230					235					240	
Phe	Asp	Ser	Thr	Xaa	Xaa	Met	Arg	Thr	Ser	Ile	Phe	Cys	Arg	Gly	Ile
			245						250					255	
Cys	Asp	Asn	Ala	Gln	Cys	Asp	Gln	Thr	His	Cys	Pro	Gln	Thr	Gln	Thr
			260					265					270		

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1312

(D) OTHER INFORMATION: / Ceres Seq. ID 1566011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

tccctgaagc	gtctctttct	tcctctgccc	ttctgttttt	ttgttttcgt	cgtctctctc	60
tcccgctctg	aaaaaatcgc	agaatccgtc	atgtctctccg	cgcgtaaatc	aactggctcc	120
gcgcgcagcg	cacccggaggt	tgacaagatg	ttctttctgt	accagtgcaa	caaacacgct	180
acaactctcaa	ttctctctac	cgctgatcct	ttttgtccaa	tttgtaaacca	agggtttctt	240
gaagaatcag	aagaccctaa	ccctaataca	tcctccaatt	tcaacccctaa	ctctctctgat	300
tcctttttcc	ccatggccga	tcctttctcc	accttgctcc	cgctcatatt	cggctcttcc	360
gctgcgcctc	cttccggcat	ggacttcatg	agcttattcg	gtccttcgat	gcaaccacag	420
gctcgttcca	ctcagcagaa	tcctcagttc	gacgcgtttg	atcgcgtttac	gtttcttcag	480
aatcatctcc	agactttgcg	atctagcggg	acgcactttg	agttcgtgat	cgagaatcat	540
ccttgatcgc	caggttaatg	tatgcctggg	aatttcgggt	attactctct	tggtccaggt	600
cttgagcagt	tgattcagca	actagctgag	aatgatccca	atcggttacg	aactcctcct	660
gcttcccaat	ccgccattga	tgctctctcc	actgttaagg	taacgaagga	tatgttgaaa	720
tccgagatga	accaatcgcc	ggtgtgtatg	gatgagtttg	aggatgtagg	cgatgttaag	780
catagtcctt	gtaagcagct	ctttcatcag	gactgtttgc	tccttggtgt	ggagttgcgt	840
aattcgtgtc	ctgttttgtc	attccaggtg	Cctacgggat	attcctgatta	tgagaacagg	900
agtcacaggaa	gtcagggggc	tggtgatgga	cgaggatcgg	ttgaggggtca	cgagacgcgc	960
aggttttagta	tacaactctc	tggccggttc	aggagacaa	atggctctcg	ttcagggctg	1020
ggagcacctg	gtgctggtgg	aggtaatctt	gagacacagg	gtgaagattt	ggatgagaaa	1080
tgtgttggtc	agtcattgct	tgaaactggt	atcagaagga	tatctatccc	aagtctccca	1140

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

1	Ser	Ser	Asp	Gly	5	Ser	Phe	Leu	Pro	Ser	Ser	Ser	Arg	Phe	Phe	Cys	Phe
Val	Val	Ser	Leu	Ser	Arg	Ser	Glu	Lys	Phe	Ala	Glu	Ser	Val	Met	Ser		
			20					25					30				
Ser	Gly	Val	Asn	Ser	Thr	Gly	Ser	Ala	Ala	Ala	Ala	Pro	Glu	Val	Asp		
		35					40					45					
Lys	Met	Phe	Cys	Tyr	Gln	Cys	Asn	Gln	Thr	Val	Thr	Ile	Ser	Ile			
	50				55						60						
Ser	Ser	Ser	Ala	Asp	Pro	Phe	Cys	Pro	Ile	Cys	Asn	Gln	Gly	Phe	Leu		
65				70						75					80		
Glu	Glu	Tyr	Glu	Asp	Asn	Pro	Asn	Gln	Ser	Leu	Asn	Phe	Asn	Phe	Pro		
				85				90					95				
Asn	Ser	Ser	Asp	Ser	Phe	Phe	Pro	Met	Ala	Asp	Pro	Phe	Ser	Thr	Leu		
			100					105					110				
Leu	Pro	Leu	Ile	Phe	Gly	Ser	Ser	Ala	Ala	Ala	Pro	Ser	Gly	Met	Asp		
		115					120					125					
Phe	Met	Ser	Leu	Phe	Gly	Pro	Ser	Met	Gln	Pro	Gln	Ala	Arg	Ser	Thr		
	130					135					140						
Gln	Gln	Asn	Pro	Gln	Ser	Asp	Ala	Phe	Asp	Pro	Phe	Thr	Phe	Leu	Glu		
145					150					155					160		
Asn	His	Leu	Gln	Thr	Leu	Arg	Ser	Ser	Gly	Thr	His	Phe	Glu	Phe	Val		
			165						170					175			
Ile	Glu	Asn	His	Pro	Ser	Asp	Pro	Gly	Asn	Arg	Met	Pro	Gly	Asn	Phe		
		180						185					190				
Gly	Asp	Tyr	Phe	Phe	Gly	Pro	Gly	Leu	Glu	Gln	Leu	Ile	Gln	Gln	Leu		
		195					200					205					
Ala	Glu	Asn	Asp	Pro	Asn	Arg	Tyr	Gly	Thr	Pro	Pro	Ala	Ser	Lys	Ser		
		210				215					220						
Ala	Ile	Asp	Ala	Leu	Pro	Thr	Val	Lys	Val	Thr	Lys	Asp	Met	Leu	Lys		
225					230					235				240			
Ser	Glu	Met	Asn	Gln	Cys	Ala	Val	Cys	Met	Asp	Glu	Phe	Glu	Asp	Gly		
			245					250					255				
Ser	Asp	Val	Lys	Gln	Met	Pro	Cys	Lys	His	Val	Phe	His	Gln	Asp	Cys		
		260						265					270				
Leu	Leu	Pro	Trp	Leu	Glu	Leu	His	Asn	Ser	Cys	Pro	Val	Cys	Arg	Phe		
		275					280					285					
Gln	Leu	Pro	Thr	Asp	Asp	Pro	Asp	Tyr	Glu	Asn	Arg	Ser	Gln	Gly	Ser		
		290				295					300						
Gln	Gly	Ser	Gly	Asp	Gly	Arg	Gly	Ser	Val	Glu	Gly	Gln	Gln	Thr	Pro		
305				310						315					320		
Arg	Phe	Ser	Ile	Gln	Leu	Pro	Trp	Pro	Phe	Arg	Arg	Gln	Asp	Gly	Ser		
			325						330				335				

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..328
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Met	Ser	Ser	Gly	Val	Asn	Ser	Thr	Gly	Ser	Ala	Ala	Ala	Ala	Pro	Glu
1				5				10						15	
Val	Asp	Lys	Met	Phe	Phe	Cys	Tyr	Gln	Cys	Asn	Gln	Thr	Val	Thr	Ile
		20						25					30		
Ser	Ile	Ser	Ser	Ser	Ala	Asp	Pro	Phe	Cys	Pro	Ile	Cys	Asn	Gln	Gly
		35					40					45			
Phe	Leu	Glu	Glu	Tyr	Glu	Asp	Pro	Asn	Pro	Asn	Gln	Ser	Leu	Asn	Phe
		50				55					60				
Asn	Pro	Asn	Ser	Ser	Asp	Ser	Phe	Phe	Pro	Met	Ala	Asp	Pro	Phe	Ser
				70						75				80	
Thr	Leu	Leu	Pro	Leu	Ile	Phe	Gly	Ser	Ser	Ala	Ala	Ala	Pro	Ser	Gly
			85					90						95	
Met	Asp	Phe	Met	Ser	Leu	Phe	Gly	Pro	Ser	Met	Gln	Pro	Gln	Ala	Arg
			100					105					110		
Ser	Thr	Gln	Gln	Asn	Pro	Gln	Ser	Asp	Ala	Phe	Asp	Pro	Phe	Thr	Phe
			115					120					125		
Leu	Gln	Asn	His	Leu	Gln	Thr	Leu	Arg	Ser	Ser	Gly	Thr	His	Phe	Glu
			130				135				140				
Phe	Val	Ile	Glu	Asn	His	Pro	Ser	Asp	Pro	Gly	Asn	Arg	Met	Pro	Gly
			145				150				155			160	
Asn	Phe	Gly	Asp	Tyr	Phe	Phe	Gly	Pro	Gly	Leu	Glu	Gln	Leu	Ile	Gln
			165						170					175	
Gln	Leu	Ala	Glu	Asn	Asp	Pro	Asn	Arg	Tyr	Gly	Thr	Pro	Pro	Ala	Ser
			180					185					190		
Lys	Ser	Ala	Ile	Asp	Ala	Leu	Pro	Thr	Val	Lys	Val	Thr	Lys	Asp	Met
			195				200					205			
Leu	Lys	Ser	Glu	Met	Asn	Gln	Cys	Ala	Val	Cys	Met	Asp	Glu	Phe	Glu
			210				215				220				
Asp	Gly	Ser	Asp	Val	Lys	Gln	Met	Pro	Cys	Lys	His	Val	Phe	His	Gln
			225			230				235				240	
Asp	Cys	Leu	Leu	Pro	Trp	Leu	Glu	Leu	His	Asn	Ser	Cys	Pro	Val	Cys
			245					250						255	
Arg	Phe	Glu	Leu	Pro	Thr	Asp	Asp	Pro	Asp	Tyr	Glu	Asn	Arg	Ser	Gln
			260				265						270		
Gly	Ser	Gln	Gly	Ser	Gly	Asp	Gly	Arg	Gly	Ser	Val	Glu	Gly	Gln	Gln
			275				280					285			
Thr	Pro	Arg	Phe	Ser	Ile	Gln	Leu	Pro	Trp	Pro	Phe	Arg	Arg	Gln	Asp
			290				295				300				
Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ala	Pro	Gly	Ala	Gly	Gly	Gly	Asn	Leu
			305			310				315					320
Glu	Thr	Arg	Gly	Glu	Asp	Leu	Asp								
						325									

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..309

(D) OTHER INFORMATION: / Ceres Seq. ID 1566014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Met	Phe	Phe	Cys	Tyr	Gln	Cys	Asn	Gln	Thr	Val	Thr	Ile	Ser	Ile	Ser
1			5					10					15		
Ser	Ser	Ala	Asp	Pro	Phe	Cys	Pro	Ile	Cys	Asn	Gln	Gly	Phe	Leu	Glu
		20						25				30			
Glu	Tyr	Glu	Asp	Pro	Asn	Pro	Asn	Gln	Ser	Leu	Asn	Phe	Asn	Pro	Asn
	35					40					45				
Ser	Ser	Asp	Ser	Phe	Phe	Pro	Met	Ala	Asp	Pro	Phe	Ser	Thr	Leu	Leu
	50				55						60				
Pro	Leu	Ile	Phe	Gly	Ser	Ser	Ala	Ala	Ala	Pro	Ser	Gly	Met	Asp	Phe
65				70					75					80	
Met	Ser	Leu	Phe	Gly	Pro	Ser	Met	Gln	Pro	Gln	Ala	Arg	Ser	Thr	Gln
			85					90					95		
Gln	Asn	Pro	Gln	Ser	Asp	Ala	Phe	Asp	Pro	Phe	Thr	Phe	Leu	Gln	Asn
		100						105					110		
His	Leu	Gln	Thr	Leu	Arg	Ser	Ser	Gly	Thr	His	Phe	Glu	Phe	Val	Ile
	115					120						125			
Glu	Asn	His	Pro	Ser	Asp	Pro	Gly	Asn	Arg	Met	Pro	Gly	Asn	Phe	Gly
	130				135						140				
Asp	Tyr	Phe	Phe	Gly	Pro	Gly	Leu	Glu	Gln	Leu	Ile	Gln	Gln	Leu	Ala
145				150					155					160	
Glu	Asn	Asp	Pro	Asn	Arg	Tyr	Gly	Thr	Pro	Pro	Ala	Ser	Lys	Ser	Ala
			165						170					175	
Ile	Asp	Ala	Leu	Pro	Thr	Val	Lys	Val	Thr	Lys	Asp	Met	Leu	Lys	Ser
		180						185					190		
Glu	Met	Asn	Gln	Cys	Ala	Val	Cys	Met	Asp	Glu	Phe	Glu	Asp	Gly	Ser
		195						200					205		
Asp	Val	Lys	Gln	Met	Pro	Cys	Lys	His	Val	Phe	His	Gln	Asp	Cys	Leu
	210					215						220			
Leu	Pro	Trp	Leu	Glu	Leu	His	Asn	Ser	Cys	Pro	Val	Cys	Arg	Phe	Glu
225					230					235				240	
Leu	Pro	Thr	Asp	Asp	Pro	Asp	Tyr	Glu	Asn	Arg	Ser	Gln	Gly	Ser	Gln
			245						250					255	
Gly	Ser	Gly	Asp	Gly	Arg	Gly	Ser	Val	Glu	Gly	Gln	Gln	Thr	Pro	Arg
		260						265					270		
Phe	Ser	Ile	Gln	Leu	Pro	Trp	Pro	Phe	Arg	Arg	Gln	Asp	Gly	Ser	Gly
		275						280					285		
Ser	Gly	Ser	Gly	Ala	Pro	Gly	Ala	Gly	Gly	Gly	Asn	Leu	Glu	Thr	Arg
	290					295					300				
Gly	Glu	Asp	Leu	Asp											
305															

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 766 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..766

(D) OTHER INFORMATION: / Ceres Seq. ID 1566024

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

acgtgtcctc	agcttgaaca	gataattctg	cgactcttga	gaaaggaaga	cgaaggaagg	60
agaatagttag	aagaagaaga	aaggagagtg	cttgatgatat	ctacgtagaaa	ggaagatggc	120
cttatctcaaa	gtgtctcgct	ctctcgccct	ttctcttccc	aattctgggtg	ccctaagagc	180
agccacaatc	acaaacccaa	cttctacatg	tcgggtttcat	gttccgcaac	ttgctggaat	240

ccgatccacc ttgccttctg gttctcctct cttgccattg aagttgagta tgacccgtag 300
aggaggaaac agagcagcat cagtttccat aagaagttag caaagtacag aaggaagcag 360
tggtttgat atatggcttg gtcgtggcgc catggttggt ttgacagttg ccattactgt 420
tgaaatttcc actggaanaa gacttcttga gaattttgga gtacgaagtc cattgCctac 480
ggttgcttta gctgttacag cattgggttg ggttctagct gcggttttca tcttccaatc 540
ttcttctaaa aactgatcaa caagaatctt gtttgtagt ctgccgagga tcatttttctt 600
gtattaagaa tcttgatata tatatcactg taacttctac atccatcagt ggaaaaaatc 660
ttacattctt agtttttttt ggcaacatac atgatctata catgtctttt ggccaaatct 720
tatttttgta tttttaaaac atgatctata acatgtatta agtttg

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1566025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Met Ala Leu Ser Gln Val Ser Ala Ser Leu Ala Phe Ser Leu Pro Asn
1 5 10 15
Ser Gly Ala Leu Lys Leu Ala Thr Ile Thr Asn Pro Thr Ser Thr Cys
20 25 30
Arg Val His Val Pro Gln Leu Ala Gly Ile Arg Ser Thr Phe Ala Ser
35 40 45
Gly Ser Pro Leu Leu Pro Leu Lys Leu Ser Met Thr Arg Arg Gly Gly
50 55 60
Asn Arg Ala Ala Ser Val Ser Ile Arg Ser Glu Gln Ser Thr Glu Gly
65 70 75 80
Ser Ser Gly Leu Asp Ile Trp Leu Gly Arg Gly Ala Met Val Gly Phe
85 90 95
Ala Val Ala Ile Thr Val Glu Ile Ser Thr Gly Lys Gly Leu Leu Glu
100 105 110
Asn Phe Gly Val Ala Ser Pro Leu Pro Thr Val Ala Leu Ala Val Thr
115 120 125
Ala Leu Val Gly Val Leu Ala Ala Val Phe Ile Phe Gln Ser Ser Ser
130 135 140
Lys Asn
145

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1566026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Met Thr Arg Arg Gly Gly Asn Arg Ala Ala Ser Val Ser Ile Arg Ser
1 5 10 15
Glu Gln Ser Thr Glu Gly Ser Ser Gly Leu Asp Ile Trp Leu Gly Arg
20 25 30
Gly Ala Met Val Gly Phe Ala Val Ala Ile Thr Val Glu Ile Ser Thr
35 40 45
Gly Lys Gly Leu Leu Glu Asn Phe Gly Val Ala Ser Pro Leu Pro Thr
50 55 60

Val Ala Leu Ala Val Thr Ala Leu Val Gly Val Leu Ala Ala Val Phe
65 70 75 80
Ile Phe Gln Ser Ser Ser Lys Asn
95

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1610

(D) OTHER INFORMATION: / Ceres Seq. ID 1566031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

```
tctcttttct ttcactctct gttttgttct ttatgcctcg agaattgatg tggattttttc 60
atatattcagt taactcttagc taattgactt gaaattcaat gaaaagattc aatttttgggt 120
ttaattaaagc aagttgtgag atagatgaac gaatttgttg accaattgcg ttttacaggga 180
tacggttgggt gctctatgaa gtcttataga ttatctgaac ttagtctctc ccaagttgat 240
agtttgaagt cagccctcgc cattgacctc tcttctatt tcgccactgt gaacccgatt 300
atcgatgctg ttcgtagcaa tggggataat gctgtcaaag aatacactga aagatttgac 360
aaagtccagc tgaataaagt tgtggaagat atgtctgagc ttctgtgtcc tgagctcgat 420
tccaaatgtca aagaagcggt tgcgtgtgag tatgacaaca tatatgcgtt tcaactgacc 480
caaaaagtc aa ctgagaaaag cggtgagaat atgaaaaggtg tcagatgtaa aaggggtgca 540
agatctattg gcctcttagg tcTtTaWkt gcctggtgga acagctgttt tgccatcaac 600
ggcctttgatg ctgtctattc ctgctcaaat tgctggatgt aaaaacagttg ttcttgcaac 660
tccaccaagt aagatgagaa gcatttgtaa ggaaggttctg tattgcgcca agagggctgg 720
tgtaactcac atactcaaa ctggtggagc gcaggtcata gctgccatgg cctggggagc 780
agatcttctg ccaagagttg agaagatttt tggctcctggg aaccagtatg tcacagctgc 840
taagatgatt ctccaaacaa gcgagggcaat ggtctcaatc gatatgcctg ctggtccttc 900
agaagtctca gttattgtcg actgaacatgc tagtccagtt tacattgcag cagactactc 960
ttctcaggcg gagcatggtc cagatagtc aagtgttctt gtatgtgtgg gcgagtaggt 1020
agatctcaac gccatcgaag aagaatttgc caagcagtg aaaaagccttc ctgagaggaga 1080
gtttgtctca aagcactaaa gtcacagttt cacagtggtt gctcgagata tgattgagcg 1140
aatatctttc tcaaatctat atgcacccga acatttgatc atcaatgtca aagacgctga 1200
gaaatgggag ggactgatt agaacgcagg ctcggttttc ataggacat ggaactccaga 1260
gagtggtggg gattatgcga gcgggacaaa ccacgttctt ccaacatagc gatatgcagg 1320
aatgtacagt ggcgtctctc tcgactcttt cctaaaagttc atgactgtac aatctttgac 1380
agaggaaaggt ctgagaaaac tcggccctta ttagcaact atggctgaaa tcgaaggttt 1440
agatgcacac aagagagccg ttactctcag actcaaggt atcgaagcca aacagctctgc 1500
ataatccaat tgagatttat attcagacaa aagagcgcaa aattcttttt gtattgtatg 1560
aacatatttg gtttctcgag attggaatac aataaaataa gagatgttgg
```

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..298

(D) OTHER INFORMATION: / Ceres Seq. ID 1566032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

```
Met Leu Ala Ile Pro Ala Gln Ile Ala Gly Cys Lys Thr Val Leu
1 5 10 15
Ala Thr Pro Pro Ser Lys Asp Gly Ser Ile Cys Lys Glu Val Leu Tyr
20 25 30
Cys Ala Lys Arg Ala Gly Val Thr His Ile Leu Lys Ala Gly Gly Ala
35 40 45
```

Gln Ala Ile Ala Ala Met Ala Trp Gly Thr Asp Ser Cys Pro Lys Val
50 55 60
Glu Lys Ile Phe Gly Pro Gly Asn Gln Tyr Val Thr Ala Ala Lys Met
65 70 75 80
Ile Leu Gln Asn Ser Glu Ala Met Val Ser Ile Asp Met Pro Ala Gly
85 90 95
Pro Ser Glu Val Leu Val Ile Ala Asp Glu His Ala Ser Pro Val Tyr
100 105 110
Ile Ala Ala Asp Leu Leu Ser Gln Ala Glu His Gly Pro Asp Ser Gln
115 120 125
Val Val Leu Val Val Val Gly Asp Ser Val Asp Leu Asn Ala Ile Glu
130 135 140
Glu Glu Ile Ala Lys Gln Cys Lys Ser Leu Pro Arg Gly Glu Phe Ala
145 150 155 160
Ser Lys Ala Leu Ser His Ser Phe Thr Val Phe Ala Arg Asp Met Ile
165 170 175
Glu Ala Ile Ser Phe Ser Asn Leu Tyr Ala Pro Glu His Leu Ile Ile
180 185 190
Asn Val Lys Asp Ala Glu Lys Trp Glu Gly Leu Ile Glu Asn Ala Gly
195 200 205
Ser Val Phe Ile Gly Pro Trp Thr Pro Glu Ser Val Gly Asp Tyr Ala
210 215 220
Ser Gly Thr Asn His Val Leu Pro Thr Tyr Gly Tyr Ala Arg Met Tyr
225 230 235 240
Ser Gly Val Ser Leu Asp Ser Phe Leu Lys Phe Met Thr Val Gln Ser
245 250 255
Leu Thr Glu Glu Gly Leu Arg Asn Leu Gly Pro Tyr Val Ala Thr Met
260 265 270
Ala Glu Ile Glu Gly Leu Asp Ala His Lys Arg Ala Val Thr Leu Arg
275 280 285
Leu Lys Asp Ile Glu Ala Lys Gln Leu Ala
290 295

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..245
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Met Ala Trp Gly Thr Asp Ser Cys Pro Lys Val Glu Lys Ile Phe Gly
1 5 10 15
Pro Gly Asn Gln Tyr Val Thr Ala Ala Lys Met Ile Leu Gln Asn Ser
20 25 30
Glu Ala Met Val Ser Ile Asp Met Pro Ala Gly Pro Ser Glu Val Leu
35 40 45
Val Ile Ala Asp Glu His Ala Ser Pro Val Tyr Ile Ala Ala Asp Leu
50 55 60
Leu Ser Gln Ala Glu His Gly Pro Asp Ser Gln Val Val Leu Val Val
65 70 75 80
Val Gly Asp Ser Val Asp Leu Asn Ala Ile Glu Glu Glu Ile Ala Lys
85 90 95
Gln Cys Lys Ser Leu Pro Arg Gly Glu Phe Ala Ser Lys Ala Leu Ser
100 105 110
His Ser Phe Thr Val Phe Ala Arg Asp Met Ile Glu Ala Ile Ser Phe
115 120 125
Ser Asn Leu Tyr Ala Pro Glu His Leu Ile Ile Asn Val Lys Asp Ala

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..472

(D) OTHER INFORMATION: / Ceres Seq. ID 1566045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

aattcatttc	ataatcatatc	acctctctac	atttgttact	actttctctt	aacttgtttt	60
caaaagagaaa	tcacaatcta	tctgttccaa	gatgagtc	tacagccaaa	accaatcttc	120
aggagcttat	cctacgcccgc	cagtgtctac	cgccctctac	gtggcaccgc	caccgctagg	180
ttaccacaacg	aacgacacaa	gtcatgccac	ggtggcaacg	gtggagacaa	agtccaaggg	240
tgatggattc	ttaaaaaggct	gtcttgcggc	catgtgtgtg	tgttgtgtcc	tcgacgcatg	300
cttctgaaga	cttagatgggt	ttattttgat	tattctttga	ttttgtttta	ccaaaatgat	360
ctgactaggt	ttatgacatt	tggtacttct	atttgttaat	tcatttctat	atcaactctt	420
ctWttKgc	at	tgtgtaattt	tataaattcc	taatatatcg	ttgtttttct	ct

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1566046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Asn	Ser	Phe	His	Asn	His	Thr	Pro	Leu	Tyr	Ile	Cys	Tyr	Tyr	Phe	Leu
1			5					10						15	
Leu	Thr	Cys	Phe	Gln	Arg	Glu	Ile	Thr	Ile	Tyr	Leu	Phe	Gln	Asp	Glu
			20					25					30		
Ser	Ile	Gln	Pro	Lys	Pro	Ile	Phe	Arg	Ser	Leu	Ser	Tyr	Ala	Ala	Ser
			35				40					45			
Val	Tyr	Arg	Pro	Leu	Arg	Gly	Thr	Ala	Thr	Ala	Arg	Leu	Pro	Asn	Glu
			50				55				60				
Arg	His	Lys	Ser	Cys	His	Gly	Gly	Asn	Gly	Gly	Asp	Lys	Val	Gln	Gly
65					70				75					80	

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1566047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Met	Ser	Gln	Tyr	Ser	Gln	Asn	Gln	Ser	Ser	Gly	Ala	Tyr	Pro	Thr	Pro
1			5					10						15	
Pro	Val	Ser	Thr	Gly	Pro	Tyr	Val	Ala	Pro	Pro	Pro	Leu	Gly	Tyr	Pro
			20					25					30		
Thr	Asn	Asp	Thr	Ser	His	Ala	Thr	Val	Ala	Thr	Val	Glu	Thr	Lys	Ser
			35				40					45			
Lys	Gly	Asp	Gly	Phe	Leu	Lys	Gly	Cys	Leu	Ala	Ala	Met	Cys	Cys	Cys
			50				55				60				
Cys	Val	Leu	Asp	Ala	Cys	Phe									
65					70										

(2) INFORMATION FOR SEQ ID NO:170:

(A) LENGTH: 1268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..1268

SEQUENCE DESCRIPTION: SEQ ID NO:170:

atgtaagagat	gacccaagc	tgcggctgctt	agctcagaat	aaagtgtgaag	accgtgacga	120
agtgtagagat	gatcatcggc	tggctagagat	tatctcagatt	atactcagaa	aagaagaaga	160
atcgcaggaat	caagagaaata	gagacgagga	tgatgatgaa	gatgccttgg	aagaagaag	180
aagaagaatt	aagggaaga	atcttagact	agcacaagag	gaggctctgt	tactctctt	200
aagaagaaga	gatgatagat	aacgagaaga	agaggagag	gaggagtctt	agtcacgac	300
tgattcgga	gatgatatgc	ctgttgattgc	cttgattaa	ccgtgttttg	ctccgaaagc	360
tgagagagat	acaattcgag	agcgagagag	gcttgaggct	aagaagaaga	tacctgaga	420
atttagcaag	agaaattagg	agcacaagaa	atgagagaca	aagcaaatgt	tggttgaga	480
agttgagaaa	gatgaagaga	tacggagaaga	catactattg	gagagaacta	attctggaga	540
tgtggaact	gatcagcaac	tcaatgaagc	tgaggagatg	gaagttgtga	agacacagga	600
gattgttag	atcaagagag	aaagaagaag	aaggcgaaat	atgctgagag	agagggaaga	660
aatagagaag	tggaggaata	tgacagagca	ggagagagga	gatggggaga	ggaagaatacc	720
gaacaacctt	tcagctcaac	cgaaaaagaa	atggaaactt	atgcagaat	attaccataa	780
gggtgccttc	ttcacggcag	attctgatga	tgaggcaggt	tctcgtgga	ccgatggtat	840
atttcacgoc	gattctctcg	ctctcaagcg	agaagatagg	tgtgacaat	cgattctccc	900
caaaagttag	caagctcaagc	atccttggct	tagtggaaga	actaaattga	ctcaacctgt	960
caatgaagac	acaaacagatt	ggagataacc	gtggacatcc	aatgatcttc	tacgtgaaa	1020
atacaacag	aaaatggcag	cgctggatgc	tccaatcgca	aaacccaaga	ggagcagaag	1080
gatgaagaat	tgggagacct	aaacccgaac	aaactttact	tgtttgtgtt	ttaataatcca	1140
atgatcgac	agtggtgatg	ggtagtagaaa	aaacatcgta	actcttctat	cagttatgtc	1200
cttgagctct	ctaaatccta	gtaataaaaa	atattgctca	aaagaatgaa	gacctaacat	1260
aattcgatt						

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

FEATURE:

(B) LOCATION: 1..366

(D) OTHER INFORMATION: / Ceres Seq. ID 1566049

Arg	Lys	Asp	Asp	Pro	Arg	Leu	Arg	Arg	Leu	Ala	Gln	Thr	Lys	Val	Glu
1				5					10				15		
Asn	Arg	Asp	Glu	Val	Arg	Ala	Asp	His	Arg	Arg	Ile	Arg	Gln	Ala	Glu
			20					25					30		
Ile	Ile	Ser	Thr	Glu	Glu	Glu	Glu	Ser	Arg	Asn	Gln	Glu	Asn	Arg	Asp
		35					40					45			
Glu	Asp	Asp	Asp	Glu	Asp	Ala	Leu	Glu	Glu	Arg	Arg	Arg	Arg	Ile	Lys
		50				55					60				
Glu	Lys	Asn	Leu	Arg	Leu	Ala	Gln	Glu	Glu	Ala	Ala	Leu	Leu	Pro	Leu
65					70					75				80	
Glu	Glu	Glu	Asp	Glu	Ile	Gln	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Ser
			85					90						95	
Glu	Tyr	Glu	Thr	Asp	Ser	Glu	Asp	Asp	Met	Pro	Gly	Ile	Ala	Leu	Ile
			100					105					110		
Lys	Pro	Val	Phe	Val	Pro	Lys	Ala	Glu	Arg	Asp	Thr	Ile	Ala	Glu	Arg
		115					120					125			

Glu Arg Leu Glu Ala Glu Glu Glu Ala Leu Glu Glu Leu Ala Lys Arg
130 135 140
Lys Leu Glu Gln Arg Lys Ile Glu Thr Lys Gln Ile Val Val Glu Glu
145 150 155 160
Val Arg Lys Asp Glu Glu Ile Arg Lys Asn Ile Leu Leu Glu Glu Ala
165 170 175
Asn Ile Gly Asp Val Glu Thr Asp Asp Glu Leu Asn Glu Ala Glu Glu
180 185 190
Tyr Glu Val Trp Lys Thr Arg Glu Ile Gly Arg Ile Lys Arg Glu Arg
195 200 205
Asp Ala Arg Glu Ala Met Leu Arg Glu Arg Glu Glu Ile Glu Lys Leu
210 215 220
Arg Asn Met Thr Glu Gln Glu Arg Arg Asp Trp Glu Arg Lys Asn Pro
225 230 235 240
Lys Pro Ser Ser Ala Gln Pro Lys Lys Lys Asn Phe Met Gln Lys
245 250 255
Tyr Tyr His Lys Gly Ala Phe Phe Gln Ala Asp Pro Asp Asp Glu Ala
260 265 270
Gly Ser Ala Gly Thr Asp Gly Ile Phe Gln Arg Asp Phe Ser Ala Pro
275 280 285
Thr Gly Glu Asp Arg Leu Asp Lys Ser Ile Leu Pro Lys Val Met Gln
290 295 300
Val Lys His Phe Gly Arg Ser Gly Arg Thr Lys Trp Thr His Leu Val
305 310 315 320
Asn Glu Asp Thr Thr Asp Trp Ser Asn Pro Trp Thr Ser Asn Asp Pro
325 330 335
Leu Arg Glu Lys Tyr Asn Lys Lys Met Ala Gly Met Asp Ala Pro Ile
340 345 350
Ala Lys Pro Lys Gly Ser Lys Lys Met Lys Asp Trp Glu Thr
355 360 365

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..261
(D) OTHER INFORMATION: / Ceres Seq. ID 1566050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met Pro Gly Ile Ala Leu Ile Lys Pro Val Phe Val Pro Lys Ala Glu
1 5 10 15
Arg Asp Thr Ile Ala Glu Arg Glu Arg Leu Glu Ala Glu Glu Ala
20 25 30
Leu Glu Glu Leu Ala Lys Arg Lys Leu Glu Gln Arg Lys Ile Glu Thr
35 40 45
Lys Gln Ile Val Val Glu Glu Val Arg Lys Asp Glu Glu Ile Arg Lys
50 55 60
Asn Ile Leu Leu Glu Glu Ala Asn Ile Gly Asp Val Glu Thr Asp Asp
65 70 75 80
Glu Leu Asn Glu Ala Glu Glu Tyr Glu Val Trp Lys Thr Arg Glu Ile
85 90 95
Gly Arg Ile Lys Arg Glu Arg Asp Ala Arg Glu Ala Met Leu Arg Glu
100 105 110
Arg Glu Glu Ile Glu Lys Leu Arg Asn Met Thr Glu Gln Glu Arg Arg
115 120 125
Asp Trp Glu Arg Lys Asn Pro Lys Pro Ser Ser Ala Gln Pro Lys Lys
130 135 140
Lys Trp Asn Phe Met Gln Lys Tyr Tyr His Lys Gly Ala Phe Phe Gln

145	150	155	160
Ala Asp Pro Asp	Asp Glu Ala Gly	Ser Ala Gly Thr	Asp Gly Ile Phe
	165	170	175
Gln Arg Asp Phe	Ser Ala Pro Thr	Gly Glu Asp Arg	Leu Asp Lys Ser
	180	185	190
Ile Leu Pro Lys	Val Met Gln Val	Lys His Phe Gly	Arg Ser Gly Arg
	195	200	205
Thr Lys Trp Thr	His Leu Val Asn	Glu Asp Thr Thr	Asp Trp Ser Asn
	210	215	220
Pro Trp Thr Ser	Asn Asp Pro Leu	Arg Glu Lys Tyr	Asn Lys Lys Met
	225	230	235
Ala Gly Met Asp	Ala Pro Ile Ala	Lys Pro Lys Gly	Ser Lys Lys Met
	245	250	255
Lys Asp Trp Glu	Thr		
	260		

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1018 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1018

(D) OTHER INFORMATION: / Ceres Seq. ID 1566062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

gaccatcgac	catcgctcgtc	tctcgcgagc	tcagttgaaa	gatgttaacg	gctgatatac	60
caccaaatca	gtcaatctac	ataaaacata	tcaatgagaa	gatcaagaaa	gaagagctga	120
agaggtctct	tactgtgttg	ttctctcagt	ttggaagatt	acttgatgtg	gttgcgttaa	180
agactcctaa	gtctcgggga	caagcatggg	ttgtttttac	tgaagtcacc	gctgctagca	240
acgctgtccg	tcagatgcag	aactttcctt	tctatgataa	gcctatgcgg	atacaatag	300
caaaatcaaa	gtcagattat	gttactaaag	cgaagggcto	ttttgttcca	aaagaaaaga	360
agatgaagca	agCaagagaa	agttgaaagg	aagcgacatg	ctgaagaaac	tcaacaacca	420
agcatgccta	atggcgcaac	tactcagaac	ggaatgcctg	tgccaatttc	tctttctcgc	480
atcatcccaa	caatacaata	ttatcttctg	acagacgtca	ttatcgcaac	ttagtctgtg	540
aatttctgtt	tcttaatacc	cgtctctgtg	atttccacgc	ctcctttcca	gccgagtggg	600
caagacacga	tgcacacaaa	caacatactc	ttcattcata	atcttcccat	tgagacgaat	660
agtatgatgc	ttcagctcgt	ctttgagcaa	taccacggat	tcaaaagagat	aagaatgatc	720
gaagcaaaac	ccggaattgc	gtttgtggag	tatgaagacg	atgttcagtc	ttccatggcc	780
atgcaggtct	tccagggttt	caagatcact	ccgcagaatc	caatgggtcgt	ctcttttggc	840
aaagaagtga	aaccagagtt	ttgttatgcg	gatgaatggg	aatgatatac	taattagtag	900
ctgtttaaaa	gcaaacctgc	ttattttatt	tggttcgttt	ccgattagtg	gtgtgaatga	960
ccccgaagct	ttagaccaga	atgtaatgag	atcgaagaat	tgagagtgat	ttggttgg	

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1566063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Met Thr Ala Asp	Ile Pro Pro Asn	Gln Ser Ile	Tyr Ile Lys His
1	5	10	15
Ile Asn Glu Lys	Ile Lys Lys Glu	Glu Leu Lys Arg	Ser Leu Tyr Cys
	20	25	30
Leu Phe Ser Gln	Phe Gly Arg Leu	Leu Asp Val Val	Ala Leu Lys Thr

(2) INFORMATION FOR SEQ ID NO:175:

(A) LENGTH: 83 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..83

SEQUENCE DESCRIPTION: SEQ ID NO:175:

[illegible]

(1) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
MOLECULE TYPE: peptide

(A) NAM

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:176:

										5					10					15				
Leu	Arg	Arg	Ile	Gln	Trp	Ser	Ser	Leu	Leu	Pro	Arg	Ser	Glu	Asn	Gln									
										20					25					30				
Ser	Phe	Val	Met	Arg	Met	Asn	Gly	Asn	Asp	Ile	Leu	Ile	Ser	Ser	Cys									
										35					40					45				
Leu	Lys	Ala	Asn	Cys	Leu	Ile	Leu	Phe	Gly	Ser	Phe	Pro	Ile	Ser	Gly									
										50					55					60				
Val	Asn	Asp	Pro	Glu	Ala	Leu	Asp	Gln	Asn	Val	Met	Arg	Ser	Lys	Asn									
										65					70					75				
																				80				

(i) SEQUENCE CHARACTERISTICS:

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..111
(D) OTHER INFORMATION: / Ceres Seq. ID 1566102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```
Met Thr Ile Arg Glu Ser Phe Glu His Ile Pro Gln Trp Leu Glu Glu
1      5      10      15
Leu Arg Val His Ala Asp Lys Asn Ile Val Ile Ile Leu Ile Gly Asn
20      25      30
Lys Thr Asp Leu Glu Asn Gln Arg Ser Val Pro Val Glu Asp Ala Lys
35      40      45
Glu Phe Ala Glu Lys Glu Gly Leu Phe Phe Leu Glu Thr Xaa Ala Leu
50      55      60
Asn Ser Thr Asn Val Glu Asn Ser Phe Asn Thr Leu Leu Thr Glu Ile
65      70      75
Phe Asn Lys Val Asn Lys Lys Asn Leu Ala Lys Thr Thr Val Ser Cys
85      90      95
Ser Ser Gln Val Ser Leu Leu Arg Pro Pro Cys Val Ala Ala Xaa
100     105     110
```

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 579 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..579
(D) OTHER INFORMATION: / Ceres Seq. ID 1566103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```
gcgtagtac aaaaatatc tgataaatag ataaataaac atctttctat tcgtaaggac      60
gacaaaatc tctcaggttc tctagaattg tcagaatcat ttctaaggg aggtaaaaag      120
ggatcagtac cggagcaaaa cacagagaag cttctctggc agtcaagcga cgtcgctgat      180
agcgtgact ccaagttcgc gtgttgctcg tggagggtcc ttacgaggc tcgcgcgaag      240
ttgtacgcgc tgggacattc tgatcgtcgg aaactttact tctccatcaa gatgggaatt      300
gctttggcac tctgttcttt cgtcatcttt ctcaaagaac cgtctcaaga tgctagtaaa      360
ttcgcagttt gggcgattct caccgtcgtt ctcatcttgc agtattacgt cggagcaact      420
ttgggtaaag gattcaatag agcattagcg acaatgttag ctgaggagact tgctctcgcc      480
gtcgcgcagC tctctgtttt agcaggagag tttgaagaag tcatcatcgt aatctgcata      540
ttccttgtag gKttttTggt gctagtatt tgaaActat
```

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..155
(D) OTHER INFORMATION: / Ceres Seq. ID 1566104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

```
Met Gly Gly Lys Met Gly Ser Val Pro Glu Gln Asn Thr Glu Lys Leu
1      5      10      15
Leu Trp Gln Ser Ser Asp Val Ala Asp Ser Arg Asp Ser Lys Phe Arg
20      25      30
Cys Cys Ser Trp Arg Ala Leu Tyr Glu Ala Pro Ala Lys Leu Tyr Ala
35      40      45
Leu Gly His Ser Asp Arg Arg Lys Leu Tyr Phe Ser Ile Lys Met Gly
50      55      60
Ile Ala Leu Ala Leu Cys Ser Phe Val Ile Phe Leu Lys Glu Pro Leu
```


Met Gly Ile Ala Leu Ala Leu Cys Ser Phe Val Ile Phe Leu Lys Glu
1 5 10 15
Pro Leu Gln Asp Ala Ser Lys Phe Ala Val Trp Ala Ile Leu Thr Val
20 25 30
Val Leu Ile Phe Glu Tyr Tyr Val Gly Ala Thr Leu Val Lys Gly Phe
35 40 45

Asn Arg Ala Leu Gly Thr Met Leu Ala Gly Gly Leu Ala Leu Gly Val
50 55 60
Ala Gln Leu Ser Val Leu Ala Gly Glu Phe Glu Val Ile Ile Val
65 70 75 80
Ile Cys Ile Phe Leu Ala Xaa Phe Leu Val Leu Val Ile
85 90

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..939
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ctatctctca	tcacacatctt	agttcatgtt	cgagtttctc	tgcttcaatt	acaaagaatg	60
gctgcttcaa	gtgctgtcac	cgcaaaactac	gtctccaagc	cacctccatt	cgcactggat	120
gctttggagc	cgcatatgag	caaacaaact	ctggagtctc	actggggaaa	acatcacaga	180
gcttacgtgg	acaaacctcaa	gaaacaggtt	cttggaaaccg	agcttgaagg	caagccctta	240
gagcacatta	tcacacagcac	ttacaacaat	ggtgatcttc	tccttgcttt	caacaacgct	300
gctcaggcgt	ggaaccacga	gttctcttgg	gagtcaatga	aaccagggtg	tggaggaaaa	360
ccatcaggag	agcttcttgc	tttgcttgaa	agagatttca	cttcttatga	gaagttctat	420
gaagagttca	atgctgtctg	agccactcag	tttgagctgt	gctgggctgt	gcttgcttat	480
tcaaatgaaa	aactcaaatg	agtgaatact	cccaatgctg	tgaatccctt	tgtgctctgc	540
tttttccca	ttgctttacca	ttgatgtctg	ggagcatgct	tactaccttg	acttccagaa	600
ccgaagacca	gattacataa	agacattcat	gaccaatctt	gtgtcttggg	aagctgttaag	660
tgccagactt	gaggccgcga	aggctgtctc	tgcttaagca	aattttctga	caatttgact	720
tcagtgacag	tgagttctgc	atcaccgaag	tctcttataa	aattattgtc	gctgtaataa	780
ggacacagct	ctcttgttgt	gtatgtgtca	cagagttctt	cattttgctt	gtgtaatgaa	840
caattaaaca	tgctcttttc	tgagtggtgt	tgcgttttgt	gtgtgtcaag	tttttcatcg	900
ttctctttat	taaaactcaa	ttggcaccta	ccatcagtg			

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..187
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Leu Ser Leu Ile His Ile Leu Val His Val Arg Val Ser Leu Leu Gln	
1 5 10 15	
Leu Gln Arg Met Ala Ala Ser Ser Ala Val Thr Ala Asn Tyr Val Leu	
20 25 30	
Lys Pro Pro Pro Phe Ala Leu Asp Ala Leu Glu Pro His Met Ser Lys	
35 40 45	
Gln Thr Leu Glu Phe His Trp Gly Lys His His Arg Ala Tyr Val Asp	
50 55 60	
Asn Leu Lys Lys Gln Val Leu Gly Thr Glu Leu Glu Gly Lys Pro Leu	
65 70 75 80	
Glu His Ile Ile His Ser Thr Tyr Asn Asn Gly Asp Leu Leu Pro Ala	
85 90 95	
Phe Asn Asn Ala Ala Gln Ala Trp Asn His Glu Phe Phe Trp Glu Ser	
100 105 110	
Met Lys Pro Gly Gly Gly Lys Pro Ser Gly Glu Leu Leu Ala Leu	

Met	Ser	Lys	Gln	Thr	Leu	Glu	Phe	His	Trp	Gly	Lys	His	His	Arg	Ala
1			5						10					15	
Tyr	Val	Asp	Asn	Leu	Lys	Lys	Gln	Val	Leu	Gly	Thr	Glu	Leu	Glu	Gly
		20						25					30		
Lys	Pro	Leu	Glu	His	Ile	Ile	His	Ser	Thr	Tyr	Asn	Asn	Gly	Asp	Leu
	35						40					45			

```

Leu Pro Ala Phe Asn Asn Ala Ala Gln Ala Trp Asn His Glu Phe Phe
  50                      55                      60
Trp Glu Ser Met Lys Pro Gly Gly Gly Lys Pro Ser Gly Glu Leu
  65                      70                      75                      80
Leu Ala Leu Leu Glu Arg Asp Phe Thr Ser Tyr Glu Lys Phe Tyr Glu
                      85                      90                      95
Glu Phe Asn Ala Ala Ala Thr Gln Phe Gly Ala Gly Trp Ala Trp
          100                      105                      110
Leu Ala Tyr Ser Asn Glu Lys Leu Lys Val Val Lys Thr Pro Asn Ala
          115                      120                      125
Val Asn Pro Leu Val Leu Gly Ser Phe Pro Ile Ala Tyr His
          130                      135                      140

```

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1217
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

```

ctcgaaacttg tttttggttc atctctcaaaa accaaaaatca ctaaagaggga gaagattgct      60
aaagtttgat aaaaacttcc aaaaatcaatg gctgatagga tcaaaggtcc atggagtctc      120
gaagaagacg acgagcttcg taggcttggt gttaaatacg gtccaagaaa ctggacagtg      180
attagcaaat ctattcccg gtagatcgggg aaatcggtgc gttacgggtg gtgcaaccag      240
ctttcgccgc aaagttagca toggccgttt tcggtcgagg aagacgagac gatcgacagt      300
gctcacgctc agttcggtta taaatggggc acgattgctc gtcttctcaa cggctcgtaac      360
gacacgcgcg tgaagaatca ctggaactcg acgctcaaga ggaatgcggc cgtttacgac      420
catcgggggtt acgattggtt ggaggatcat cgcccggtta agagatcggt gaatgcggga      480
tctccacctg ttgttactgg gctttacatg agcccaggaa gcccaactgg atctgatgtc      540
agtgattcaa gtactatccc gatattacct tccgttgagc ttttcaagcc tgtgcctaga      600
cctgggtgctg wtgtgctacc gcytctctatc gaaacgtcgt ctcttctcga tgatccaccg      660
aMttcggttaa gctttgctact tccgttggtcc gacgtaagcg aggagtcaaa ccgtagccac      720
gagtcaacga atatcaacaa caccacttgc agccgccaca accacaacaa tacggtgtgc      780
tttatgccctg ttatgggtgg gtttagaggt gcgattgagg aaatggggaa gtcttttccc      840
ggtaacggag gcgagtttat gcggtggtg caagagatga ttaaggcgga agtgaggagt      900
tatactgcagc agatgcaacg gaacaatggt gcgcgattcg tcggaggatt cattgataat      960
ggcatgattc cgatgctca aattggagtt gggagaatcg agtagacaaa gtaggagatt      1020
taggaaactg tttaaattgg aagaagaagaa aaatgctctg tttttttctc ctttgattaa      1080
ggcttaagaa ttttgggttt taaggaaatg tataaggaaa atcagtgaaa caaagctcga      1140
gagctggggga cgtagtgaac aagacgaaga tcaaaattctc cttaagctat tcaggaaaat      1200
aaaataaatt tttattt

```

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..305
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

```

Met Ala Asp Arg Ile Lys Gly Pro Trp Ser Pro Glu Glu Asp Glu Gln
  1           5           10           15
Leu Arg Arg Leu Val Val Lys Tyr Gly Pro Arg Asn Trp Thr Val Ile
          20           25           30

```

```

Ser Lys Ser Ile Pro Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp
      35              40              45
Cys Asn Gln Leu Ser Pro Gln Val Glu His Arg Pro Phe Ser Ala Glu
      50              55              60
Glu Asp Glu Thr Ile Ala Arg Ala His Ala Gln Phe Gly Asn Lys Trp
      65              70              75
Ala Thr Ile Ala Arg Leu Leu Asn Gly Arg Thr Asp Asn Ala Val Lys
      85              90              95
Asn His Trp Asn Ser Thr Leu Lys Arg Lys Cys Gly Gly Tyr Asp His
      100             105             110
Arg Gly Tyr Asp Gly Ser Glu Asp His Arg Pro Val Lys Arg Ser Val
      115             120             125
Ser Ala Gly Ser Pro Pro Val Val Thr Gly Leu Tyr Met Ser Pro Gly
      130             135             140
Ser Pro Thr Gly Ser Asp Val Ser Asp Ser Ser Thr Ile Pro Ile Leu
      145             150             155
Pro Ser Val Glu Leu Phe Lys Pro Val Pro Arg Pro Gly Ala Xaa Val
      165             170             175
Leu Pro Xaa Pro Ile Glu Thr Ser Ser Ser Ser Asp Asp Pro Pro Xaa
      180             185             190
Ser Leu Ser Leu Ser Leu Pro Gly Ala Asp Val Ser Glu Glu Ser Asn
      195             200             205
Arg Ser His Glu Ser Thr Asn Ile Asn Asn Thr Thr Ser Ser Arg His
      210             215             220
Asn His Asn Asn Thr Val Ser Phe Met Pro Phe Ser Gly Gly Phe Arg
      225             230             235
Gly Ala Ile Glu Glu Met Gly Lys Ser Phe Pro Gly Asn Gly Gly Glu
      245             250             255
Phe Met Ala Val Val Gln Glu Met Ile Lys Ala Glu Val Arg Ser Tyr
      260             265             270
Met Thr Glu Met Gln Arg Asn Asn Gly Gly Gly Phe Val Gly Gly Phe
      275             280             285
Ile Asp Asn Gly Met Ile Pro Met Ser Gln Ile Gly Val Gly Arg Ile
      290             295             300
Glu
305

```

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

```

Met Ser Pro Gly Ser Pro Thr Gly Ser Asp Val Ser Asp Ser Ser Thr
1      5      10      15
Ile Pro Ile Leu Pro Ser Val Glu Leu Phe Lys Pro Val Pro Arg Pro
      20      25      30
Gly Ala Xaa Val Leu Pro Xaa Pro Ile Glu Thr Ser Ser Ser Asp
      35      40      45
Asp Pro Pro Xaa Ser Leu Ser Leu Ser Leu Pro Gly Ala Asp Val Ser
      50      55      60
Glu Glu Ser Asn Arg Ser His Glu Ser Thr Asn Ile Asn Asn Thr Thr
      65      70      75
Ser Ser Arg His Asn His Asn Asn Thr Val Ser Phe Met Pro Phe Ser
      85      90      95
Gly Gly Phe Arg Gly Ala Ile Glu Glu Met Gly Lys Ser Phe Pro Gly

```

Asn	Gly	Gly	Glu	Phe	Met	Ala	Val	Val	Gln	Glu	Met	Ile	Lys	Ala	Glu
115							120						125		
Val	Arg	Ser	Tyr	Met	Thr	Glu	Met	Gln	Arg	Asn	Asn	Gly	Gly	Gly	Phe
130							135					140			
Val	Gly	Gly	Phe	Ile	Asp	Asn	Gly	Met	Ile	Pro	Met	Ser	Gln	Ile	Gly
145						150				155				160	
Val	Gly	Arg	Ile	Glu											

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..702
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

aaaaactcgct	ctccgggtgat	cgctctttcgg	tcagattctt	ataagcgtgc	ttgattttca	60
aatcaagttt	gtttctttat	ctccagagtt	tatcatctct	tatgtgactg	tgttaaaatg	120
aattttcttaa	actcagctgc	atccatttgc	agaagagtta	gtctgaggga	actcatcatc	180
gaggttctctg	cttatactgg	cagcagcatt	tccgatgggt	cttcaagtgg	gttgagtttg	240
gtcttggaagc	gttgggctac	taagaaaaacc	gctggttcta	caaagaacgg	tcgtgactct	300
aatcccaagt	tcttctgtgt	taagaaattc	ggaggagaga	gtgtgatacc	tggaaacatc	360
atagttctgt	aacgtggaac	tcggtttcat	cctggagact	atgtcgggat	tggtaaggac	420
cataactctgt	ttgcactgaa	ggaaggacga	gtcagggttc	agaaaaagca	gattacagga	480
cgcaaatgga	ttcatgttga	tccaataggt	ggctcatgtc	ttcacccat	ctacacaaaa	540
gcgcagctgt	caaaatcgac	taagttgaac	acagcttcat	agcaaaactg	acaatctaaa	600
cgtgtctctg	tttcttcttt	tagattatat	gatctctcvt	agtaaaaagt	gatggtatct	660
tagaatctca	acactcattt	caataacagc	tgctgttttg	tt		

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Met	Asn	Phe	Leu	Asn	Ser	Ala	Ala	Ser	Ile	Cys	Arg	Arg	Val	Ser	Leu
1			5						10					15	
Arg	Glu	Leu	Ile	Thr	Glu	Val	Pro	Ala	Tyr	Thr	Gly	Ser	Ser	Ile	Ser
			20					25					30		
Asp	Gly	Ser	Ser	Ser	Gly	Leu	Ser	Leu	Val	Leu	Lys	Arg	Trp	Ala	Thr
			35				40					45			
Lys	Lys	Thr	Ala	Gly	Ser	Thr	Lys	Asn	Gly	Arg	Asp	Ser	Asn	Pro	Lys
			50			55					60				
Phe	Leu	Gly	Val	Lys	Lys	Phe	Gly	Gly	Glu	Ser	Val	Ile	Pro	Gly	Asn
			65			70				75				80	
Ile	Ile	Val	Arg	Gln	Arg	Gly	Thr	Arg	Phe	His	Pro	Gly	Asp	Tyr	Val
			85						90					95	
Gly	Ile	Gly	Lys	Asp	His	Thr	Leu	Phe	Ala	Leu	Lys	Glu	Gly	Arg	Val
			100					105					110		
Arg	Phe	Glu	Lys	Ser	Lys	Ile	Thr	Gly	Arg	Lys	Trp	Ile	His	Val	Asp
			115					120							

Pro Ile Gly Gly His Val Leu His Pro Ile Tyr Thr Lys Ala Ala Ala
130 135 140
Ala Lys Ser Thr Lys Leu Asn Thr Ala Ser
145 150

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1239

(D) OTHER INFORMATION: / Ceres Seq. ID 1566132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

atcgagtgct	tcgcccagct	tcttcagctc	tcaccacata	atattaataa	aaagcatttt	60
ctctctttcga	ttgcttcaga	ttcgtcagct	cactctttcc	ttccagaaga	aaaccctaga	120
catctcattcg	caaaaatgtt	cagatctatg	ctcgtccgat	cttctgcctc	cgcgaagCag	180
cggtgatccg	gcggtagctt	ctctccggt	tcggtcccg	agcgtaaaat	cgccatcctt	240
ggtgcgcgcg	tggaattgg	tcagcctctt	gctctctca	tgaagcttaa	tcctcttggt	300
ttctctctct	ccctctacga	tatcgctaac	actccggag	ttgctgtgta	gtcgtgctac	360
atcaacacca	gatctgaggt	tggtggatac	atgggcgatg	ataacttggt	caagctcta	420
gaaggagctg	attctgctat	cattccaagt	ggtgtgccaa	ggaagccttg	tatgaccctg	480
gacgatcttt	taaacattaa	tgctggaatt	gtcaagaacc	ttgcaactgc	catcgcccaag	540
tactgcccac	tatgccttat	taatatgata	agcaaccctg	tgaactctac	tggtccaatt	600
cgagctgaga	tatttaagaa	ggctggatgt	tacgatgaaa	agaaaattgt	tggtgttaac	660
actcttgacg	tcgtcagggc	caggactttc	tatgctggaa	agggcaaatg	cccagtttga	720
gaagttaatg	ttccgggtgt	tggtggatcat	gctgggggta	ctattctccc	ttctctctct	780
cagggaactc	ctcaagccaa	cttgtcaagt	gacatactta	ccgcccttac	taagcgtacc	840
caagatggag	gtcagagaagt	cgtggaggca	aaagcaggaa	aaggttcacg	tacattgttc	900
atggcctatg	ccggagcatt	gttcgtgat	gcattgttga	aaggactcaa	cggtgttcca	960
gatgtcatag	aatgctcata	cgtgcaatct	acaatcacgc	agcttctctt	ctttgcctcg	1020
aagggtgaggt	tggggaagaa	tggtgtggag	gaggttcttg	actttgggac	actctcaagc	1080
tttgagaagg	aagccttggg	agcattgaag	ccagaactca	agctctccat	agaaaaggga	1140
gtcaagtttg	ccaaccagtg	attaaaccga	gtttactcgg	taatttttcc	aattttkccag	1200
ctagagttgc	ccactctctc	ttcatcgggt	tgatatcaat			

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..386

(D) OTHER INFORMATION: / Ceres Seq. ID 1566133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Ile	Glu	Cys	Leu	Ala	Gln	Leu	Leu	Gln	Ser	Pro	His	Asn	Ile	Asn
1		5						10					15	
Lys	Lys	His	Phe	Leu	Leu	Ser	Ile	Ala	Ser	Asp	Ser	Ser	Ala	His
		20						25					30	
Phe	Leu	Ser	Arg	Arg	Asn	Pro	Arg	His	Leu	Ile	Ala	Lys	Met	Phe
		35						40					45	
Ser	Met	Leu	Val	Arg	Ser	Ser	Ala	Ser	Ala	Lys	Gln	Ala	Ala	Ile
		50						55					60	
Arg	Ser	Phe	Ser	Ser	Gly	Ser	Val	Pro	Glu	Arg	Lys	Val	Ala	Ile
		65						70					75	
Gly	Ala	Ala	Gly	Gly	Ile	Gly	Gln	Pro	Leu	Ala	Leu	Leu	Met	Lys
		85						90					95	

Asn Pro Leu Val Ser Ser Leu Ser Leu Tyr Asp Ile Ala Asn Thr Pro
100 105 110
Gly Val Ala Ala Asp Val Gly His Ile Asn Thr Arg Ser Glu Val Val
115 120 125
Gly Tyr Met Gly Asp Asp Asn Leu Ala Lys Ala Leu Glu Gly Ala Asp
130 135 140
Leu Val Ile Ile Pro Ala Gly Val Pro Arg Lys Pro Gly Met Thr Arg
145 150 155 160
Asp Asp Leu Phe Asn Ile Asn Ala Gly Ile Val Lys Asn Leu Cys Thr
165 170 175
Ala Ile Ala Lys Tyr Cys Pro His Ala Leu Ile Asn Met Ile Ser Asn
180 185 190
Pro Val Asn Ser Thr Val Pro Ile Ala Ala Glu Ile Phe Lys Lys Ala
195 200 205
Gly Met Tyr Asp Glu Lys Lys Leu Phe Gly Val Thr Thr Leu Asp Val
210 215 220
Val Arg Ala Arg Thr Phe Tyr Ala Gly Lys Ala Asn Val Pro Val Ala
225 230 235 240
Glu Val Asn Val Pro Val Ile Gly Gly His Ala Gly Val Thr Ile Leu
245 250 255
Pro Leu Phe Ser Gln Ala Thr Pro Gln Ala Asn Leu Ser Ser Asp Ile
260 265 270
Leu Thr Ala Leu Thr Lys Arg Thr Gln Asp Gly Gly Thr Glu Val Val
275 280 285
Glu Ala Lys Ala Gly Lys Gly Ser Ala Thr Leu Ser Met Ala Tyr Ala
290 295 300
Gly Ala Leu Phe Ala Asp Ala Cys Leu Lys Gly Leu Asn Gly Val Pro
305 310 315 320
Asp Val Ile Glu Cys Ser Tyr Val Gln Ser Thr Thr Ile Thr Glu Leu Pro
325 330 335
Phe Phe Ala Ser Lys Val Arg Leu Gly Lys Asn Gly Val Glu Glu Val
340 345 350
Leu Asp Leu Gly Pro Leu Ser Asp Phe Glu Lys Glu Gly Leu Glu Ala
355 360 365
Leu Lys Pro Glu Leu Lys Ser Ser Ile Glu Lys Gly Val Lys Phe Ala
370 375 380
Asn Gln
385

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..341

(D) OTHER INFORMATION: / Ceres Seq. ID 1566134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Met Phe Arg Ser Met Leu Val Arg Ser Ser Ala Ser Ala Lys Gln Ala
1 5 10 15
Ala Ile Arg Arg Ser Phe Ser Ser Gly Ser Val Pro Glu Arg Lys Val
20 25 30
Ala Ile Leu Gly Ala Ala Gly Gly Ile Gly Gln Pro Leu Ala Leu Leu
35 40 45
Met Lys Leu Asn Pro Leu Val Ser Ser Leu Ser Leu Tyr Asp Ile Ala
50 55 60
Asn Thr Pro Gly Val Ala Ala Asp Val Gly His Ile Asn Thr Arg Ser
65 70 75 80
Glu Val Val Gly Tyr Met Gly Asp Asp Asn Leu Ala Lys Ala Leu Glu

[illegible]

(2) INFORMATION FOR SEO ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..33

(D) OTHER INFORMATION: / Ceres Seq. ID 1566135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Met	Leu	Val	Arg	Ser	Ser	Ala	Ser	Ala	Lys	Gln	Ala	Ala	Ile	Arg	Arg
1				5					10					15	
Ser	Phe	Ser	Ser	Gly	Ser	Val	Pro	Glu	Arg	Lys	Val	Ala	Ile	Leu	Gly
				20				25					30		
Ala	Ala	Gly	Gly	Ile	Gly	Gln	Pro	Leu	Ala	Leu	Leu	Met	Lys	Leu	Asn
		35					40					45			
Pro	Leu	Val	Ser	Ser	Leu	Ser	Leu	Tyr	Asp	Ile	Ala	Asn	Thr	Pro	Gly
	50					55					60				
Val	Ala	Ala	Asp	Val	Gly	His	Ile	Asn	Thr	Arg	Ser	Glu	Val	Val	Gly
65					70					75					80
Tyr	Met	Gly	Asp	Asp	Asn	Leu	Ala	Lys	Ala	Leu	Glu	Gly	Ala	Asp	Leu
				85				90						95	
Val	Ile	Ile	Pro	Ala	Gly	Val	Pro	Arg	Lys	Pro	Gly	Met	Thr	Arg	Asp
			100					105					110		
Asp	Leu	Phe	Asn	Ile	Asn	Ala	Gly	Ile	Val	Lys	Asn	Leu	Cys	Thr	Ala
		115				120						125			

```

Ile Ala Lys Tyr Cys Pro His Ala Leu Ile Asn Met Ile Ser Asn Pro
130 135 140
Val Asn Ser Thr Val Pro Ile Ala Ala Glu Ile Phe Lys Lys Ala Gly
145 150 155 160
Met Tyr Asp Glu Lys Lys Leu Phe Gly Val Thr Thr Leu Asp Val Val
165 170 175
Arg Ala Arg Thr Phe Tyr Ala Gly Lys Ala Asn Val Pro Val Ala Glu
180 185 190
Val Asn Val Pro Val Ile Gly Gly His Ala Gly Val Thr Ile Leu Pro
195 200 205
Leu Phe Ser Gln Ala Thr Pro Gln Ala Asn Leu Ser Ser Asp Ile Leu
210 215 220
Thr Ala Leu Thr Lys Arg Thr Gln Asp Gly Gly Thr Glu Val Val Glu
225 230 235 240
Ala Lys Ala Gly Lys Gly Ser Ala Thr Leu Ser Met Ala Tyr Ala Gly
245 250 255
Ala Leu Phe Ala Asp Ala Cys Leu Lys Gly Leu Asn Gly Val Pro Asp
260 265 270
Val Ile Glu Cys Ser Tyr Val Gln Ser Thr Ile Thr Glu Leu Pro Phe
275 280 285
Phe Ala Ser Lys Val Arg Leu Gly Lys Asn Gly Val Glu Glu Val Leu
290 295 300
Asp Leu Gly Pro Leu Ser Asp Phe Glu Lys Glu Gly Leu Glu Ala Leu
305 310 315 320
Lys Pro Glu Leu Lys Ser Ser Ile Glu Lys Gly Val Lys Phe Ala Asn
325 330 335
Gln

```

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1844 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1844
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

```

ttcaatctca ttaaagagaa aagaaacgat tagagaaaga gaagagggta gagactttctt 60
tctcttggttt ctgttagagcc tcttcttctt cttctctgtc tctgtctctgt tctctgtcttc 120
tctgtaactct tctgtgtctct ccaaaaattt gtctctccct tctctgcgcg actccacaaa 180
ttttgagctt ctttttttga agttcttgag aacaagtgaag agagcttaat atccacaaga 240
ctctctgttct tttcttaaat ggctaaagt tattggcctt atttcgatcc tgaatatgatg 300
aacttgagct cagaatctaa tctccaagt gtttctatag ataacactag ctgcaaaagaa 360
tgcaactcttg tcaaggtgga cagtatgaac aaacctggaa tactacttga agttgtgcga 420
gtcctaaccg atctcgaatc cactatcact aaagcttata tctcttctga tgggtgatgg 480
ttcatggacg tattccatgt caccgatcaa caaggaaaca aggttactga tagcaaaaacc 540
atcgattaca tcgagaaggt gtaggacca aagggtcatg cttcggtctc acaaaaacct 600
tgccctggtg aaagagtcgt gtgcattca ttaggcgacc acacatcgat agagattatt 660
gtcgtgatc gtctctggcc ttgtctggag gtttcagccg tactagcaga cctcaacatt 720
aatgtgggtg cagctgaagc atggactcac aaccgtagga ttgcgtgtgt cctctatgtg 780
aatgacaatg caactcttag agccgttgat gatccagaaa gattgtcttc catggaagaa 840
cagcttaaca atgtgtctgc tgggtgcgaa gaacaagatg agaaatttgc tgcggacgag 900
ctctccattg ggtcgactca cgttgataga aggccttcac agatgttttt cgtcgataga 960
gactacgaag cagtgactaa gcttgatgat tctgcttctt gcggatttga gcccaaaatc 1020
acggttgagc attgtgaaga gaaaggttac tccgtgataa acgtgagctg cgagatgaga 1080
ccaaagctca tgtttgatca tgtatgcacg ctacaggata tgcaatacat tgtgtttcac 1140
gccacgattt catcaagcgg ctctcatgct tctcaggagt atttcacag acacaagac 1200
ggttgcactc ttgacacaga aggagagaaa gagagagdtg tcaaatgtct agaagctgcga 1260

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2025 RELEASE UNDER E.O. 14176

```
atccatagac gagtcagcga ggggttgagt ttggagctct gcgcaaagga cacagattgga 1320
ttactgtcgg aagtgacaag gattctgaga gaggacgggc tatcagtgct gagagctgggt 1380
gtgacaacag tagggagaaca agccgtcaac gttttctatg tgaaagatgc ttcagggaat 1440
ccagtggtatg tgaagacgat tgaggcggtta cgccggagaga ttggacacag tatgatgatt 1500
gacttcaaga ataaagttcc gagcagaaaa tggaaagaag aaggtaacag cggaaacagga 1560
ggaggatggg ccaaaaccag tttcttcttt gggaatttgc ttgagaagtt actgccttga 1620
gagaaaaagt aactatgtgt ggataaaacg tactgtataaa tgtgtattat gtagatcata 1680
gagggcctta gtgtgatgta tgactttgtc agggattttg gtggtttgcc cgaagtcaaa 1740
ccgaacaaaa actggttttc ggttacttta gactttagtc atagtataat gaacatgtct 1800
ataaatgaat aatatgcaac tcttccaatt ggtaggcttg cttt
```

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 453 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..453

(D) OTHER INFORMATION: / Ceres Seq. ID 1566151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

```
Met Ala Lys Val Tyr Trp Pro Tyr Phe Asp Pro Glu Tyr Glu Asn Leu
1 5 10 15
Ser Ser Arg Ile Asn Pro Pro Ser Val Ser Ile Asp Asn Thr Ser Cys
20 25 30
Lys Glu Cys Thr Leu Val Lys Val Asp Ser Met Asn Lys Pro Gly Ile
35 40 45
Leu Leu Glu Val Val Gln Val Leu Thr Asp Leu Asp Leu Thr Ile Thr
50 55 60
Lys Ala Tyr Ile Ser Ser Asp Gly Gly Trp Phe Met Asp Val Phe His
65 70 75 80
Val Thr Asp Gln Gln Gly Asn Lys Val Thr Asp Ser Lys Thr Ile Asp
85 90 95
Tyr Ile Glu Lys Val Leu Gly Pro Lys Gly His Ala Ser Ala Ser Gln
100 105 110
Asn Thr Trp Pro Gly Lys Arg Val Gly Val His Ser Leu Gly Asp His
115 120 125
Thr Ser Ile Glu Ile Ile Ala Arg Asp Arg Pro Gly Leu Leu Ser Glu
130 135 140
Val Ser Ala Val Leu Ala Asp Leu Asn Ile Asn Val Val Ala Ala Glu
145 150 155 160
Ala Trp Thr His Asn Arg Arg Ile Ala Cys Val Leu Tyr Val Asn Asp
165 170 175
Asn Ala Thr Ser Arg Ala Val Asp Asp Pro Glu Arg Leu Ser Ser Met
180 185 190
Glu Glu Gln Leu Asn Asn Val Leu Arg Gly Cys Glu Glu Gln Asp Glu
195 200 205
Lys Phe Ala Arg Thr Ser Leu Ser Ile Gly Ser Thr His Val Asp Arg
210 215 220
Arg Leu His Gln Met Thr Phe Ala Asp Arg Asp Tyr Glu Ala Val Thr
225 230 235 240
Lys Leu Asp Asp Ser Ala Ser Cys Gly Phe Glu Pro Lys Ile Thr Val
245 250 255
Glu His Cys Glu Glu Lys Gly Tyr Ser Val Ile Asn Val Ser Cys Glu
260 265 270
Asp Arg Pro Lys Leu Met Phe Asp Ile Val Cys Thr Leu Thr Asp Met
275 280 285
Gln Tyr Ile Val Phe His Ala Thr Ile Ser Ser Ser Gly Ser His Ala
290 295 300
Ser Gln Glu Tyr Phe Ile Arg His Lys Asp Gly Cys Thr Leu Asp Thr
```

305		310		315		320
Glu Gly	Glu Lys	Glu Arg	Xaa Val	Lys Cys	Leu Glu	Ala Ala
	325			330		Ile His
Arg Arg	Val Ser	Glu Gly	Trp Ser	Leu Glu	Leu Cys	Ala Lys
	340			345		350
Val Gly	Leu Leu	Ser Glu	Val Thr	Arg Ile	Leu Arg	Glu His
	355			360		365
Ser Val	Ser Arg	Ala Gly	Val Thr	Thr Val	Gly Glu	Gln Ala
	370			375		380
Val Phe	Tyr Val	Lys Asp	Ala Ser	Gly Asn	Pro Val	Asp Val
	385			390		395
Ile Glu	Ala Leu	Arg Gly	Glu Ile	Gly His	Ser Met	Met Ile
	405			410		415
Lys Asn	Lys Val	Pro Ser	Arg Lys	Trp Lys	Glu Glu	Gly Gln
	420			425		430
Thr Gly	Gly Gly	Trp Ala	Lys Thr	Ser Phe	Phe Phe	Phe Gly
	435			440		445
Glu Lys	Leu Leu	Pro				
	450					

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..411

(D) OTHER INFORMATION: / Ceres Seq. ID 1566152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Met Asn	Lys Pro	Gly Ile	Leu Leu	Glu Val	Val Gln	Val Leu	Thr Asp
1	5			10		15	
Leu Asp	Leu Thr	Ile Thr	Lys Ala	Tyr Ile	Ser Ser	Asp Gly	Trp
	20			25		30	
Phe Met	Asp Val	Phe His	Val Thr	Asp Gln	Gln Gly	Asn Lys	Val Thr
	35			40		45	
Asp Ser	Lys Thr	Ile Asp	Tyr Ile	Glu Lys	Val Leu	Gly Pro	Lys Gly
	50			55		60	
His Ala	Ser Ala	Ser Gln	Asn Thr	Trp Pro	Gly Lys	Arg Val	Gly Val
	65			70		75	
His Ser	Leu Gly	Asp His	Thr Ser	Ile Glu	Ile Ile	Ala Arg	Asp Arg
	85			90		95	
Pro Gly	Leu Leu	Ser Glu	Val Ser	Ala Val	Leu Ala	Asp Leu	Asn Ile
	100			105		110	
Asn Val	Val Ala	Ala Glu	Ala Trp	Thr His	Asn Arg	Arg Ile	Ala Cys
	115			120		125	
Val Leu	Tyr Val	Asn Asp	Asn Ala	Thr Ser	Arg Ala	Val Asp	Asp Pro
	130			135		140	
Glu Arg	Leu Ser	Ser Met	Glu Glu	Gln Leu	Asn Asn	Val Leu	Arg Gly
	145			150		155	
Cys Glu	Glu Gln	Asp Glu	Lys Phe	Ala Arg	Thr Ser	Leu Ser	Ile Gly
	165			170		175	
Ser Thr	His Val	Asp Arg	Arg Leu	His Gln	Met Phe	Phe Ala	Asp Arg
	180			185		190	
Asp Tyr	Glu Ala	Val Thr	Lys Leu	Asp Asp	Ser Ala	Ser Cys	Gly Phe
	195			200		205	
Glu Pro	Lys Ile	Thr Val	Glu His	Cys Glu	Glu Lys	Gly Tyr	Ser Val
	210			215		220	
Ile Asn	Val Ser	Cys Glu	Asp Arg	Pro Lys	Leu Met	Phe Asp	Ile Val
	225			230		235	
							240

Cys Thr Leu Thr Asp Met Gln Tyr Ile Val Phe His Ala Thr Ile Ser
245 250 255
Ser Ser Gly Ser His Ala Ser Gln Glu Tyr Phe Ile Arg His Lys Asp
260 270
Gly Cys Thr Leu Asp Thr Glu Gly Glu Lys Glu Arg Xaa Val Lys Cys
275 280 285
Leu Glu Ala Ala Ile His Arg Arg Val Ser Glu Gly Trp Ser Leu Glu
290 295 300
Leu Cys Ala Lys Asp Arg Val Gly Leu Leu Ser Glu Val Thr Arg Ile
305 310 315 320
Leu Arg Glu His Gly Leu Ser Val Ser Arg Ala Gly Val Thr Thr Val
325 330 335
Gly Glu Gln Ala Val Asn Val Phe Tyr Val Lys Asp Ala Ser Gly Asn
340 345 350
Pro Val Asp Val Lys Thr Ile Glu Ala Leu Arg Gly Glu Ile Gly His
355 360 365
Ser Met Met Ile Asp Phe Lys Asn Lys Val Pro Ser Arg Lys Trp Lys
370 375 380
Glu Glu Gly Gln Ala Gly Thr Gly Gly Trp Ala Lys Thr Ser Phe
385 390 395 400
Phe Phe Gly Asn Leu Leu Glu Lys Leu Leu Pro
405 410

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..378

(D) OTHER INFORMATION: / Ceres Seq. ID 1566153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Met Asp Val Phe His Val Thr Asp Gln Gln Gly Asn Lys Val Thr Asp
1 5 10 15
Ser Lys Thr Ile Asp Tyr Ile Glu Lys Val Leu Gly Pro Lys Gly His
20 25 30
Ala Ser Ala Ser Gln Asn Thr Trp Pro Gly Lys Arg Val Gly Val His
35 40 45
Ser Leu Gly Asp His Thr Ser Ile Glu Ile Ala Arg Asp Arg Pro
50 55 60
Gly Leu Leu Ser Glu Val Ser Ala Val Leu Ala Asp Leu Asn Ile Asn
65 70 75 80
Val Val Ala Ala Glu Ala Trp Thr His Asn Arg Arg Ile Ala Cys Val
85 90 95
Leu Tyr Val Asn Asp Asn Ala Thr Ser Arg Ala Val Asp Asp Pro Glu
100 105 110
Arg Leu Ser Ser Met Glu Glu Gln Leu Asn Asn Val Leu Arg Gly Cys
115 120 125
Glu Glu Gln Asp Glu Lys Phe Ala Arg Thr Ser Leu Ser Ile Gly Ser
130 135 140
Thr His Val Asp Arg Arg Leu His Gln Met Phe Phe Ala Asp Arg Asp
145 150 155 160
Tyr Glu Ala Val Thr Lys Leu Asp Asp Ser Ala Ser Cys Gly Phe Glu
165 170 175
Pro Lys Ile Thr Val Glu His Cys Glu Glu Lys Gly Tyr Ser Val Ile
180 185 190
Asn Val Ser Cys Glu Asp Arg Pro Lys Leu Met Phe Asp Ile Val Cys
195 200 205
Thr Leu Thr Asp Met Gln Tyr Ile Val Phe His Ala Thr Ile Ser Ser

210	215	220
Ser Gly Ser His Ala	Ser Gln Glu Tyr Phe	Ile Arg His Lys Asp Gly
225	230	235
Cys Thr Leu Asp Thr	Glu Gly Glu Lys Glu Arg	Xaa Val Lys Cys Leu
240	245	250
Glu Ala Ala Ile His	Arg Arg Val Ser Glu Gly	Trp Ser Leu Glu Leu
255	260	265
Cys Ala Lys Asp Arg	Val Gly Leu Leu Ser Glu	Val Thr Arg Ile Leu
270	275	280
Arg Glu His Gly Leu	Ser Val Ser Arg Ala Gly	Val Thr Thr Val Gly
285	290	295
Glu Gln Ala Val Asn	Val Phe Tyr Val Lys Asp	Ala Ser Gly Asn Pro
300	305	310
Val Asp Val Lys Thr	Ile Glu Ala Leu Arg	Gly Glu Ile Gly His Ser
315	320	325
Met Met Ile Asp Phe	Lys Asn Lys Val Pro	Ser Arg Lys Trp Lys Glu
330	335	340
Glu Gly Gln Ala Gly	Thr Gly Gly Trp Ala	Lys Thr Ser Phe Phe
345	350	355
Phe Gly Asn Leu Leu	Glu Lys Leu Leu Pro	
360	365	

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..676
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

acataagtcct	ctctctttaca	ttttgaaacc	ctaatctctc	aaaaaaaaatg	tctgaagttg	60
agtaccgggtg	ctttgtcggc	ggccttgect	gggccaccaa	tgatgaagat	cttcaaaagg	120
cgttctcaca	gttcggcgac	gttatcgatt	ctaagatcat	taacgaccgc	gagagtggaa	180
gatcaagggg	attcggattc	gtcaccttca	aggacgagaa	agccatgagg	gatgcgattg	240
aagagatgaa	cggtaaaagag	ctcgatggac	gtgtcatcac	cgtgaacgag	gctcagtcga	300
gaggttagcgg	cggtggcggc	ggatactcag	gaggaggcgg	tggtggttac	gagagacgta	360
cgggaggtta	cggatctggt	ggargcgggt	gtggccgagg	atacggtggt	ggtggacgcc	420
gtgagggagg	tggctacgga	ggcgggtgat	gtggaagtta	cgccggcggt	ggtggcggtg	480
ggtaatacaa	gatagagttg	tttgcgtgct	gctgctctgt	ttttggttta	gatttgggat	540
ttgtgtcacc	actctctggt	tggttatcgt	tcgttkggtt	tacttttttg	atgaaacagt	600
ttcgtttaag	tctctcttgt	ctggatcgaa	atgttaattc	gcgtgttggt	tactaaattt	660
ataacgtttc	cttttc					

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Met Ser Glu Val Glu Tyr Arg Cys Phe Val Gly Gly Leu Ala Trp Ala
1 5 10 15
Thr Asn Asp Glu Asp Leu Gln Arg Thr Phe Ser Gln Phe Gly Asp Val
20 25 30

```

Ile Asp Ser Lys Ile Ile Asn Asp Arg Glu Ser Gly Arg Ser Arg Gly
    35          40          45
Phe Gly Phe Val Thr Phe Lys Asp Glu Lys Ala Met Arg Asp Ala Ile
    50          55          60
Glu Glu Met Asn Gly Lys Glu Leu Asp Gly Arg Val Ile Thr Val Asn
    65          70          75          80
Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Tyr Ser Gly Gly
    85          90          95
Gly Gly Gly Gly Tyr Glu Arg Arg Ser Gly Gly Tyr Gly Ser Gly Gly
    100         105         110
Xaa Gly Gly Gly Arg Gly Tyr Gly Gly Gly Arg Arg Glu Gly Gly
    115         120         125
Gly Tyr Gly Gly Gly Asp Gly Gly Ser Tyr Gly Gly Gly Gly Gly
    130         135         140

```

Trp
145

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

```

Met Arg Asp Ala Ile Glu Glu Met Asn Gly Lys Glu Leu Asp Gly Arg
 1          5          10          15
Val Ile Thr Val Asn Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Gly
    20         25         30
Gly Tyr Ser Gly Gly Gly Gly Gly Gly Tyr Glu Arg Arg Ser Gly Gly
    35         40         45
Tyr Gly Ser Gly Gly Xaa Gly Gly Gly Arg Gly Tyr Gly Gly Gly Gly
    50         55         60
Arg Arg Glu Gly Gly Gly Tyr Gly Gly Gly Asp Gly Gly Ser Tyr Gly
    65         70         75         80
Gly Gly Gly Gly Gly Trp
    85

```

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

```

Met Asn Gly Lys Glu Leu Asp Gly Arg Val Ile Thr Val Asn Glu Ala
 1          5          10          15
Gln Ser Arg Gly Ser Gly Gly Gly Gly Gly Tyr Ser Gly Gly Gly Gly
    20         25         30
Gly Gly Tyr Glu Arg Arg Ser Gly Gly Tyr Gly Ser Gly Gly Xaa Gly
    35         40         45
Gly Gly Arg Gly Tyr Gly Gly Gly Gly Arg Arg Glu Gly Gly Gly Tyr
    50         55         60
Gly Gly Gly Asp Gly Gly Ser Tyr Gly Gly Gly Gly Gly Trp

```

65

70

75

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1415
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

atgttcacatg	tgaattgttt	agttgggttt	aattctctttt	taagacaaca	tataatgtca	60
atgttatgta	cgtttttctt	gtttctctta	aacacttctt	ttgcgtttgc	attttgcgatt	120
cctaaccgac	caatagtaag	gagactatca	acgacagtga	catcaaatcc	aacagcgctct	180
ctttgtctag	ccaatggaaa	tccaatcgat	gagtgttgga	gatgcgacga	aaactgggaag	240
gacaaccgca	aaaacctcgc	ggattgcgcg	gttggtattcg	gacgcgactc	aattggcggt	300
agagccgggg	agttctacac	gggtgactgat	tcaggagacg	acaatcctct	aaatccaact	360
ccaggtagcat	tacggtagcg	tcgcgacaca	gatcaaacctc	tatggatcat	ttttgatgca	420
gacatggttaa	tacaactaaa	acaagatctt	caagtagctt	catacaaaaac	cattgatgggt	480
agaggaaata	acgtacaacat	agcttatgga	cgtgtgttaa	ctttatataa	agtttagtaac	540
attattataa	acaattctta	tattcacgat	tgtgttcccg	cgaaacggaa	tgctttatcg	600
tcgttgggag	gatactcgga	tggaagatga	atacgatat	tcgagctctg	agatattttg	660
attgatcatt	gtacgttaga	gaaatgttac	gatgggctta	ttgatgcggt	gaatggatcc	720
acggatataa	cgattttcga	tagttacatg	ttgaatcata	atgaagtcat	gcttttggttc	780
catagtgtat	agttattccg	tgatcgggat	atgcgagtta	cgatgcgctt	taactatttt	840
gggtgaaggac	ttgtccaagg	aattgccaaag	tgtaggcatg	gatattttca	catagtgaat	900
aaacatttata	gagactggaa	gatgtatgct	attgtgtgaa	gtgctaattcc	aacgatcttt	960
agccaaggaa	atgtttttac	agcttccaat	aatacagttca	ccaaggaggt	tacaagaagca	1020
gagagtgacg	atggagacaga	agaatggaag	gaatggaaact	ggaatcaaga	aggagacgaa	1080
atggtttaaag	gagcttttct	tacaccgtca	gggaagagag	attctccgag	Ctaacgcaaa	1140
ttttcagata	tggttagctcg	accagcttca	cttctcaaga	ccacacatcc	atcagtaggt	1200
gtttcttagt	gcgaaattga	ccaagcttgt	taaaaacaca	aacataagct	tgtgaccaaa	1260
tctagtgttt	gtccttcttt	ttcttttttg	ctcttctact	tggtgtggtt	atgtgttatcg	1320
taaatagtag	ttgtactgaa	tgtgatgatg	atcatagacc	caaaacaaca	ttgttcatgt	1380
tcaatttctt	taccaaaaaa	ttctttttac	gagtc			

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..410
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Met	Phe	Ile	Val	Lys	Leu	Leu	Val	Gly	Phe	Asn	Leu	Phe	Leu	Arg	Gln
1				5				10						15	
His	Ile	Met	Ser	Ile	Val	Cys	Thr	Phe	Phe	Leu	Phe	Leu	Leu	Asn	Thr
				20				25						30	
Ser	Phe	Ala	Phe	Ala	Phe	Ala	Ile	Pro	Lys	Pro	Pro	Ile	Val	Arg	Arg
				35				40						45	
Leu	Ser	Thr	Thr	Val	Thr	Ser	Asn	Ser	Thr	Ala	Ser	Ser	Cys	Ser	Ala
				50				55						60	
Asn	Gly	Asn	Pro	Ile	Asp	Glu	Cys	Trp	Arg	Cys	Asp	Glu	Asn	Trp	Lys
65				70				75						80	
Asp	Asn	Arg	Lys	Asn	Leu	Ala	Asp	Cys	Ala	Val	Gly	Phe	Gly	Arg	Asp
				85				90						95	

Ser Ile Gly Gly Arg Ala Gly Glu Phe Tyr Thr Val Thr Asp Ser Gly
100 105 110
Asp Asp Asn Pro Leu Asn Pro Thr Pro Gly Thr Leu Arg Tyr Ala Ala
115 120 125
Thr Gln Asp Gln Pro Leu Trp Ile Ile Phe Asp Arg Asp Met Val Ile
130 135 140
Gln Leu Lys Gln Asp Leu Gln Val Ala Ser Tyr Lys Thr Ile Asp Gly
145 150 155 160
Arg Gly Asn Asn Val Gln Ile Ala Tyr Gly Pro Cys Leu Thr Leu Tyr
165 170 175
Lys Val Ser Asn Ile Ile Ile Asn Asn Leu Tyr Ile His Asp Cys Val
180 185 190
Pro Ala Lys Arg Asn Ala Leu Ser Ser Leu Gly Gly Tyr Ser Asp Gly
195 200 205
Asp Gly Ile Ser Ile Phe Glu Ser Arg Asp Ile Trp Ile Asp His Cys
210 215 220
Thr Leu Glu Lys Cys Tyr Asp Gly Leu Ile Asp Ala Val Asn Gly Ser
225 230 235 240
Thr Asp Ile Thr Ile Ser Asn Ser Tyr Met Leu Asn His Asn Glu Val
245 250 255
Met Leu Leu Gly His Ser Asp Glu Tyr Ser Gly Asp Arg Asp Met Arg
260 265 270
Val Thr Ile Ala Phe Asn Tyr Phe Gly Glu Gly Leu Val Gln Arg Met
275 280 285
Pro Arg Cys Arg His Gly Tyr Phe His Ile Val Asn Asn Ile Tyr Arg
290 295 300
Asp Trp Lys Met Tyr Ala Ile Gly Gly Ser Ala Asn Pro Thr Ile Phe
305 310 315 320
Ser Gln Gly Asn Val Phe Ile Ala Ser Asn Asn Gln Phe Thr Lys Glu
325 330 335
Val Thr Lys Arg Glu Ser Ala Asp Gly Asp Glu Glu Trp Lys Glu Trp
340 345 350
Asn Trp Lys Ser Glu Gly Asp Glu Met Val Asn Gly Ala Phe Phe Thr
355 360 365
Pro Ser Gly Lys Glu Asp Ser Pro Ser Tyr Ala Lys Phe Ser Ser Met
370 375 380
Val Ala Arg Pro Ala Ser Leu Leu Lys Thr Thr His Pro Ser Val Gly
385 390 395 400
Val Leu Ser Cys Glu Ile Asp Gln Ala Cys
405 410

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..392

(D) OTHER INFORMATION: / Ceres Seq. ID 1566173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Met Ser Ile Val Cys Thr Phe Phe Leu Phe Leu Leu Asn Thr Ser Phe
1 5 10 15
Ala Phe Ala Phe Ala Ile Pro Lys Pro Pro Ile Val Arg Arg Leu Ser
20 25 30
Thr Thr Val Thr Ser Asn Ser Thr Ala Ser Ser Cys Ser Ala Asn Gly
35 40 45
Asn Pro Ile Asp Glu Cys Trp Arg Cys Asp Glu Asn Trp Lys Asp Asn
50 55 60
Arg Lys Asn Leu Ala Asp Cys Ala Val Gly Phe Gly Arg Asp Ser Ile

65 70 75 80
Gly Gly Arg Ala Gly Glu Phe Tyr Thr Val Thr Asp Ser Gly Asp Asp
85 90 95
Asn Pro Leu Asn Pro Thr Pro Gly Thr Leu Arg Tyr Ala Ala Thr Gln
100 105 110
Asp Gln Pro Leu Trp Ile Ile Phe Asp Arg Asp Met Val Ile Gln Leu
115 120 125
Lys Gln Asp Leu Gln Val Ala Ser Tyr Lys Thr Ile Asp Gly Arg Gly
130 135 140
Asn Asn Val Gln Ile Ala Tyr Gly Pro Cys Leu Thr Leu Tyr Lys Val
145 150 155 160
Ser Asn Ile Ile Ile Asn Asn Leu Tyr Ile His Asp Cys Val Pro Ala
165 170 175
Lys Arg Asn Ala Leu Ser Ser Leu Gly Tyr Ser Asp Gly Asp Gly
180 185 190
Ile Ser Ile Phe Glu Ser Arg Asp Ile Trp Ile Asp His Cys Thr Leu
195 200 205
Glu Lys Cys Tyr Asp Gly Leu Ile Asp Ala Val Asn Gly Ser Thr Asp
210 215 220
Ile Thr Ile Ser Asn Ser Tyr Met Leu Asn His Asn Glu Val Met Leu
225 230 235 240
Leu Gly His Ser Asp Glu Tyr Ser Gly Asp Arg Asp Met Arg Val Thr
245 250 255
Ile Ala Phe Asn Tyr Phe Gly Glu Gly Leu Val Gln Arg Met Pro Arg
260 265 270
Cys Arg His Gly Tyr Phe His Ile Val Asn Asn Ile Tyr Arg Asp Trp
275 280 285
Lys Met Tyr Ala Ile Gly Gly Ser Ala Asn Pro Thr Ile Phe Ser Gln
290 295 300
Gly Asn Val Phe Ile Ala Ser Asn Asn Gln Phe Thr Lys Glu Val Thr
305 310 315 320
Lys Arg Glu Ser Ala Asp Gly Asp Glu Glu Trp Lys Glu Trp Asn Trp
325 330 335
Lys Ser Glu Gly Asp Glu Met Val Asn Gly Ala Phe Phe Thr Pro Ser
340 345 350
Gly Lys Glu Asp Ser Pro Ser Tyr Ala Lys Phe Ser Ser Met Val Ala
355 360 365
Arg Pro Ala Ser Leu Leu Lys Thr Thr His Pro Ser Val Gly Val Leu
370 375 380
Ser Cys Glu Ile Asp Gln Ala Cys
385 390

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..731

(D) OTHER INFORMATION: / Ceres Seq. ID 1566181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

agtttttgtt	tgttttgggt	gttgcgagtt	gttgactata	aaacctcttc	cacttggttc	60
ttcaacttca	ctgtttctca	tctcttggtc	ttctccgctc	ccttcaatct	cactccggtc	120
tctctacgat	tcattcggtt	tatggtcttc	attgctgctt	ctgctcttat	ttcccttcaa	180
gctgctctc	gccaaactgc	gatcgcggt	aggcaagtta	aaagcttttg	caatggaaga	240
agaagcagtc	tttcttttaa	ttctccgcag	cttctctacc	gcttgactgt	ttctgcgctc	300
gcaaaacctg	agacagtgga	caaggtgtgt	gcagttgtca	gaaagcaact	ctcaactaaa	360
gaggctgacg	aaattactgc	tgccaccaaa	tttgctgcac	ttggtgctga	ttcccttgat	420
acggtggaga	ttgtgatggg	actagaggaa	gagttcggga	ttgaaatggc	ggaggagaaa	480

gcacagtcac tcgccacagt tgagcaagca Gctgcgcgtca ttgaggagct cttgtttgaa 540
aaggccaagt agaatacttt tattacatta gcaaaaacga aaaaaatcaa aaccccaaac 600
actactttat tgtttcggtta gctagagagc aattgtgtct gttgaaagat tttatgttat 660
tttggggaaa ttattacaag gcttgtatct gactttttat tttcttctaa aacattttac 720
tttcagcttc c

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Ser	Phe	Cys	Leu	Phe	Trp	Leu	Leu	Arg	Val	Cys	Asp	Tyr	Lys	Thr	Ser
1			5					10					15		
Pro	Thr	Trp	Phe	Phe	Thr	Leu	Thr	Val	Ser	His	Leu	Phe	Val	Phe	Ser
			20					25					30		
Ala	Ser	Phe	Asn	Leu	Thr	Pro	Ile	Ser	Leu	Arg	Phe	Ile	Arg	Ser	Met
			35					40				45			
Ala	Ser	Ile	Ala	Ala	Ser	Ala	Ser	Ile	Ser	Leu	Gln	Ala	Arg	Pro	Arg
			50					55				60			
Gln	Leu	Ala	Ile	Ala	Ala	Arg	Gln	Val	Lys	Ser	Phe	Ser	Asn	Gly	Arg
			65					70				75			80
Arg	Ser	Ser	Leu	Ser	Phe	Asn	Leu	Arg	Gln	Leu	Pro	Thr	Arg	Leu	Thr
			85					90					95		
Val	Ser	Cys	Ala	Ala	Lys	Pro	Glu	Thr	Val	Asp	Lys	Val	Cys	Ala	Val
			100					105					110		
Val	Arg	Lys	Gln	Leu	Ser	Leu	Lys	Glu	Ala	Asp	Glu	Ile	Thr	Ala	Ala
			115					120					125		
Thr	Lys	Phe	Ala	Ala	Leu	Gly	Ala	Asp	Ser	Leu	Asp	Thr	Val	Glu	Ile
			130					135					140		
Val	Met	Gly	Leu	Glu	Glu	Glu	Phe	Gly	Ile	Glu	Met	Ala	Glu	Glu	Lys
			145					150				155			160
Ala	Gln	Ser	Ile	Ala	Thr	Val	Glu	Gln	Ala	Ala	Ala	Leu	Ile	Glu	Glu
			165					170					175		
Leu	Leu	Phe	Glu	Lys	Ala	Lys									
			180												

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Val	Phe	Val	Cys	Phe	Gly	Cys	Cys	Glu	Phe	Val	Thr	Ile	Lys	Pro	Leu
1			5					10					15		
Pro	Leu	Gly	Ser	Ser	Leu	Ser	Leu	Phe	Leu	Ile	Ser	Ser	Ser	Ser	Pro
			20					25					30		
Pro	Pro	Ser	Ile	Ser	Leu	Arg	Ser	Leu	Tyr	Asp	Ser	Phe	Val	Leu	Trp
			35					40				45			
Leu	Pro	Leu	Leu	Leu	Leu	Leu	Phe	Pro	Phe	Lys	Leu	Val	Leu	Ala	
			50					55				60			

Asn Trp Arg Ser Arg Leu Gly Lys Leu Lys Ala Leu Ala Met Glu Glu
65 70 75 80
Glu Ala Val Phe Leu Leu Ile Ser Ala Ser Phe Leu Pro Ala
85 90

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Met Ala Ser Ile Ala Ala Ser Ala Ser Ile Ser Leu Gln Ala Arg Pro
1 5 10 15
Arg Gln Leu Ala Ile Ala Ala Arg Gln Val Lys Ser Phe Ser Asn Gly
20 25 30
Arg Arg Ser Ser Leu Ser Phe Asn Leu Arg Gln Leu Pro Thr Arg Leu
35 40 45
Thr Val Ser Cys Ala Ala Lys Pro Glu Thr Val Asp Lys Val Cys Ala
50 55 60
Val Val Arg Lys Gln Leu Ser Leu Lys Glu Ala Asp Glu Ile Thr Ala
65 70 75 80
Ala Thr Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr Val Glu
85 90 95
Ile Val Met Gly Leu Glu Glu Glu Phe Gly Ile Glu Met Ala Glu Glu
100 105 110
Lys Ala Gln Ser Ile Ala Thr Val Glu Gln Ala Ala Ala Leu Ile Glu
115 120 125
Glu Leu Leu Phe Glu Lys Ala Lys
130 135

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

gaagaaacaaa cacaaaaaatg gcgacgggtac cattgtttcac ccagttttccc tgcaaaacccc 60
taaattccaag ctcatcaaac actaaacac aatcgaaatc tccgatctcta ctaccgatta 120
actcaataaaa tcgatcggag attggagtct ctgtttcatcg gccagatttc aaaatcccgag 180
cgacggacat cgacgacgaa tgggggtcaag atggagtggg gagagtattt gcctcatctt 240
caaccgtatc ggtagcagat aaagcaatcg aatccgtgga ggagacggag aggcataaaga 300
gatcactagc ggattcggtt tacggaacacg atcgaggttt aagcgtatcg agtgatacga 360
gagctgagat cagcgagctc atcacacagc tcgagttctaa gaacccctact ccagctctcta 420
acgaagctct gtttctctc aacggcaaat ggatcctcgc ctacacgtcg ttctgggggt 480
tgttccatt gctctcacga agaattgaac cgttggttaa agtggatgag atctcacaaa 540
ccattgattc cgatagcttc accgttcaaa actctgtccg gttcgtcgtt ccgttttcca 600
caacgtcgtt tagcaccaac gctaagtttg aaatccgaag tctataaacgt gtccagatta 660
agttcgagca aggtgttata ggRactcctc agctaaccga ttcgattgaa ataccggaat 720
ccgtggaggt tcttggtcgc aaaaatcgatc tcaatccccat taaaggttta ctatcatcag 780
tccaagacac tgcttcttca gtggctagaa ccaattccaa ccaaccacca ttgaagtttt 840
ctctgcctag tgacaacacg cagtctgtgc tgcacaaac ttatctcgac aagacCttc 900

ggatctcgag aggcgatggt ggaagcgtct atgtgctcat caaagaagga agctctctct 960
taaaccctta aatcatcata actctcatca catccatagt aacatatata caagtatatga 1020
cccatctgtc tatgtttact agtgttgtaa ctgttatata gctctttac ctgttgagaga 1080
gttataaact tataatggat gttactcttg gtatactgta ctacaataca tatacataac 1140
tacatacttg aacaggcc

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..322
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Arg	Thr	Asn	Thr	Lys	Met	Ala	Thr	Val	Pro	Leu	Phe	Thr	Gln	Phe	Pro
1			5						10				15		
Cys	Lys	Thr	Leu	Asn	Pro	Ser	Ser	Ser	Asn	Thr	Lys	His	Gln	Ser	Lys
			20					25					30		
Ser	Pro	Ile	Leu	Leu	Pro	Ile	Asn	Ser	Ile	Asn	Arg	Ser	Glu	Ile	Gly
		35					40				45				
Val	Ser	Val	His	Arg	Pro	Asp	Phe	Lys	Ile	Arg	Ala	Thr	Asp	Ile	Asp
		50				55					60				
Asp	Glu	Trp	Gly	Gln	Asp	Gly	Val	Glu	Arg	Val	Phe	Ala	Ser	Ser	Ser
		65			70				75				80		
Thr	Val	Ser	Val	Ala	Asp	Lys	Ala	Ile	Glu	Ser	Val	Glu	Glu	Thr	Glu
			85					90					95		
Arg	Leu	Lys	Arg	Ser	Leu	Ala	Asp	Ser	Leu	Tyr	Gly	Thr	Asp	Arg	Gly
			100				105					110			
Leu	Ser	Val	Ser	Ser	Asp	Thr	Arg	Ala	Glu	Ile	Ser	Glu	Leu	Ile	Thr
		115				120						125			
Gln	Leu	Glu	Ser	Lys	Asn	Pro	Thr	Pro	Ala	Pro	Asn	Glu	Ala	Leu	Phe
		130				135					140				
Leu	Leu	Asn	Gly	Lys	Trp	Ile	Leu	Ala	Tyr	Thr	Ser	Phe	Val	Gly	Leu
		145			150					155				160	
Phe	Pro	Leu	Leu	Ser	Arg	Arg	Ile	Glu	Pro	Leu	Val	Lys	Val	Asp	Glu
			165						170					175	
Ile	Ser	Gln	Thr	Ile	Asp	Ser	Asp	Ser	Phe	Thr	Val	Gln	Asn	Ser	Val
			180				185						190		
Arg	Phe	Ala	Gly	Pro	Phe	Ser	Thr	Thr	Ser	Phe	Ser	Thr	Asn	Ala	Lys
		195					200					205			
Phe	Glu	Ile	Arg	Ser	Pro	Lys	Arg	Val	Gln	Ile	Lys	Phe	Glu	Gln	Gly
		210				215					220				
Val	Ile	Xaa	Thr	Pro	Gln	Leu	Thr	Asp	Ser	Ile	Glu	Ile	Pro	Glu	Ser
		225			230				235					240	
Val	Glu	Val	Leu	Gly	Gln	Lys	Ile	Asp	Leu	Asn	Pro	Ile	Lys	Gly	Leu
			245					250					255		
Leu	Thr	Ser	Val	Gln	Asp	Thr	Ala	Ser	Ser	Val	Ala	Arg	Thr	Ile	Ser
			260				265					270			
Asn	Gln	Pro	Pro	Leu	Lys	Phe	Ser	Leu	Pro	Ser	Asp	Asn	Thr	Gln	Ser
		275				280					285				
Trp	Leu	Leu	Thr	Thr	Tyr	Leu	Asp	Lys	Asp	Leu	Arg	Ile	Ser	Arg	Gly
		290				295					300				
Asp	Gly	Gly	Ser	Val	Tyr	Val	Leu	Ile	Lys	Glu	Gly	Ser	Ser	Leu	Leu
		305			310				315					320	
Asn	Pro														

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..317
(D) OTHER INFORMATION: / Ceres Seq. ID 1566187
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:
Met Ala Thr Val Pro Leu Phe Thr Gln Phe Pro Cys Lys Thr Leu Asn
1 5 10 15
Pro Ser Ser Ser Asn Thr Lys His Gln Ser Lys Ser Pro Ile Leu Leu
20 25 30
Pro Ile Asn Ser Ile Asn Arg Ser Glu Ile Gly Val Ser Val His Arg
35 40 45
Pro Asp Phe Lys Ile Arg Ala Thr Asp Ile Asp Asp Glu Trp Gly Gln
50 55 60
Asp Gly Val Glu Arg Val Phe Ala Ser Ser Ser Thr Val Ser Val Ala
65 70 75 80
Asp Lys Ala Ile Glu Ser Val Glu Glu Thr Glu Arg Leu Lys Arg Ser
85 90 95
Leu Ala Asp Ser Leu Tyr Gly Thr Asp Arg Gly Leu Ser Val Ser Ser
100 105 110
Asp Thr Arg Ala Glu Ile Ser Glu Leu Ile Thr Gln Leu Glu Ser Lys
115 120 125
Asn Pro Thr Pro Ala Pro Asn Glu Ala Leu Phe Leu Leu Asn Gly Lys
130 135 140
Trp Ile Leu Ala Tyr Thr Ser Phe Val Gly Leu Phe Pro Leu Leu Ser
145 150 155 160
Arg Arg Ile Glu Pro Leu Val Lys Val Asp Glu Ile Ser Gln Thr Ile
165 170 175
Asp Ser Asp Ser Phe Thr Val Gln Asn Ser Val Arg Phe Ala Gly Pro
180 185 190
Phe Ser Thr Thr Ser Phe Ser Thr Asn Ala Lys Phe Glu Ile Arg Ser
195 200 205
Pro Lys Arg Val Gln Ile Lys Phe Glu Gln Gly Val Ile Xaa Thr Pro
210 215 220
Gln Leu Thr Asp Ser Ile Glu Ile Pro Glu Ser Val Glu Val Leu Gly
225 230 235 240
Gln Lys Ile Asp Leu Asn Pro Ile Lys Gly Leu Leu Thr Ser Val Gln
245 250 255
Asp Thr Ala Ser Ser Val Ala Arg Thr Ile Ser Asn Gln Pro Pro Leu
260 265 270
Lys Phe Ser Leu Pro Ser Asp Asn Thr Gln Ser Trp Leu Leu Thr Thr
275 280 285
Tyr Leu Asp Lys Asp Leu Arg Ile Ser Arg Gly Asp Gly Gly Ser Val
290 295 300
Tyr Val Leu Ile Lys Glu Gly Ser Ser Leu Leu Asn Pro
305 310 315
(2) INFORMATION FOR SEQ ID NO:215:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 655 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..655
(D) OTHER INFORMATION: / Ceres Seq. ID 1566214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:
aatggttact tttacttctc ctctcttctc tcttgttcca tctttcatgt gaaagagaga 60
gttgaatttt gcagatgagt atgagaagaa gcaaaagcgga agggaaagag agcttacgag 120
aactgagtga ggaagagaaa gaagaagaag aaactgaaga tgaagatact tttgaagaag 180
aagaggcttt ggagaagaag cagaaaagga aagctacaag tagtagtgga gtttgcagg 240
tcgagagttg taccgcggat ataagcaaaag ccaaacagta ccacaaacga cacaaagtct 300
gcagcttttca tgccaaagct cctcatgttc ggatctcttg tcttcaccaa cgtttctgcc 360
aacaatgcag caggttttcac gcgctcagtg agtttgatga agccaagcgg agttgcagga 420
gacgcttagc tggacacaac gagagaaggg ggaagagcac aactgactaa agacgggtgaa 480
acgtgtgaga tccCggtttg aaggttaatg aaacaggGct ttgGcttact ctctctgtgc 540
agtctctttt agctccttgt aatcctctgt gtctctgtct gtccccata ttacctgtaa 600
tcaaagctat ctgctaaacc tacgacatgg ttaataaat gcattgagac ttagc

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1566215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Met	Ser	Met	Arg	Arg	Ser	Lys	Ala	Glu	Gly	Lys	Arg	Ser	Leu	Arg	Glu
1			5					10					15		
Leu	Ser	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Thr	Glu	Asp	Glu	Asp	Thr	
			20					25					30		
Phe	Glu	Glu	Glu	Glu	Ala	Leu	Glu	Lys	Lys	Gln	Lys	Gly	Lys	Ala	Thr
			35				40					45			
Ser	Ser	Ser	Gly	Val	Cys	Gln	Val	Glu	Ser	Cys	Thr	Ala	Asp	Ile	Ser
			50				55				60				
Lys	Ala	Lys	Gln	Tyr	His	Lys	Arg	His	Lys	Val	Cys	Gln	Phe	His	Ala
65				70						75				80	
Lys	Ala	Pro	His	Val	Arg	Ile	Ser	Gly	Leu	His	Gln	Arg	Phe	Cys	Gln
			85						90					95	
Gln	Cys	Ser	Arg	Phe	His	Ala	Leu	Ser	Glu	Phe	Asp	Glu	Ala	Lys	Arg
			100					105					110		
Ser	Cys	Arg	Arg	Arg	Leu	Ala	Gly	His	Asn	Glu	Arg	Arg	Arg	Lys	Ser
			115				120						125		
Thr	Thr	Asp													
															130

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1566216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Met	Arg	Arg	Ser	Lys	Ala	Glu	Gly	Lys	Arg	Ser	Leu	Arg	Glu	Leu	Ser
1				5						10				15	
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Thr	Glu	Asp	Glu	Asp	Thr	Phe	Glu
				20				25						30	
Glu	Glu	Glu	Ala	Leu	Glu	Lys	Lys	Gln	Lys	Gly	Lys	Ala	Thr	Ser	Ser
			35				40					45			
Ser	Gly	Val	Cys	Gln	Val	Glu	Ser	Cys	Thr	Ala	Asp	Ile	Ser	Lys	Ala

50					55					60					
Lys	Gln	Tyr	His	Lys	Arg	His	Lys	Val	Cys	Gln	Phe	His	Ala	Lys	Ala
65				70					75					80	
Pro	His	Val	Arg	Ile	Ser	Gly	Leu	His	Gln	Arg	Phe	Cys	Gln	Gln	Cys
				85					90					95	
Ser	Arg	Phe	His	Ala	Leu	Ser	Glu	Phe	Asp	Glu	Ala	Lys	Arg	Ser	Cys
				100				105					110		
Arg	Arg	Arg	Leu	Ala	Gly	His	Asn	Glu	Arg	Arg	Arg	Lys	Ser	Thr	Thr
			115				120						125		

Asp

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..631
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

atatttatat	tttccaataa	tctcaaaaaa	aaActctctg	attcgaaaaa	tgaaatttga	60
ttttgacaaa	aaaaaaatga	gctacgacag	agtcccaccg	gaatcgatct	ctcctccagg	120
ataccaatct	cactatccac	ctccggggtta	tccatcagca	ccgccaccgc	cgggatatcc	180
ttctctctcg	tcgcatcacg	aaggatatcc	tccacctcac	ccttacggag	gatatccacc	240
acgcctctca	cgtccttacg	aaggcggtta	tcaagggtac	tgcgcggag	gagggttatcc	300
tcacagcatc	caaggaccac	cacctctctc	tccgccgcaa	aattacgacc	actgccatca	360
tgatcatcac	cattaccaag	attctgactc	tggttgcttc	tctttcatcc	gtggctgtct	420
tgctgctctt	tgctgttgct	gtttgttgga	ggaatgctgc	ttctgagaat	gcgcgcagtc	480
tctgtggtac	tcgtgtgtta	ctgtcagcat	tatgtgtcta	atcgaagaca	tatgccataa	540
cactctatgt	cttatatgta	tccatcaaaa	taaacattg	tgagtttga	atgcagttcc	600
ttcagaaatg	tgtggaataa	tgtttcacaa	t			

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Tyr	Leu	Tyr	Phe	Pro	Ile	Ile	Ser	Lys	Lys	Asn	Ser	Leu	Ile	Arg	Lys
1				5				10				15			
Val	Lys	Phe	Asp	Phe	Asp	Lys	Lys	Lys	Met	Ser	Tyr	Asp	Arg	Val	Pro
			20					25				30			
Pro	Glu	Ser	Tyr	Pro	Pro	Pro	Gly	Tyr	Gln	Ser	His	Tyr	Pro	Pro	Pro
			35				40				45				
Gly	Tyr	Pro	Ser	Ala	Pro	Pro	Pro	Gly	Tyr	Pro	Ser	Pro	Pro	Pro	Ser
			50				55				60				
His	His	Glu	Gly	Tyr	Pro	Pro	Pro	Gln	Pro	Tyr	Gly	Gly	Tyr	Pro	Pro
			65				70			75			80		
Pro	Ser	Ser	Arg	Pro	Tyr	Glu	Gly	Gly	Tyr	Gln	Gly	Tyr	Phe	Ala	Gly
			85				90				95				
Gly	Gly	Tyr	Pro	His	Gln	His	His	Gly	Pro	Pro	Pro	Pro	Pro	Pro	Pro
			100				105				110				
Gln	Asn	Tyr	Asp	His	Cys	His	His	Asp	His	His	His	Tyr	Gln	Asp	Ser

115 120 125
Asp Ser Gly Cys Phe Ser Phe Ile Arg Gly Cys Leu Ala Ala Leu Cys
130 135 140
Cys Cys Cys Leu Leu Glu Glu Cys Cys Phe
145 150

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Met	Ser	Tyr	Asp	Arg	Val	Pro	Pro	Glu	Ser	Tyr	Pro	Pro	Pro	Gly	Tyr
1			5					10						15	
Gln	Ser	His	Tyr	Pro	Pro	Pro	Gly	Tyr	Pro	Ser	Ala	Pro	Pro	Pro	Pro
			20				25					30			
Gly	Tyr	Pro	Ser	Pro	Pro	Ser	His	His	Glu	Gly	Tyr	Pro	Pro	Pro	Gln
		35					40				45				
Pro	Tyr	Gly	Gly	Tyr	Pro	Pro	Pro	Ser	Ser	Arg	Pro	Tyr	Glu	Gly	Gly
		50				55				60					
Tyr	Gln	Gly	Tyr	Phe	Ala	Gly	Gly	Tyr	Pro	His	Gln	His	His	Gly	
		65			70			75			80				
Pro	Pro	Pro	Pro	Pro	Pro	Pro	Gln	Asn	Tyr	Asp	His	Cys	His	His	Asp
				85				90			95				
His	His	His	Tyr	Gln	Asp	Ser	Asp	Ser	Gly	Cys	Phe	Ser	Phe	Ile	Arg
			100				105				110				
Gly	Cys	Leu	Ala	Ala	Leu	Cys	Cys	Cys	Leu	Leu	Glu	Gly	Cys	Cys	
		115				120					125				
Phe															

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..771
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

aaaaaattag	tctgtcgaag	catcgtgaaa	atgatcgtac	ttctctgttg	ttccgctttct	60
tcatactcga	tctgtcgtcgt	cttttcctgc	gcgctttctc	tgtttctact	ctctgaaact	120
tctctaggag	ctccttctgc	catcaatggc	ttgccaatcg	tgaggaatat	tagtgacctt	180
cctcaggata	actatggaag	accaggtctt	tccacatga	ctgttgctgg	ctccgtattg	240
catggaatga	aagagggttg	aatatggctt	cagacatttg	ctccaggttc	agagacacca	300
attcacaggc	actcctgtga	agagggtttt	gttctcctaa	agggcagtg	tactctgtat	360
ctcgtcgaaa	cacatggaaa	tttccctggg	aaaccaatcg	aatttccaat	ctttgccaac	420
agtacaattc	atatcccgat	caatgatgct	catcagggtc	aaaacacccg	tcattgaggac	480
ctgcaggtgt	tgggttatcat	atctcggcgc	ccattataaaa	tcttcatcta	cgaagactgg	540
tttatgccac	acaactgctgc	aaggctgaag	ttCccttact	attgggatga	gcaatgcatt	600
caagaatcac	aaaaagacga	gctttaaagc	aaagtccgag	gctaaaagca	agcacacctt	660
ttagatagta	aaatcatatg	tgagggtttt	tgacActacg	tagatactgg	taaatgtggca	720
aggattttac	atgaatgttg	ttgttaccag	aaagtaata	aatgttcaag	c	

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..208
(D) OTHER INFORMATION: / Ceres Seq. ID 1566224
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Lys	Lys	Leu	Val	Arg	Arg	Ser	Ile	Val	Lys	Met	Ile	Val	Leu	Ser	Val
1				5				10					15		
Gly	Ser	Ala	Ser	Ser	Ser	Pro	Ile	Val	Val	Phe	Ser	Val	Ala	Leu	
		20					25					30			
Leu	Leu	Phe	Tyr	Phe	Ser	Glu	Thr	Ser	Leu	Gly	Ala	Pro	Cys	Pro	Ile
		35					40				45				
Asn	Gly	Leu	Pro	Ile	Val	Arg	Asn	Ile	Ser	Asp	Leu	Pro	Gln	Asp	Asn
	50					55				60					
Tyr	Gly	Arg	Pro	Gly	Leu	Ser	His	Met	Thr	Val	Ala	Gly	Ser	Val	Leu
65				70				75						80	
His	Gly	Met	Lys	Glu	Val	Glu	Ile	Trp	Leu	Gln	Thr	Phe	Ala	Pro	Gly
			85					90				95			
Ser	Glu	Thr	Pro	Ile	His	Arg	His	Ser	Cys	Glu	Glu	Val	Phe	Val	Leu
			100					105				110			
Leu	Lys	Gly	Ser	Gly	Thr	Leu	Tyr	Leu	Ala	Glu	Thr	His	Gly	Asn	Phe
		115				120					125				
Pro	Gly	Lys	Pro	Ile	Glu	Phe	Pro	Ile	Phe	Ala	Asn	Ser	Thr	Ile	His
	130				135						140				
Ile	Pro	Ile	Asn	Asp	Ala	His	Gln	Val	Lys	Asn	Thr	Gly	His	Glu	Asp
145				150					155					160	
Leu	Gln	Val	Leu	Val	Ile	Ile	Ser	Arg	Pro	Pro	Ile	Lys	Ile	Phe	Ile
			165					170				175			
Tyr	Glu	Asp	Trp	Phe	Met	Pro	His	Thr	Ala	Ala	Arg	Leu	Lys	Phe	Pro
		180						185				190			
Tyr	Tyr	Trp	Asp	Glu	Gln	Cys	Ile	Gln	Glu	Ser	Gln	Lys	Asp	Glu	Leu
		195					200					205			

- (2) INFORMATION FOR SEQ ID NO:223:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..198
(D) OTHER INFORMATION: / Ceres Seq. ID 1566225
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Met	Ile	Val	Leu	Ser	Val	Gly	Ser	Ala	Ser	Ser	Ser	Pro	Ile	Val	Val
1				5				10					15		
Val	Phe	Ser	Val	Ala	Leu	Leu	Leu	Phe	Tyr	Phe	Ser	Glu	Thr	Ser	Leu
			20					25				30			
Gly	Ala	Pro	Cys	Pro	Ile	Asn	Gly	Leu	Pro	Ile	Val	Arg	Asn	Ile	Ser
		35					40				45				
Asp	Leu	Pro	Gln	Asp	Asn	Tyr	Gly	Arg	Pro	Gly	Leu	Ser	His	Met	Thr
	50				55					60					
Val	Ala	Gly	Ser	Val	Leu	His	Gly	Met	Lys	Glu	Val	Glu	Ile	Trp	Leu
65					70					75				80	

Gln	Thr	Phe	Ala	Pro	Gly	Ser	Glu	Thr	Pro	Ile	His	Arg	His	Ser	Cys	
				85					90					95		
Glu	Glu	Val	Phe	Val	Leu	Leu	Lys	Gly	Ser	Gly	Thr	Leu	Tyr	Leu	Ala	
				100				105					110			
Glu	Thr	His	Gly	Asn	Phe	Pro	Gly	Lys	Pro	Ile	Glu	Phe	Pro	Ile	Phe	
				115				120					125			
Ala	Asn	Ser	Thr	Ile	His	Ile	Pro	Ile	Asn	Asp	Ala	His	Gln	Val	Lys	
				130				135				140				
Asn	Thr	Gly	His	Glu	Asp	Leu	Gln	Val	Leu	Val	Ile	Ile	Ser	Arg	Pro	
				145				150				155			160	
Pro	Ile	Lys	Ile	Phe	Ile	Tyr	Glu	Asp	Trp	Phe	Met	Pro	His	Thr	Ala	
				165				170					175			
Ala	Arg	Leu	Lys	Phe	Pro	Tyr	Tyr	Trp	Asp	Glu	Gln	Cys	Ile	Gln	Glu	
				180				185					190			
Ser	Gln	Lys	Asp	Glu	Leu											
				195												

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Met	Thr	Val	Ala	Gly	Ser	Val	Leu	His	Gly	Met	Lys	Glu	Val	Glu	Ile	
1				5				10					15			
Trp	Leu	Gln	Thr	Phe	Ala	Pro	Gly	Ser	Glu	Thr	Pro	Ile	His	Arg	His	
				20				25					30			
Ser	Cys	Glu	Glu	Val	Phe	Val	Leu	Leu	Lys	Gly	Ser	Gly	Thr	Leu	Tyr	
				35				40				45				
Leu	Ala	Glu	Thr	His	Gly	Asn	Phe	Pro	Gly	Lys	Pro	Ile	Glu	Phe	Pro	
				50				55				60				
Ile	Phe	Ala	Asn	Ser	Thr	Ile	His	Ile	Pro	Ile	Asn	Asp	Ala	His	Gln	
				65				70				75			80	
Val	Lys	Asn	Thr	Gly	His	Glu	Asp	Leu	Gln	Val	Leu	Val	Ile	Ile	Ser	
				85				90					95			
Arg	Pro	Pro	Ile	Lys	Ile	Phe	Ile	Tyr	Glu	Asp	Trp	Phe	Met	Pro	His	
				100				105					110			
Thr	Ala	Ala	Arg	Leu	Lys	Phe	Pro	Tyr	Tyr	Trp	Asp	Glu	Gln	Cys	Ile	
				115				120					125			
Gln	Glu	Ser	Gln	Lys	Asp	Glu	Leu									
				130				135								

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1256
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

aaacaaaaca	caggtttggt	cggagaaggc	tttattaatc	cacttgtcct	ccctctcagac	60
tctacaaagt	caaagtgtgt	cactttacct	ataaaaacgc	ttctctttca	atggctctct	120
cttctgtgtt	cttgcgtctg	attctcttct	cttctctctac	taacctctgt	tcaaatcacc	180

```

atctcccccac tttcttcccc aagaatcatc tcatttgctc tcattccact tctctctgct 240
tcgaatcgct ctoggttttca tgcgtcgcaa ctggatctac caagaaatca tccgatactc 300
ggagaaagggt aaagagcatg gctacgacaa atataggaaa gaggaggag aaagagctcg 360
agatttatga tctcgaagAg aatttagcga ttgatttgcc taaattcaca gcagatctct 420
ccgataagtt ttgtaaagag agaggcgctt tcaccgtcgt tgtctccggt ggctctctca 480
tcaaatcact ccgaaaatta gtagaatctc cttagcttga tctctatagat tgggcaagggt 540
ggcattttttt ctgggttgac gagagagttg ttcccaagaa tcacgatgat agcaactata 600
aactcgttta tgatagtatt ctatcccaag taccaattcc gcttggaat gtatatgcga 660
tcaacgaagc cctctccgct gaggtcgtag cggatgatta cgagacctcg ctcaaacatt 720
tggtcaacac caacattctc cgtgtatctg aatcaactgg ctttcccaaa ttgtatctca 780
tgctctaggt tatgggacct gatggtcatc tggcatcatt attccctggg catggtctct 840
gcaacgagag caagaaatgg gtagtttcaa tctctgactc tccaaaacca ccgtctgaga 900
gaatcacctt cactgtcccc gtcatacaat catctgcaca tgtagctcta gttgtttcgg 960
gttctgggaa agctgaagct gtggaggcag ctttaaaagaa gactgggaat gtaccacctg 1020
ctggttctgt ttctgctgaa gacgagttgg tttggtctct ggacaaaacca gcatcttcca 1080
agctctaaaa acagggtgga tgcttcccat tccagtgaa ttaccaatgt gactagctcg 1140
gtttagtttt tggattttga ctcttttggt ctctccattt atgttgtggg aagagaactg 1200
tgtgataaaa gcgtgtactt tacatggaaa taatgaacta atcaatggtt tctctg

```

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..325

(D) OTHER INFORMATION: / Ceres Seq. ID 1566235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

```

Met Ala Ser Ser Ser Cys Phe Leu Arg Ser Ile Leu Phe Ser Ser Pro
1      5      10      15
Thr Asn Leu Arg Ser Asn His His Leu Pro Thr Phe Phe Pro Lys Asn
20     25
His Leu Ile Cys Ser His Ser Thr Ser Ser Arg Phe Glu Ser Leu Ser
35     40     45
Val Ser Ser Ile Gly Thr Gly Ser Thr Lys Lys Ser Ser Asp Thr Arg
50     55     60
Arg Lys Val Lys Ser Met Ala Thr Thr Asn Ile Gly Lys Glu Glu Lys
65     70     75     80
Lys Arg Val Glu Ile Tyr Asp Leu Glu Glu Asn Leu Ala Ile Asp Leu
85     90     95
Ala Lys Phe Thr Ala Asp Leu Ser Asp Lys Phe Cys Lys Glu Arg Gly
100    105    110
Ala Phe Thr Val Val Val Ser Gly Gly Ser Leu Ile Lys Ser Leu Arg
115    120    125
Lys Leu Val Glu Ser Pro Tyr Val Asp Ser Ile Asp Trp Ala Arg Trp
130    135    140
His Phe Phe Trp Val Asp Glu Arg Val Val Pro Lys Asn His Asp Asp
145    150    155    160
Ser Asn Tyr Lys Leu Ala Tyr Asp Ser Phe Leu Ser Lys Val Pro Ile
165    170    175
Pro Pro Gly Asn Val Tyr Ala Ile Asn Glu Ala Leu Ser Ala Glu Ala
180    185    190
Ala Ala Asp Asp Tyr Glu Thr Cys Leu Lys His Leu Val Asn Thr Asn
195    200    205
Ile Leu Arg Val Ser Glu Ser Thr Gly Phe Pro Lys Phe Asp Leu Met
210    215    220
Leu Leu Gly Met Gly Pro Asp Gly His Val Ala Ser Leu Phe Pro Gly
225    230    235    240
His Gly Leu Cys Asn Glu Ser Lys Lys Trp Val Ser Ile Ser Asp

```

245 250 255
Ser Pro Lys Pro Pro Ser Glu Arg Ile Thr Phe Thr Phe Pro Val Ile
260 265 270
Asn Ser Ser Ala His Val Ala Leu Val Val Cys Gly Ser Gly Lys Ala
275 280 285
Glu Ala Val Glu Ala Ala Leu Lys Lys Thr Gly Asn Val Pro Pro Ala
290 295 300
Gly Ser Val Ser Ala Glu Asp Glu Leu Val Trp Phe Leu Asp Lys Pro
305 310 315 320
Ala Ser Ser Lys Leu
325

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1566236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Met Ala Thr Thr Asn Ile Gly Lys Glu Glu Lys Lys Arg Val Glu Ile
1 5 10 15
Tyr Asp Leu Glu Glu Asn Leu Ala Ile Asp Leu Ala Lys Phe Thr Ala
20 25 30
Asp Leu Ser Asp Lys Phe Cys Lys Glu Arg Gly Ala Phe Thr Val Val
35 40 45
Val Ser Gly Gly Ser Leu Ile Lys Ser Leu Arg Lys Leu Val Glu Ser
50 55 60
Pro Tyr Val Asp Ser Ile Asp Trp Ala Arg Trp His Phe Phe Trp Val
65 70 75 80
Asp Glu Arg Val Val Pro Lys Asn His Asp Asp Ser Asn Tyr Lys Leu
85 90 95
Ala Tyr Asp Ser Phe Leu Ser Lys Val Pro Ile Pro Pro Gly Asn Val
100 105 110
Tyr Ala Ile Asn Glu Ala Leu Ser Ala Glu Ala Ala Asp Asp Tyr
115 120 125
Glu Thr Cys Leu Lys His Leu Val Asn Thr Asn Ile Leu Arg Val Ser
130 135 140
Glu Ser Thr Gly Phe Pro Lys Phe Asp Leu Met Leu Leu Gly Met Gly
145 150 155 160
Pro Asp Gly His Val Ala Ser Leu Phe Pro Gly His Gly Leu Cys Asn
165 170 175
Glu Ser Lys Lys Trp Val Val Ser Ile Ser Asp Ser Pro Lys Pro Pro
180 185 190
Ser Glu Arg Ile Thr Phe Thr Phe Pro Val Ile Asn Ser Ser Ala His
195 200 205
Val Ala Leu Val Val Cys Gly Ser Gly Lys Ala Glu Ala Val Glu Ala
210 215 220
Ala Leu Lys Lys Thr Gly Asn Val Pro Pro Ala Gly Ser Val Ser Ala
225 230 235 240
Glu Asp Glu Leu Val Trp Phe Leu Asp Lys Pro Ala Ser Ser Lys Leu
245 250 255

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 640 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..640
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566237
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:
aactaccacc aattcaatcc attgctcaaa ctctcttctc atctctcaaca caccaccctt 60
acctaccctc atctctctct ctgcaacaga gcacaaaaat ggattctgca tcgtccaaca 120
ccaaagctat agaccctcca ctccacatgt tgggtttcga gttcgatgaa ttatctccga 180
cacgtatcac aggtgcgctt cctgtttctc ccgtctgctg ccagcctttc aaggtgttac 240
acggtgggtg atctgctttg atagccgagt ctttagcaag tatgggagct cacatggcct 300
ctgggtttcaa aagggtgcgt ggaattcaac tctcaatcaa ccatttgaag agtgcgtgatc 360
ttggagacct tgtcttcgcc gaagcaactc ctgtaagcac aggggaagact attcagggttt 420
gggaagtcga gttattggaaa acaacacaga aagataaagc taacaaaatc Tttaatatct 480
tcctctagag ttacacttat ctgtaattcta cctatccctg ataacgccaa agatgcagca 540
aacatgctca aaatggctgc aaagtgttag atttcttcag gcttttttgt ttactcttga 600
ttgtatgtaa tgaccatct tctcgaattt gataataagc
(2) INFORMATION FOR SEQ ID NO:229:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..161
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566238
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:
Leu Pro Pro Ile Gln Ser Ile Ala Gln Thr Leu Leu Ser Ser Leu Thr
1 5 10 15
His Pro Pro Tyr Leu Pro Pro Ser Leu Gln Gln Ser Thr Lys
20 25 30
Met Asp Ser Ala Ser Ser Asn Thr Lys Ala Ile Asp Pro Pro Leu His
35 40 45
Met Leu Gly Phe Glu Phe Asp Glu Leu Ser Pro Thr Arg Ile Thr Gly
50 55 60
Arg Leu Pro Val Ser Pro Val Cys Cys Gln Pro Phe Lys Val Leu His
65 70 75 80
Gly Gly Val Ser Ala Leu Ile Ala Glu Ser Leu Ala Ser Met Gly Ala
85 90 95
His Met Ala Ser Gly Phe Lys Arg Val Ala Gly Ile Gln Leu Ser Ile
100 105 110
Asn His Leu Lys Ser Ala Asp Leu Gly Asp Leu Val Phe Ala Glu Ala
115 120 125
Thr Pro Val Ser Thr Gly Lys Thr Ile Gln Val Trp Glu Val Lys Leu
130 135 140
Trp Lys Thr Thr Gln Lys Asp Lys Ala Asn Lys Ile Phe Asn Ile Phe
145 150 155 160
Leu

(2) INFORMATION FOR SEQ ID NO:230:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..129
(D) OTHER INFORMATION: / Ceres Seq. ID 1566239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```
Met Asp Ser Ala Ser Ser Asn Thr Lys Ala Ile Asp Pro Pro Leu His
1          5          10          15
Met Leu Gly Phe Glu Phe Asp Glu Leu Ser Pro Thr Arg Ile Thr Gly
20          25          30
Arg Leu Pro Val Ser Pro Val Cys Cys Gln Pro Phe Lys Val Leu His
35          40          45
Gly Gly Val Ser Ala Leu Ile Ala Glu Ser Leu Ala Ser Met Gly Ala
50          55          60
His Met Ala Ser Gly Phe Lys Arg Val Ala Gly Ile Gln Leu Ser Ile
65          70          75
Asn His Leu Lys Ser Ala Asp Leu Gly Asp Leu Val Phe Ala Glu Ala
85          90          95
Thr Pro Val Ser Thr Gly Lys Thr Ile Gln Val Trp Glu Val Lys Leu
100         105         110
Trp Lys Thr Thr Gln Lys Asp Lys Ala Asn Lys Ile Phe Asn Ile Phe
115         120         125
Leu
```

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..113
(D) OTHER INFORMATION: / Ceres Seq. ID 1566240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```
Met Leu Gly Phe Glu Phe Asp Glu Leu Ser Pro Thr Arg Ile Thr Gly
1          5          10          15
Arg Leu Pro Val Ser Pro Val Cys Cys Gln Pro Phe Lys Val Leu His
20          25          30
Gly Gly Val Ser Ala Leu Ile Ala Glu Ser Leu Ala Ser Met Gly Ala
35          40          45
His Met Ala Ser Gly Phe Lys Arg Val Ala Gly Ile Gln Leu Ser Ile
50          55          60
Asn His Leu Lys Ser Ala Asp Leu Gly Asp Leu Val Phe Ala Glu Ala
65          70          75
Thr Pro Val Ser Thr Gly Lys Thr Ile Gln Val Trp Glu Val Lys Leu
85          90          95
Trp Lys Thr Thr Gln Lys Asp Lys Ala Asn Lys Ile Phe Asn Ile Phe
100         105         110
Leu
```

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1090 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1090
(D) OTHER INFORMATION: / Ceres Seq. ID 1566241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

actcttttctt	cttctctctcg	tgtctgtttg	tcacttttaga	gtactcttctt	cttcttctctt	60
gttaagcggtt	ctctctcgac	ttgatacttt	tctccagtaa	gggtttgcaa	agatgaagct	120
tgatactagt	gggttcgaga	cttccatgcc	tatgatitga	tttggtctga	gcagtgatat	180
gcttgatgag	cttctctctg	tacctctgtt	tgatctaccc	cgtactaaag	agtttgatgg	240
atttcagaaa	aaagctaaa	acatgttgaa	gcatgcaaaa	ggaaacacca	ctctcgcttt	300
tatcttcaaa	gggtgtgtta	tggtcgctgc	tgattctcgg	gctagcatgg	gaggtatat	360
ctcttcacaa	tctgtgaaga	agattattga	aatcaatcct	tatatgctcg	gtacaatggc	420
tgaggagcgt	gctgattgcc	aattctggca	cagaaatctt	ggaataaagt	gcgcctacaa	480
tgagctggca	aacaagagga	gaatctctgt	tccggagcgt	tcgaaacttc	ttcgcaaat	540
gctctattca	taccgtggaa	tgggacttct	tggtgtgtaca	atgattgctg	gatggagcga	600
aactggtccc	ggactatact	atgtcgacaa	cgaaggagga	cgctcaagg	gagacaggtt	660
ttcagtcggt	tctggttcac	catatgctta	cggtgtgctg	gacagcggtg	acaaatatga	720
tatgtcagtt	gaagaagcgt	ccgagttaga	ggagatcaat	ctaccatcgc	acattccgtg	780
atggagccag	tggtggagtt	gctagcgtgt	accacgttgg	tcccgaagga	tggaagaaac	840
tatcaggaga	tgatgttggg	gagctacact	accattacta	ccccgtggca	ccagctaccg	900
cagaacaagt	catggaggaa	gcaacagccg	aataaaaaatc	ctgttttagtt	ttctaactgt	960
tcactccctt	tcttgtgtgt	gcatttttgt	gtagtatata	ctgagttgtc	tctagctgaa	1020
gcttgggtat	tctattttat	tgatctgaaa	tggtgctcgc	ggattattct	ctataagatt	1080
ctcttttctt						

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..222
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

Met	Lys	Leu	Asp	Thr	Ser	Gly	Phe	Glu	Thr	Ser	Met	Pro	Met	Ile	Gly
1			5					10						15	
Phe	Gly	Ser	Ser	Ser	Asp	Met	Leu	Asp	Glu	Leu	Ser	Ser	Val	Pro	Ser
			20					25					30		
Phe	Asp	Leu	Pro	Arg	Thr	Lys	Glu	Phe	Asp	Gly	Phe	Gln	Lys	Lys	Ala
			35				40					45			
Lys	Asp	Met	Leu	Lys	His	Ala	Lys	Gly	Thr	Thr	Thr	Leu	Ala	Phe	Ile
			50			55					60				
Phe	Lys	Gly	Gly	Val	Met	Val	Ala	Ala	Asp	Ser	Arg	Ala	Ser	Met	Gly
65				70					75					80	
Gly	Tyr	Ile	Ser	Ser	Gln	Ser	Val	Lys	Lys	Ile	Ile	Glu	Ile	Asn	Pro
			85						90					95	
Tyr	Met	Leu	Gly	Thr	Met	Ala	Gly	Gly	Ala	Ala	Asp	Cys	Gln	Phe	Trp
			100				105						110		
His	Arg	Asn	Leu	Gly	Ile	Lys	Cys	Arg	Leu	His	Glu	Leu	Ala	Asn	Lys
		115				120					125				
Arg	Arg	Ile	Ser	Val	Ser	Gly	Ala	Ser	Lys	Leu	Leu	Ala	Asn	Met	Leu
		130				135					140				
Tyr	Ser	Tyr	Arg	Gly	Met	Gly	Leu	Ser	Val	Gly	Thr	Met	Ile	Ala	Gly
145				150						155				160	
Trp	Asp	Glu	Thr	Gly	Pro	Gly	Leu	Tyr	Tyr	Val	Asp	Asn	Glu	Gly	Gly
			165						170				175		
Arg	Leu	Lys	Gly	Asp	Arg	Phe	Ser	Val	Gly	Ser	Gly	Ser	Pro	Tyr	Ala
			180				185						190		
Tyr	Gly	Val	Leu	Asp	Ser	Gly	Tyr	Lys	Tyr	Asp	Met	Ser	Val	Glu	Glu
			195				200				205				
Ala	Ser	Glu	Leu	Glu	Glu	Ile	Asn	Leu	Pro	Cys	Asp	Ile	Pro		
		210				215					220				

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 211 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..211
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566243
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:
Met Pro Met Ile Gly Phe Gly Ser Ser Ser Asp Met Leu Asp Glu Leu
1 5 10 15
Ser Ser Val Pro Ser Phe Asp Leu Pro Arg Thr Lys Glu Phe Asp Gly
 20 25 30
Phe Gln Lys Lys Ala Lys Asp Met Leu Lys His Ala Lys Gly Thr Thr
 35 40 45
Thr Leu Ala Phe Ile Phe Lys Gly Gly Val Met Val Ala Ala Asp Ser
 50 55 60
Arg Ala Ser Met Gly Gly Tyr Ile Ser Ser Gln Ser Val Lys Lys Ile
65 70 75 80
Ile Glu Ile Asn Pro Tyr Met Leu Gly Thr Met Ala Gly Gly Ala Ala
 85 90 95
Asp Cys Gln Phe Trp His Arg Asn Leu Gly Ile Lys Cys Arg Leu His
 100 105 110
Glu Leu Ala Asn Lys Arg Arg Ile Ser Val Ser Gly Ala Ser Lys Leu
 115 120 125
Leu Ala Asn Met Leu Tyr Ser Tyr Arg Gly Met Gly Leu Ser Val Gly
130 135 140
Thr Met Ile Ala Gly Trp Asp Glu Thr Gly Pro Gly Leu Tyr Tyr Val
145 150 155 160
Asp Asn Glu Gly Gly Arg Leu Lys Gly Asp Arg Phe Ser Val Gly Ser
 165 170 175
Gly Ser Pro Tyr Ala Tyr Gly Val Leu Asp Ser Gly Tyr Lys Tyr Asp
 180 185 190
Met Ser Val Glu Glu Ala Ser Glu Leu Glu Glu Ile Asn Leu Pro Cys
 195 200 205
Asp Ile Pro
210
(2) INFORMATION FOR SEQ ID NO:235:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..209
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566244
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:
Met Ile Gly Phe Gly Ser Ser Ser Asp Met Leu Asp Glu Leu Ser Ser
1 5 10 15
Val Pro Ser Phe Asp Leu Pro Arg Thr Lys Glu Phe Asp Gly Phe Gln
 20 25 30
Lys Lys Ala Lys Asp Met Leu Lys His Ala Lys Gly Thr Thr Leu
 35 40 45
Ala Phe Ile Phe Lys Gly Gly Val Met Val Ala Ala Asp Ser Arg Ala
50 55 60
Ser Met Gly Gly Tyr Ile Ser Ser Gln Ser Val Lys Lys Ile Ile Glu
65 70 75 80

Ile	Asn	Pro	Tyr	Met	Leu	Gly	Thr	Met	Ala	Gly	Gly	Ala	Ala	Asp	Cys	
				85						90				95		
Gln	Phe	Trp	His	Arg	Asn	Leu	Gly	Ile	Lys	Cys	Arg	Leu	His	Glu	Leu	
			100					105					110			
Ala	Asn	Lys	Arg	Arg	Ile	Ser	Val	Ser	Gly	Ala	Ser	Lys	Leu	Leu	Ala	
		115					120					125				
Asn	Met	Leu	Tyr	Ser	Tyr	Arg	Gly	Met	Gly	Leu	Ser	Val	Gly	Thr	Met	
	130					135						140				
Ile	Ala	Gly	Trp	Asp	Glu	Thr	Gly	Pro	Gly	Leu	Tyr	Tyr	Val	Asp	Asn	
	145				150					155				160		
Glu	Gly	Gly	Arg	Leu	Lys	Gly	Asp	Arg	Phe	Ser	Val	Gly	Ser	Gly	Ser	
			165						170					175		
Pro	Tyr	Ala	Tyr	Gly	Val	Leu	Asp	Ser	Gly	Tyr	Lys	Tyr	Asp	Met	Ser	
			180					185					190			
Val	Glu	Glu	Ala	Ser	Glu	Leu	Glu	Glu	Ile	Asn	Leu	Pro	Cys	Asp	Ile	
			195				200						205			

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1498 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1498

(D) OTHER INFORMATION: / Ceres Seq. ID 1566253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

aggaagaaga	gaacacctgat	tctattcttg	aggaacctga	agattctaac	atcaaagctg	60
ttactttctg	tgaacacacca	tatacatcag	caagtagatt	tgaagacttg	aactgtgtcac	120
ctgaattgat	gaaggcttg	tacgttgaga	tgaattctga	aaagcctagc	aagatccaaag	180
ctattagttt	gactatgata	atgacgcgcg	cacacaagca	tctgattgcc	caggctcata	240
acggatctgg	aaagacgact	tgtttcgttc	tgtgaatgtt	gagtcgtgtt	gatccacat	300
tgagagagcc	tcaagctctc	tgtatttgtc	ccactagaga	attagctaat	cagaatatgg	360
aagtctctca	gaagatgggg	aagtttactg	ggatcactgc	tgagttggct	gtgCctgact	420
caacgagagg	tgacccggcg	gcaacaagag	gagctcctgt	tctgtgctat	gttgtgattg	480
gcaccctctg	aagccttaag	aaatggatgg	catttaagag	actaggtcta	aatcattttga	540
agattctggg	ttttgatgag	gctgcaccata	tgcttgctac	ggatgggttt	agggatgatt	600
ctttgaagat	aatgaagagc	attggggagag	ttaatcccaa	tttccaggtt	ctctttttct	660
cggaacattt	taacgaaact	gtcaaaagatt	ttgttgcgcg	gacagtcaaa	gatccccacc	720
aattgtttgt	caaaagagag	gatctggcct	togactcggt	gaagcagtat	aaagtgtgtt	780
gcocgaaagg	gcaaaacaaa	atcgaaagta	tcaaggatca	gattatggag	cttgggggata	840
ttgggcaaac	cattatcttt	gtgaaaacaa	aagcgttctg	ctcaaaaagt	gcacaaagcc	900
ttgcgggaaa	tgggatatga	cgttaccagt	gtccatggta	atctgactga	atcggaacag	960
gataagatag	ttaaaagatg	taaagaatgc	cttactcaag	tgctcatatg	taccgatgtc	1020
attgcaagag	gtttttgacca	acagcgggtg	aatttgggtg	tcaattataa	tcttccactt	1080
aaatatgaaa	ctggagagcc	agattatgag	gtgtaccttc	acaggggttg	gagagctggc	1140
cggtttctgc	gcaaaaggagc	ggttttcaac	tgtctgcttg	atgatggctg	ggataaagag	1200
gtgattggaga	agatcagaga	gtattttgaa	gcaaatgtca	aggagatcaa	gtcgtggaga	1260
tcagaggaag	agataaagag	tgcattaaag	gaagctggctt	tgtctgacga	gtgaggaaga	1320
gagacagcat	gtgttcaaac	catcttaaaa	gaactatgct	tctgtttttc	tgagattgtt	1380
ttaagaaaaga	aacttgtata	cctctttgag	gttttctgt	aattctttgt	tctgatttgt	1440
gagattttca	gacttttgat	attttttgtt	aagggaaaag	gaaaacattt	tttatgtc	

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..305

SEQUENCE DESCRIPTION: SEQ ID NO:237:

Glu Glu Lys Pro Asp Ser Ile Leu Glu Glu P

Ile
305

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..263

(D) OTHER INFORMATION: / Ceres Seq. ID 1566255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Met Lys Gly Leu Tyr Val Glu Met Lys Phe Glu Lys Pro Ser Lys Ile
1 5 10 15
Gln Ala Ile Ser Leu Pro Met Ile Met Thr Pro Pro His Lys His Leu

Met	Lys	Phe	Glu	Lys	Pro	Ser	Lys	Ile	Gln	Ala	Ile	Ser	Leu	Pro	Met
1			5					10						15	
Ile	Met	Thr	Pro	Pro	His	Lys	His	Leu	Ile	Ala	Gln	Ala	His	Asn	Gly
			20					25					30		
Ser	Gly	Lys	Thr	Thr	Cys	Phe	Val	Leu	Gly	Met	Leu	Ser	Arg	Val	Asp
		35				40					45				
Pro	Thr	Leu	Arg	Glu	Pro	Gln	Ala	Leu	Cys	Ile	Cys	Pro	Thr	Arg	Glu
		50				55					60				
Leu	Ala	Asn	Gln	Asn	Met	Glu	Val	Leu	Gln	Lys	Met	Gly	Lys	Phe	Thr
65				70						75				80	
Gly	Ile	Thr	Ala	Glu	Leu	Ala	Val	Pro	Asp	Ser	Thr	Arg	Gly	Ala	Pro
			85					90					95		
Ala	Ala	Thr	Arg	Gly	Ala	Pro	Val	Ser	Ala	His	Val	Val	Ile	Gly	Thr
			100					105					110		
Pro	Gly	Thr	Leu	Lys	Lys	Trp	Met	Ala	Phe	Lys	Arg	Leu	Gly	Leu	Asn
			115				120					125			
His	Leu	Lys	Ile	Leu	Val	Phe	Asp	Glu	Ala	Asp	His	Met	Leu	Ala	Thr
130						135					140				

Asp Gly Phe Arg Asp Asp Ser Leu Lys Ile Met Lys Asp Ile Gly Arg	
145 150 155 160	
Val Asn Pro Asn Phe Gln Val Leu Leu Phe Ser Ala Thr Phe Asn Glu	
165 170 175	
Thr Val Lys Asp Phe Val Ala Arg Thr Val Lys Asp Pro Asn Gln Leu	
180 185 190	
Phe Val Lys Arg Glu Asp Leu Ala Phe Asp Ser Val Lys Gln Tyr Lys	
195 200 205	
Val Val Cys Pro Lys Glu Gln Asn Lys Ile Glu Val Ile Lys Asp Gln	
210 215 220	
Ile Met Glu Leu Gly Asp Ile Gly Gln Thr Ile Ile Phe Val Lys Thr	
225 230 235 240	
Lys Ala Phe Cys Ser Lys Gly Ala Gln Ser Pro Cys Gly Asn Gly Ile	
245 250 255	

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 637 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..637
(D) OTHER INFORMATION: / Ceres Seq. ID 1566257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

acgatacc	caaa	ctcttctt	cttccctt	cttctctt	ctcttctt	60
cacgttt	cag	ctatata	ctctata	tacatta	ttgatctt	120
tgcttcc	aat	aaactcca	gaacagct	ctctttt	cttcttct	180
atggag	agag	aagacttg	ta	gattga	acgaatgt	240
ctcagac	ttt	cttaca	gaag	ccttggt	ctg	300
atagaga	aaag	atgaag	ctaa	gatgaa	attt	360
tcggatt	cca	acaagag	gct	tttgtat	gac	420
actgga	atgg	ctgattt	cat	aaatgag	atg	480
ggggac	gaaa	atttag	agga	atttga	agag	540
aatcaat	tca	aaactcg	ttc	atctt	ctgc	600
tttgttc	cat	tgcatg	att	ctaat	caatg	

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..135
(D) OTHER INFORMATION: / Ceres Seq. ID 1566258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Met Glu Arg Glu Asp Leu Tyr Ala Val Leu Asp Leu Asn Asn Glu Cys	
1 5 10 15	
Thr Gln Gly Asp Leu Arg Leu Ser Tyr Lys Asn Leu Val Leu Lys Trp	
20 25 30	
His Pro Asp Arg Phe Leu Glu Glu Ile Glu Lys Asp Glu Ala Lys Met	
35 40 45	
Lys Phe Gln Ser Ile Gln Arg Ala Tyr Ser Val Leu Ser Asp Ser Asn	
50 55 60	
Lys Arg Leu Leu Tyr Asp Val Gly Ala Tyr Asp Ser Asp Asp Asp Glu	
65 70 75 80	

Thr Gly Met Ala Asp Phe Ile Asn Glu Met Val Thr Leu Met Ala Gln
85 90 95
Thr Gln Ser Thr Gly Asp Glu Asn Leu Glu Glu Phe Glu Glu Leu Phe
100 105 110
Gln Glu Leu Leu Lys Asp Asp Val Asn Gln Phe Lys Thr Arg Ser Ser
115 120 125
Phe Val Phe Met Phe Ala Ile
130 135

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1566259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Met Lys Phe Gln Ser Ile Gln Arg Ala Tyr Ser Val Leu Ser Asp Ser
1 5 10 15
Asn Lys Arg Leu Leu Tyr Asp Val Gly Ala Tyr Asp Ser Asp Asp
20 25 30
Glu Thr Gly Met Ala Asp Phe Ile Asn Glu Met Val Thr Leu Met Ala
35 40 45
Gln Thr Gln Ser Thr Gly Asp Glu Asn Leu Glu Glu Phe Glu Glu Leu
50 55 60
Phe Gln Glu Leu Leu Lys Asp Asp Val Asn Gln Phe Lys Thr Arg Ser
65 70 75 80
Ser Phe Val Phe Met Phe Ala Ile
85

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..477

(D) OTHER INFORMATION: / Ceres Seq. ID 1566268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

cgggttgccg caccctgcttc gcttctcttc tctcgtcttc tactcaggac tcgtttactc 60
tttcaaaagct aagcttttcaa gatgcaaaac gaagagggtc aagtcactga gctttacatt 120
cctaggaaat gttctgctac taaccgggtg atcacatcca aggatcatgc ctctgttcag 180
ctcaacattg gtcattttaga tgctaattgac ttgtacacgc gacagttcac aacctttgtc 240
ctctgcggtt ttgtccgtgc tcaggggagac gctgacagtg gtgtcgacag gttgtggcag 300
aagaagaagg ttgaagccaa acaaaactaa gagcttaatc tgtcttggtt ttgtcgaat 360
cttgtttttt tttttccgaa agatttgctc atactgaagt aatgattttg gotttgggtc 420
gtggaaacta acttaataac ttttgtgcac catgtcttct aatttttcac cagttcg

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1566269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Met	Gln	Asn	Glu	Glu	Gly	Gln	Val	Thr	Glu	Leu	Tyr	Ile	Pro	Arg	Lys	
1			5						10					15		
Cys	Ser	Ala	Thr	Asn	Arg	Leu	Ile	Thr	Ser	Lys	Asp	His	Ala	Ser	Val	
		20						25				30				
Gln	Leu	Asn	Ile	Gly	His	Leu	Asp	Ala	Asn	Gly	Leu	Tyr	Thr	Gly	Gln	
		35					40					45				
Phe	Thr	Thr	Phe	Ala	Leu	Cys	Gly	Phe	Val	Arg	Ala	Gln	Gly	Asp	Ala	
	50				55						60					
Asp	Ser	Gly	Val	Asp	Arg	Leu	Trp	Gln	Lys	Lys	Val	Glu	Ala	Lys		
65				70					75					80		
Gln	Asn															

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1566270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Met	Leu	Met	Ala	Cys	Thr	Pro	Asp	Ser	Ser	Gln	Pro	Leu	Leu	Ser	Ala	
1			5						10					15		
Val	Leu	Ser	Val	Leu	Arg	Glu	Thr	Leu	Thr	Val	Val	Ser	Thr	Gly	Cys	
		20						25				30				
Gly	Arg	Arg	Arg	Arg	Leu	Lys	Pro	Asn	Lys	Thr	Lys	Ser	Leu	Ile	Cys	
		35					40					45				
Leu	Val	Phe	Cys	Arg	Ile	Leu	Phe	Phe	Phe	Phe	Arg	Lys	Ile	Ala	Ser	
	50				55						60					
Tyr																
65																

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1566271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Met	Ala	Cys	Thr	Pro	Asp	Ser	Ser	Gln	Pro	Leu	Leu	Ser	Ala	Val	Leu	
1			5						10					15		
Ser	Val	Leu	Arg	Glu	Thr	Leu	Thr	Val	Val	Ser	Thr	Gly	Cys	Gly	Arg	
		20						25				30				
Arg	Arg	Arg	Leu	Lys	Pro	Asn	Lys	Thr	Lys	Ser	Leu	Ile	Cys	Leu	Val	
		35					40					45				
Phe	Cys	Arg	Ile	Leu	Phe	Phe	Phe	Phe	Arg	Lys	Ile	Ala	Ser	Tyr		
	50			55							60					

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 988 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..988
(D) OTHER INFORMATION: / Ceres Seq. ID 1566276
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

aaaagaagac	ttttgtaag	aaataaacac	acaactaaag	agatgtcgtc	aaccttggac	60
aacgaagagt	caggactcgg	tgattcaaat	cgttcgacgg	aagtagatag	cgcgacgga	120
ggaaacttca	cggtttacga	gtctcgattc	cagtcgcagc	ggtttgactc	ttccttctct	180
aattttgact	cccaaccgga	gaaagagtca	gacttaccag	gcggcgattc	atctccttca	240
cccgaacctc	aatctccgcc	gtcgtataat	agtttcgatg	atacaaacgg	ttcgatcttg	300
ccgccaccat	cgggccatgga	gaaagaggaa	ggtttcgctc	ttagagagtg	gcgaaggcta	360
aatgctctga	gatctggaaga	gaaagaaaaa	gaagagaaa	aaatggttca	acaaattcta	420
gaagcagcag	agcaatataa	ggctgagttc	tatagcaaac	gtaacgttac	tattgaaaaa	480
aacaagaaac	taaaaccgga	gaaagagaag	ttttttttgg	agaatcaaga	aaagtttttac	540
gctgaagctg	acaaaaacaa	ttggaaggcg	attgcagaac	tcattcctcg	tgaagtgcga	600
gtttatagaga	atagagggaa	caagaagaaa	acagcaacca	taactgtaac	ccaggggacca	660
aagccaggga	agcccatcta	tctgtGctcg	tatgcgtcaa	gtgctcacga	aactcaagca	720
caatccggcca	actcatatga	agccaaaact	gccttcacca	tctggagctg	accggaatgt	780
gagtgctgagt	gaacagggtca	cagttacaga	gaagttgtag	ttgtgtatgt	gacaaagttaa	840
cttctctcttg	attgatgtta	aacgcgtctt	actttgttag	cttcctcatc	gttcagcttc	900
gactattggt	tgttttgatt	tcgtcttttg	tcttaccatt	gttggtttcc	cacacagttt	960
ttactcttga	tgtatatata	atatattc				

(2) INFORMATION FOR SEQ ID NO:248:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 242 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..242
(D) OTHER INFORMATION: / Ceres Seq. ID 1566277
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Met	Ser	Ser	Thr	Leu	Ser	Asn	Glu	Glu	Ser	Gly	Leu	Gly	Asp	Ser	Asn	
1				5					10					15		
Arg	Ser	Thr	Glu	Val	Asp	Ser	Gly	Asp	Gly	Gly	Asn	Phe	Thr	Ala	Tyr	
			20					25					30			
Glu	Ser	Arg	Phe	Gln	Ser	Gln	Arg	Phe	Asp	Ser	Ser	Phe	Ser	Asn	Phe	
			35					40				45				
Asp	Ser	Gln	Pro	Glu	Lys	Glu	Ser	Asp	Leu	Pro	Gly	Gly	Asp	Ser	Ser	
			50					55				60				
Pro	Arg	Pro	Glu	Thr	Gln	Ser	Pro	Pro	Ser	Ile	Asn	Ser	Phe	Asp	Asp	
			65					70			75			80		
Thr	Asn	Gly	Ser	Ile	Leu	Pro	Pro	Pro	Ser	Ala	Met	Glu	Lys	Glu	Glu	
			85						90				95			
Gly	Phe	Ala	Leu	Arg	Glu	Trp	Arg	Arg	Leu	Asn	Ala	Leu	Arg	Leu	Glu	
			100					105					110			
Glu	Lys	Glu	Lys	Glu	Glu	Lys	Glu	Met	Val	Gln	Gln	Ile	Leu	Glu	Ala	
			115					120				125				
Ala	Glu	Gln	Tyr	Lys	Ala	Glu	Phe	Tyr	Ser	Lys	Arg	Asn	Val	Thr	Ile	
			130					135				140				
Glu	Asn	Asn	Lys	Lys	Leu	Asn	Arg	Glu	Lys	Glu	Lys	Phe	Phe	Leu	Glu	
			145					150				155			160	
Asn	Gln	Glu	Lys	Phe	Tyr	Ala	Glu	Ala	Asp	Lys	Asn	Asn	Trp	Lys	Ala	
			165						170					175		
Ile	Ala	Glu	Leu	Ile	Pro	Arg	Glu	Val	Pro	Val	Ile	Glu	Asn	Arg	Gly	
			180					185						190		

Asn Lys Lys Lys Thr Ala Thr Ile Thr Val Ile Gln Gly Pro Lys Pro
195 200 205
Gly Lys Pro Thr Asp Leu Cys Ser Tyr Ala Ser Ser Ala His Glu Thr
210 215 220
Gln Ala Gln Ser Ala Asn Ser Tyr Glu Ala Lys Thr Ala Leu Thr Ile
225 230 235 240
Trp Ser

(2) INFORMATION FOR SEQ ID NO:249:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1566278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

Met Glu Lys Glu Glu Phe Ala Leu Arg Glu Trp Arg Arg Leu Asn
1 5 10 15
Ala Leu Arg Leu Glu Glu Lys Glu Lys Glu Lys Glu Met Val Gln
20 25 30
Gln Ile Leu Glu Ala Ala Glu Gln Tyr Lys Ala Glu Phe Tyr Ser Lys
35 40 45
Arg Asn Val Thr Ile Glu Asn Asn Lys Lys Leu Asn Arg Glu Lys Glu
50 55 60
Lys Phe Phe Leu Glu Asn Gln Glu Lys Phe Tyr Ala Glu Ala Asp Lys
65 70 75 80
Asn Asn Trp Lys Ala Ile Ala Glu Leu Ile Pro Arg Glu Val Pro Val
85 90 95
Ile Glu Asn Arg Gly Asn Lys Lys Lys Thr Ala Thr Ile Thr Val Ile
100 105 110
Gln Gly Pro Lys Pro Gly Lys Pro Thr Asp Leu Cys Ser Tyr Ala Ser
115 120 125
Ser Ala His Glu Thr Gln Ala Gln Ser Ala Asn Ser Tyr Glu Ala Lys
130 135 140
Thr Ala Leu Thr Ile Trp Ser
145 150

(2) INFORMATION FOR SEQ ID NO:250:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1566279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Met Val Gln Gln Ile Leu Glu Ala Ala Glu Gln Tyr Lys Ala Glu Phe
1 5 10 15
Tyr Ser Lys Arg Asn Val Thr Ile Glu Asn Asn Lys Lys Leu Asn Arg
20 25 30
Glu Lys Glu Lys Phe Phe Leu Glu Asn Gln Glu Lys Phe Tyr Ala Glu
35 40 45
Ala Asp Lys Asn Asn Trp Lys Ala Ile Ala Glu Leu Ile Pro Arg Glu
50 55 60
Val Pro Val Ile Glu Asn Arg Gly Asn Lys Lys Lys Thr Ala Thr Ile

65	70	75	80
Thr Val Ile Gln Gly Pro Lys Pro Gly Lys Pro Thr Asp Leu Cys Ser			
	85	90	95
Tyr Ala Ser Ser Ala His Glu Thr Gln Ala Gln Ser Ala Asn Ser Tyr			
	100	105	110
Glu Ala Lys Thr Ala Leu Thr Ile Trp Ser			
	115	120	

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1643 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1643
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

aaagaaaaga	ccttattcac	acagggtcgt	tttgcgaagC	tcactcgtca	cgatgacctat	60
gatggatata	gcgaaggga	agacagtgat	gtgtctgtta	acagaccag	aaggaactca	120
tttaggttct	gccatgtata	ttctcctaaa	ggctgtgtct	ttgcaactta	ctcagctcgt	180
caatagggtc	ctcgacaacg	aggagatggt	accttacagt	ttctatgtat	cgacgcaaga	240
gcttcttgta	cagatggga	cgactctgga	gaaaaacaaa	gtgtctgtgg	agaagggttt	300
gacgattggt	tatcaacaac	aagctgtttt	tcgaattcgt	cctgttaacc	gttgctcaca	360
gacaattgct	ggctacggcg	aagctgttct	ttgtgtttcg	tttagtcctg	atggaaagca	420
attagctagt	gggtcagggt	atactactgt	caggcttttg	gatctctaca	ctgaaactcc	480
attgtttact	tgcaaaaggcc	acaagaattg	ggttctcaca	gtgcgtggt	ctcgtgatgg	540
taagcatctt	gtgagtggta	gtaaatccgg	tgaaatctgt	tgttggaatc	caaagaaagg	600
agaaattgaa	ggcagccocac	ttacgggtca	caagaatagg	attactggta	tctcgtggga	660
accagttcac	cttagttctc	catgccgtcg	atttgtgact	tctagttaag	atggggatgc	720
aaggatttgg	gatatttacc	tgaaaaaatc	tattatttgt	ctcagtgggc	acacacttgc	780
tgtgacttgt	gtcaaatggg	gcggagatgg	aattatttat	acaggttcgc	aagattgtac	840
gattaagatg	tgggagacta	ctcaggggaa	gcttattcgt	gaattgaagg	ggcatgggca	900
ttggattaac	tcctctgcgt	tgagcacaga	atatgttctt	cgaaacaggag	cttttgacca	960
cactggaaga	caatatccctc	caaatgaaga	aaagcaaaag	gcgctcgaaa	gatacaacaa	1020
aacaaaaggg	gattccctgt	aaagattagt	ctcaggttct	gatgatttca	ctatgttctt	1080
ttgggaacca	tcgtgttagca	aacaacctaa	aaagcgctta	accggtcctc	aacagcttgt	1140
aaatcatatc	tattttctac	ctgatgggaa	atggatttga	atgtgactgt	tcgataaaat	1200
agttaggtta	tggaaatgta	tcacaggaca	atttgttaca	gttttccggg	gccatgtttg	1260
acctgtttat	caggtcagtt	gtcccgaga	cagttagattg	cttttgagtg	cgagtaaaaga	1320
ctctactctc	aaagatttggg	aaattaggac	gaaaaagtta	aaacaagatc	ttctcgttca	1380
tgcgtgatgc	gtttttcggg	tgagattggag	tccagatgga	gagaaagtgc	ttctcgtgtg	1440
taaagataga	gtgttgaagc	tatggaaggg	ttaaaatgga	agaccatttt	ggagtttttg	1500
tttactcaac	caacacttat	tttacacata	tttatctatt	tcgccttggt	tgggtttctac	1560
acataaatgc	ttctctatgg	gtctcttttt	gatcttatgc	ttagtaaaac	aactcttttt	1620
tcttacctca	agttgttact	gtc				

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..490
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Lys Lys Arg Pro Tyr Ser His Arg Ser Ser Leu Arg Ser Ser Ser Ser			
1	5	10	15

Thr	Met	Thr	Met	Met	Asp	Thr	Asp	Glu	Gly	Lys	Thr	Val	Met	Cys	Leu	
			20					25					30			
Leu	Thr	Asp	Pro	Glu	Gly	Thr	His	Leu	Gly	Ser	Ala	Met	Tyr	Ile	Pro	
		35				40						45				
Gln	Lys	Ala	Gly	Pro	Leu	Gln	Leu	Thr	Gln	Leu	Val	Asn	Arg	Phe	Leu	
		50				55					60					
Asp	Asn	Glu	Glu	Met	Leu	Pro	Tyr	Ser	Phe	Tyr	Val	Ser	Asp	Glu	Glu	
65				70					75					80		
Leu	Leu	Val	Pro	Val	Gly	Thr	Tyr	Leu	Glu	Lys	Asn	Lys	Val	Ser	Val	
				85					90					95		
Glu	Lys	Val	Leu	Thr	Ile	Val	Tyr	Gln	Gln	Gln	Ala	Val	Phe	Arg	Ile	
			100					105					110			
Arg	Pro	Val	Asn	Arg	Cys	Ser	Gln	Thr	Ile	Ala	Gly	His	Ala	Glu	Ala	
		115					120					125				
Val	Leu	Cys	Val	Ser	Phe	Ser	Pro	Asp	Gly	Lys	Gln	Leu	Ala	Ser	Gly	
		130				135					140					
Ser	Gly	Asp	Thr	Thr	Val	Arg	Leu	Trp	Asp	Leu	Tyr	Thr	Glu	Thr	Pro	
145				150					155					160		
Leu	Phe	Thr	Cys	Lys	Gly	His	Lys	Asn	Trp	Val	Leu	Thr	Val	Ala	Trp	
				165					170					175		
Ser	Pro	Asp	Gly	Lys	His	Leu	Val	Ser	Gly	Ser	Lys	Ser	Gly	Glu	Ile	
		180					185						190			
Cys	Cys	Trp	Asn	Pro	Lys	Lys	Gly	Glu	Leu	Glu	Gly	Ser	Pro	Leu	Thr	
		195					200					205				
Gly	His	Lys	Lys	Trp	Ile	Thr	Gly	Ile	Ser	Trp	Glu	Pro	Val	His	Leu	
		210				215					220					
Ser	Ser	Pro	Cys	Arg	Arg	Phe	Val	Thr	Ser	Ser	Lys	Asp	Gly	Asp	Ala	
225				230					235					240		
Arg	Ile	Trp	Asp	Ile	Thr	Leu	Lys	Lys	Ser	Ile	Ile	Cys	Leu	Ser	Gly	
				245					250					255		
His	Thr	Leu	Ala	Val	Thr	Cys	Val	Lys	Trp	Gly	Gly	Asp	Gly	Ile	Ile	
		260					265					270				
Tyr	Thr	Gly	Ser	Gln	Asp	Cys	Thr	Ile	Lys	Met	Trp	Glu	Thr	Thr	Gln	
		275					280					285				
Gly	Lys	Leu	Ile	Arg	Glu	Leu	Lys	Gly	His	Gly	His	Trp	Ile	Asn	Ser	
		290				295					300					
Leu	Ala	Leu	Ser	Thr	Glu	Tyr	Val	Leu	Arg	Thr	Gly	Ala	Phe	Asp	His	
				310					315					320		
Thr	Gly	Arg	Gln	Tyr	Pro	Pro	Asn	Glu	Glu	Lys	Gln	Lys	Ala	Leu	Glu	
				325					330					335		
Arg	Tyr	Asn	Lys	Thr	Lys	Gly	Asp	Ser	Pro	Glu	Arg	Leu	Val	Ser	Gly	
		340					345						350			
Ser	Asp	Asp	Phe	Thr	Met	Phe	Leu	Trp	Glu	Pro	Ser	Val	Ser	Lys	Gln	
		355					360					365				
Pro	Lys	Lys	Arg	Leu	Thr	Gly	His	Gln	Gln	Leu	Val	Asn	His	Val	Tyr	
		370				375					380					
Phe	Ser	Pro	Asp	Gly	Lys	Trp	Ile	Ala	Ser	Ala	Ser	Phe	Asp	Lys	Ser	
385				390					395					400		
Val	Arg	Leu	Trp	Asn	Gly	Ile	Thr	Gly	Gln	Phe	Val	Thr	Val	Phe	Arg	
				405					410					415		
Gly	His	Val	Gly	Pro	Val	Tyr	Gln	Val	Ser	Trp	Ser	Ala	Asp	Ser	Arg	
		420					425						430			
Leu	Leu	Leu	Ser	Gly	Ser	Lys	Asp	Ser	Thr	Leu	Lys	Ile	Trp	Glu	Ile	
		435					440					445				
Arg	Thr	Lys	Lys	Leu	Lys	Gln	Asp	Leu	Pro	Gly	His	Ala	Asp	Glu	Val	
		450				455					460					
Phe	Ala	Val	Asp	Trp	Ser	Pro	Asp	Gly	Glu	Lys	Val	Val	Ser	Gly	Gly	
465				470					475					480		
Lys	Asp	Arg	Val	Leu	Lys	Leu	Trp	Lys	Gly							
				485					490							

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 473 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..473
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566292
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Met	Thr	Met	Met	Asp	Thr	Asp	Glu	Gly	Lys	Thr	Val	Met	Cys	Leu	Leu
1			5						10				15		
Thr	Asp	Pro	Glu	Gly	Thr	His	Leu	Gly	Ser	Ala	Met	Tyr	Ile	Pro	Gln
		20					25						30		
Lys	Ala	Gly	Pro	Leu	Gln	Leu	Thr	Gln	Leu	Val	Asn	Arg	Phe	Leu	Asp
		35					40					45			
Asn	Glu	Glu	Met	Leu	Pro	Tyr	Ser	Phe	Tyr	Val	Ser	Asp	Glu	Glu	Leu
	50				55				60						
Leu	Val	Pro	Val	Gly	Thr	Tyr	Leu	Glu	Lys	Asn	Lys	Val	Ser	Val	Glu
65				70					75					80	
Lys	Val	Leu	Thr	Ile	Val	Tyr	Gln	Gln	Gln	Ala	Val	Phe	Arg	Ile	Arg
			85						90				95		
Pro	Val	Asn	Arg	Cys	Ser	Gln	Thr	Ile	Ala	Gly	His	Ala	Glu	Ala	Val
		100					105						110		
Leu	Cys	Val	Ser	Phe	Ser	Pro	Asp	Gly	Lys	Gln	Leu	Ala	Ser	Gly	Ser
		115					120					125			
Gly	Asp	Thr	Thr	Val	Arg	Leu	Trp	Asp	Leu	Tyr	Thr	Glu	Thr	Pro	Leu
	130				135						140				
Phe	Thr	Cys	Lys	Gly	His	Lys	Asn	Trp	Val	Leu	Thr	Val	Ala	Trp	Ser
145			150						155					160	
Pro	Asp	Gly	Lys	His	Leu	Val	Ser	Gly	Ser	Lys	Ser	Gly	Glu	Ile	Cys
			165						170					175	
Cys	Trp	Asn	Pro	Lys	Lys	Gly	Glu	Leu	Glu	Gly	Ser	Pro	Leu	Thr	Gly
		180					185						190		
His	Lys	Lys	Trp	Ile	Thr	Gly	Ile	Ser	Trp	Glu	Pro	Val	His	Leu	Ser
		195					200					205			
Ser	Pro	Cys	Arg	Arg	Phe	Val	Thr	Ser	Ser	Lys	Asp	Gly	Asp	Ala	Arg
	210					215					220				
Ile	Trp	Asp	Ile	Thr	Leu	Lys	Lys	Ser	Ile	Ile	Cys	Leu	Ser	Gly	His
225				230					235					240	
Thr	Leu	Ala	Val	Thr	Cys	Val	Lys	Trp	Gly	Gly	Asp	Gly	Ile	Ile	Tyr
			245						250				255		
Thr	Gly	Ser	Gln	Asp	Cys	Thr	Ile	Lys	Met	Trp	Glu	Thr	Thr	Gln	Gly
		260						265					270		
Lys	Leu	Ile	Arg	Glu	Leu	Lys	Gly	His	Gly	His	Trp	Ile	Asn	Ser	Leu
		275					280					285			
Ala	Leu	Ser	Thr	Glu	Tyr	Val	Leu	Arg	Thr	Gly	Ala	Phe	Asp	His	Thr
	290					295					300				
Gly	Arg	Gln	Tyr	Pro	Pro	Asn	Glu	Glu	Lys	Gln	Lys	Ala	Leu	Glu	Arg
305				310					315					320	
Tyr	Asn	Lys	Thr	Lys	Gly	Asp	Ser	Pro	Glu	Arg	Leu	Val	Ser	Gly	Ser
			325						330					335	
Asp	Asp	Phe	Thr	Met	Phe	Leu	Trp	Glu	Pro	Ser	Val	Ser	Lys	Gln	Pro
		340					345						350		
Lys	Lys	Arg	Leu	Thr	Gly	His	Gln	Gln	Leu	Val	Asn	His	Val	Tyr	Phe
		355					360					365			
Ser	Pro	Asp	Gly	Lys	Trp	Ile	Ala	Ser	Ala	Ser	Phe	Asp	Lys	Ser	Val
	370				375						380				
Arg	Leu	Trp	Asn	Gly	Ile	Thr	Gly	Gln	Phe	Val	Thr	Val	Phe	Arg	Gly
385					390				395						400

His Val Gly Pro Val Tyr Gln Val Ser Trp Ser Ala Asp Ser Arg Leu
405 410 415
Leu Leu Ser Gly Ser Lys Asp Ser Thr Leu Lys Ile Trp Glu Ile Arg
420 425 430
Thr Lys Lys Leu Lys Gln Asp Leu Pro Gly His Ala Asp Glu Val Phe
435 440 445
Ala Val Asp Trp Ser Pro Asp Gly Glu Lys Val Val Ser Gly Gly Lys
450 455 460
Asp Arg Val Leu Lys Leu Trp Lys Gly
465 470

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1566293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Met Met Asp Thr Asp Glu Gly Lys Thr Val Met Cys Leu Leu Thr Asp
1 5 10 15
Pro Glu Gly Thr His Leu Gly Ser Ala Met Tyr Ile Pro Gln Lys Ala
20 25 30
Gly Pro Leu Gln Leu Thr Gln Leu Val Asn Arg Phe Leu Asp Asn Glu
35 40 45
Glu Met Leu Pro Tyr Ser Phe Tyr Val Ser Asp Glu Glu Leu Leu Val
50 55 60
Pro Val Gly Thr Tyr Leu Glu Lys Asn Lys Val Ser Val Glu Lys Val
65 70 75 80
Leu Thr Ile Val Tyr Gln Gln Gln Ala Val Phe Arg Ile Arg Pro Val
85 90 95
Asn Arg Cys Ser Gln Thr Ile Ala Gly His Ala Glu Ala Val Leu Cys
100 105 110
Val Ser Phe Ser Pro Asp Gly Lys Gln Leu Ala Ser Gly Ser Gly Asp
115 120 125
Thr Thr Val Arg Leu Trp Asp Leu Tyr Thr Glu Thr Pro Leu Phe Thr
130 135 140
Cys Lys Gly His Lys Asn Trp Val Leu Thr Val Ala Trp Ser Pro Asp
145 150 155 160
Gly Lys His Leu Val Ser Gly Ser Lys Ser Gly Glu Ile Cys Cys Trp
165 170 175
Asn Pro Lys Lys Gly Glu Leu Glu Gly Ser Pro Leu Thr Gly His Lys
180 185 190
Lys Trp Ile Thr Gly Ile Ser Trp Glu Pro Val His Leu Ser Ser Pro
195 200 205
Cys Arg Arg Phe Val Thr Ser Ser Lys Asp Gly Asp Ala Arg Ile Trp
210 215 220
Asp Ile Thr Leu Lys Lys Ser Ile Ile Cys Leu Ser Gly His Thr Leu
225 230 235 240
Ala Val Thr Cys Val Lys Trp Gly Gly Asp Gly Ile Ile Tyr Thr Gly
245 250 255
Ser Gln Asp Cys Thr Ile Lys Met Trp Glu Thr Thr Gln Gly Lys Leu
260 265 270
Ile Arg Glu Leu Lys Gly His Gly His Trp Ile Asn Ser Leu Ala Leu
275 280 285
Ser Thr Glu Tyr Val Leu Arg Thr Gly Ala Phe Asp His Thr Gly Arg
290 295 300
Gln Tyr Pro Pro Asn Glu Lys Lys Ala Leu Glu Arg Tyr Asn

305 310 315 320
Lys Thr Lys Gly Asp Ser Pro Glu Arg Leu Val Ser Gly Ser Asp Asp
325 330 335
Phe Thr Met Phe Leu Trp Glu Pro Ser Val Ser Lys Gln Pro Lys Lys
340 345 350
Arg Leu Thr Gly His Gln Gln Leu Val Asn His Val Tyr Phe Ser Pro
355 360 365
Asp Gly Lys Trp Ile Ala Ser Ala Ser Phe Asp Lys Ser Val Arg Leu
370 375 380
Trp Asn Gly Ile Thr Gly Gln Phe Val Thr Val Phe Arg Gly His Val
385 390 395 400
Gly Pro Val Tyr Gln Val Ser Trp Ser Ala Asp Ser Arg Leu Leu Leu
405 410 415
Ser Gly Ser Lys Asp Ser Thr Leu Lys Ile Trp Glu Ile Arg Thr Lys
420 425 430
Lys Leu Lys Gln Asp Leu Pro Gly His Ala Asp Glu Val Phe Ala Val
435 440 445
Asp Trp Ser Pro Asp Gly Glu Lys Val Val Ser Gly Gly Lys Asp Arg
450 455 460
Val Leu Lys Leu Trp Lys Gly
465 470

(2) INFORMATION FOR SEQ ID NO:255:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 944 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..944
(D) OTHER INFORMATION: / Ceres Seq. ID 1566297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

attttttttc ataattgtat caaattgtga gaggaaaaaa agaatttcaa gaaatggaga 60
aggaaggact cgggcttgag ataacggagc tgagattggg gcttcggggg agagatgtgg 120
cagagaagat gatgaagaag agagcttttca cggagatgaa tatgacgtcg tcgggttagta 180
atagtgatca atgtgaaagc ggcgtcggtt catctgggtg tgacgtgag aaggttaagt 240
attcgcgggc ggcGaaaagc caggtgggtg ggtggccacc ggtttgttct taccggaaga 300
aaaacagctg taaggaaagct tcgaccacga aagtggtgStt agggatgtg aaagtgaagca 360
tgagatgggt gctttatttg aggaagatgg atcttgggtc gagccaaggc tatgatgatc 420
tagcttttct tcttgataag ctcttcggtt tccgtggcat cggtgtggcc ttgaaagatg 480
gtgacaaact cgaatacgtt accatatacg aagacaaaga tggagactgg atgctcgcgg 540
gtgatghacc ttgggggatg tGttctagag tcatgcaaga ggttgagaat aatgaaaaa 600
tcggatgcta ccgggttttg gctgcagcct agaggagtag acgagtgatg atgacttgaa 660
caagaagcaa ggagctgggt catataatta atcttaaat tgatcatcaa gatcctttag 720
aacatttttc ctattcatgt tatataaata tatatgttat agtatattat ttgcaacaaa 780
atttcaagtt atggtttgca taattatctt cagaaagaca gctatatata tatcacactc 840
ttgttttttg agtgtttgagt taataacatta atctgtttca atattatttg ttatttcgga 900
cttatatatg tgtgtagaaa catatgtaat aagtatccat tatt

(2) INFORMATION FOR SEQ ID NO:256:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..192
(D) OTHER INFORMATION: / Ceres Seq. ID 1566298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Met Glu Lys Glu Gly Leu Gly Leu Glu Ile Thr Glu Leu Arg Leu Gly
1 5 10 15
Leu Pro Gly Arg Asp Val Ala Glu Lys Met Met Lys Lys Arg Ala Phe
20 25 30
Thr Glu Met Asn Met Thr Ser Ser Gly Ser Asn Ser Asp Gln Cys Glu
35 40 45
Ser Gly Val Val Ser Ser Gly Gly Asp Ala Glu Lys Val Asn Asp Ser
50 55 60
Pro Ala Ala Lys Ser Gln Val Val Gly Trp Pro Val Cys Ser Tyr
65 70 75 80
Arg Lys Lys Asn Ser Cys Lys Glu Ala Ser Thr Thr Lys Val Xaa Leu
85 90 95
Gly Tyr Val Lys Val Ser Met Asp Gly Val Pro Tyr Leu Arg Lys Met
100 105 110
Asp Leu Gly Ser Ser Gln Gly Tyr Asp Asp Leu Ala Phe Ser Leu Asp
115 120 125
Lys Leu Phe Gly Phe Arg Gly Ile Gly Val Ala Leu Lys Asp Gly Asp
130 135 140
Asn Cys Glu Tyr Val Thr Ile Tyr Glu Asp Lys Asp Gly Asp Trp Met
145 150 155 160
Leu Ala Gly Asp Xaa Pro Trp Gly Met Cys Ser Arg Val Met Gln Glu
165 170 175
Val Glu Asn Asn Glu Lys Ile Gly Cys Tyr Arg Val Trp Ala Ala Ala
180 185 190

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1566299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Met Met Lys Lys Arg Ala Phe Thr Glu Met Asn Met Thr Ser Ser Gly
1 5 10 15
Ser Asn Ser Asp Gln Cys Glu Ser Gly Val Val Ser Ser Gly Gly Asp
20 25 30
Ala Glu Lys Val Asn Asp Ser Pro Ala Ala Lys Ser Gln Val Val Gly
35 40 45
Trp Pro Pro Val Cys Ser Tyr Arg Lys Lys Asn Ser Cys Lys Glu Ala
50 55 60
Ser Thr Thr Lys Val Xaa Leu Gly Tyr Val Lys Val Ser Met Asp Gly
65 70 75 80
Val Pro Tyr Leu Arg Lys Met Asp Leu Gly Ser Ser Gln Gly Tyr Asp
85 90 95
Asp Leu Ala Phe Ser Leu Asp Lys Leu Phe Gly Phe Arg Gly Ile Gly
100 105 110
Val Ala Leu Lys Asp Gly Asp Asn Cys Glu Tyr Val Thr Ile Tyr Glu
115 120 125
Asp Lys Asp Gly Asp Trp Met Leu Ala Gly Asp Xaa Pro Trp Gly Met
130 135 140
Cys Ser Arg Val Met Gln Glu Val Glu Asn Asn Glu Lys Ile Gly Cys
145 150 155 160
Tyr Arg Val Trp Ala Ala Ala
165

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..166
(D) OTHER INFORMATION: / Ceres Seq. ID 1566300
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Met	Lys	Lys	Arg	Ala	Phe	Thr	Glu	Met	Asn	Met	Thr	Ser	Ser	Gly	Ser
1			5					10						15	
Asn	Ser	Asp	Gln	Cys	Glu	Ser	Gly	Val	Ser	Ser	Gly	Gly	Asp	Ala	
			20					25					30		
Glu	Lys	Val	Asn	Asp	Ser	Pro	Ala	Ala	Lys	Ser	Gln	Val	Val	Gly	Trp
			35					40				45			
Pro	Pro	Val	Cys	Ser	Tyr	Arg	Lys	Lys	Asn	Ser	Cys	Lys	Glu	Ala	Ser
			50					55				60			
Thr	Thr	Lys	Val	Xaa	Leu	Gly	Tyr	Val	Lys	Val	Ser	Met	Asp	Gly	Val
65								70				75			80
Pro	Tyr	Leu	Arg	Lys	Met	Asp	Leu	Gly	Ser	Ser	Gln	Gly	Tyr	Asp	Asp
								85				90		95	
Leu	Ala	Phe	Ser	Leu	Asp	Lys	Leu	Phe	Gly	Phe	Arg	Gly	Ile	Gly	Val
								100				105		110	
Ala	Leu	Lys	Asp	Gly	Asp	Asn	Cys	Glu	Tyr	Val	Thr	Ile	Tyr	Glu	Asp
								115				120		125	
Lys	Asp	Gly	Asp	Trp	Met	Leu	Ala	Gly	Asp	Xaa	Pro	Trp	Gly	Met	Cys
								130				135		140	
Ser	Arg	Val	Met	Gln	Glu	Val	Glu	Asn	Asn	Glu	Lys	Ile	Gly	Cys	Tyr
								145				150		155	160
Arg	Val	Trp	Ala	Ala	Ala										
															165

(2) INFORMATION FOR SEQ ID NO:259:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..2363
(D) OTHER INFORMATION: / Ceres Seq. ID 1566353
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

actcaaacgc	tgcattctcat	gcagaacccgt	actacccttc	ctttaaagat	gtcaaaaattg	60
ttgtccccga	aatttcttgt	gaaacacagat	gttogaagaa	gtttcagaat	cttaattgtt	120
ctcacgagct	aagaactacc	acagctacgg	aggatcaatt	gccgggtgta	tctaattgat	180
ctaaacagga	ccgtggctta	gagttattga	cccataacat	ggacaacggt	ggaaaaaacc	240
aagcaactca	acaagatttt	caaaagttcag	taagattaa	tgatcaacct	ttttgttcaa	300
actcgacac	agatccagaa	gctcaaaact	tgatcacgga	tgaggaattg	tgtagggttc	360
tttttccga	taacatgaaa	gatagcagta	catcttctgg	tgagcaaggt	cggaaatatg	420
ttgacctcta	aaacggcaaa	ggatctcttt	gttctcaggc	tgcaaaaacc	catgctcatg	480
aaaactggaaa	agttccagct	taccgtggc	atccttcaag	ttctgagggc	ctggccgggtc	540
ataatttgt	ccctttgtg	gattcagact	tgaaggactc	acttttacc	cgtaatgatt	600
ccaacgctcc	tatacaaggt	tgtcgcttt	ttggagctac	cgaattagaa	tgtaaagact	660
atacaaatga	cggtttcac	gatacttacg	gacattgaac	ttcccatg	aatgatgata	720
atggtgtgt	ccagagaaca	caggggctgt	catataattc	caaggattct	ttgaagctag	780
tacctttgaa	tagtttttct	tctccttcta	gagtgaacaa	gatttatatt	ctcattgaac	840
ataagcgcgc	tgaaaaagac	aaaggagctc	tttgttatga	acctccacgt	tttccaagtg	900
cagatatctc	tttcttcagc	tgtgatcttg	taccatcaaa	tagtgactta	cggcaagagt	960

acagtcctctt	tggtatccgt	cagttgatga	tttcttcaat	gaattgtaca	actccggttaa	1020
ggttatggga	ttcacccgtt	caecatagga	gcctctgatg	catgctttaa	gatactcgca	1080
aaagttttta	tggtgcacga	tccatcttaa	agaagcggca	tcgagacttg	ctttcacctg	1140
tgcttgatag	aaagaaagac	aaaaagctta	aaagggtctg	gacttctccc	ttggcctaag	1200
atttttcggc	cttagatgta	atgcttgatg	aaggagatga	ttgcattgac	ctctgctccg	1260
cagagttctc	tgaagataaa	aatatatgtg	cctccccttc	catagccaga	gataacagaa	1320
atttgctcat	attctcggtt	tatcaagaaa	tgattccgat	agatgaggaa	ccaaagggaaa	1380
ccttagaatc	agggtggagt	acttctatgc	aaaatgaaaa	tgatgtaat	gacggtgggtg	1440
cttcacgtaa	aaatgaccaa	gaaactctct	gaagtttttt	tgagttacga	ctgtgtctct	1500
ctggtagtag	tcgagctaga	ccagataaca	aagttaatgc	aagtgcgaaa	gatctatcaa	1560
accagacaaa	aatatcattc	gggtgatttt	caacagaaga	aatgtcatca	gaacctctat	1620
gcacagtga	ctctattcct	ttatctgcga	tcgataaaa	taaacactga	gagaccagct	1680
ttgatattga	aaacttcaac	atatgtgatg	gaactccgtt	cagaaaaactc	cttgataccc	1740
catcaccttg	gaaatctcct	ttactctttg	gttcttctct	gcaaaagtcca	aagttgcttc	1800
cagaaatcac	atttggagat	attgggtgtt	ttatgagtcc	cgccgagaga	agtttatgat	1860
ccataggact	gatgaagcat	ttgagtgaac	actcagctac	ggcatatgca	gatgccttgg	1920
aagttctggg	taatgacaca	cctgaatcga	tactcaagaa	gagacagctg	aacaagtcca	1980
ttcaaggaaa	agaaaatcag	caccagcttc	atgatcagct	tgggaaccga	tcccacgtgg	2040
agtgctcgcc	cttagacttc	agcgattgtg	ggacaccagg	gaaagctaa	gtacCttcgg	2100
cttctccggg	aggctactca	agcccatcat	cttacctttt	gaagagtgtc	agatagagaa	2160
gggtgggttt	gttcatagag	ttctgaaggg	agtcctcgct	tcaatttttt	gatcccatgt	2220
gtgtatgtct	tttttatctc	ctcctgtctc	aattttcttg	tttctaattt	ttttaaatgt	2280
gtagatctct	caactctgga	catcatacca	ttgattaaat	agcgaaaaag	taactgttgc	2340
tcaagtaatt	aacttgtaac	tcc				

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..717
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1566354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Ser	Asn	Ala	Ala	Ser	His	Ala	Glu	Pro	Tyr	Tyr	Pro	Ser	Phe	Lys	Asp
1			5						10					15	
Val	Lys	Ile	Val	Val	Pro	Glu	Ile	Ser	Cys	Glu	Thr	Glu	Cys	Ser	Lys
			20					25					30		
Lys	Phe	Gln	Asn	Leu	Asn	Cys	Ser	His	Glu	Leu	Arg	Thr	Thr	Thr	Ala
			35				40					45			
Thr	Glu	Asp	Gln	Leu	Pro	Gly	Val	Ser	Asn	Asp	Ala	Lys	Gln	Asp	Arg
			50				55				60				
Gly	Leu	Glu	Leu	Leu	Thr	His	Asn	Met	Asp	Asn	Gly	Gly	Lys	Asn	Gln
			65			70			75					80	
Ala	Leu	Gln	Gln	Asp	Phe	Gln	Ser	Ser	Val	Arg	Leu	Ser	Asp	Gln	Pro
			85					90					95		
Phe	Leu	Ser	Asn	Ser	Asp	Thr	Asp	Pro	Glu	Ala	Gln	Thr	Leu	Ile	Thr
			100				105						110		
Asp	Glu	Glu	Cys	Cys	Arg	Val	Leu	Phe	Pro	Asp	Asn	Met	Lys	Asp	Ser
			115				120					125			
Ser	Thr	Ser	Ser	Gly	Glu	Gln	Gly	Arg	Asn	Met	Val	Asp	Pro	Gln	Asn
			130				135				140				
Gly	Lys	Gly	Ser	Leu	Cys	Ser	Gln	Ala	Ala	Glu	Thr	His	Ala	His	Glu
			145				150			155				160	
Thr	Gly	Lys	Val	Pro	Ala	Leu	Pro	Trp	His	Pro	Ser	Ser	Ser	Glu	Gly
			165					170						175	
Leu	Ala	Gly	His	Asn	Cys	Val	Pro	Leu	Leu	Asp	Ser	Asp	Leu	Lys	Asp
			180					185					190		
Ser	Leu	Leu	Pro	Arg	Asn	Asp	Ser	Asn	Ala	Pro	Ile	Gln	Gly	Cys	Arg

195	200	205
Leu Phe Gly Ala Thr Glu	Leu Glu Cys Lys Thr Asp	Thr Asn Asp Gly
210	215	220
Phe Ile Asp Thr Tyr Glu	His Val Thr Ser His	Gly Asn Asp Asp Asn
225	230	235
Gly Gly Phe Pro Glu Gln Gln Gly	Leu Ser Tyr Ile Pro	Lys Asp Ser
245	250	255
Leu Lys Leu Val Pro Leu Asn Ser Phe	Ser Ser Pro Ser Arg	Val Asn
260	265	270
Lys Ile Tyr Phe Pro Ile Asp Asp	Lys Pro Ala Glu Lys	Asp Lys Gly
275	280	285
Ala Leu Cys Tyr Glu Pro Pro Arg Phe	Pro Ser Ala Asp Ile Pro	Phe
290	295	300
Phe Ser Cys Asp Leu Val Pro Ser Asn Ser	Asp Leu Arg Gln Glu Tyr	
305	310	315
Ser Pro Phe Gly Ile Arg Gln Leu Met	Ile Ser Ser Met Asn	Cys Thr
325	330	335
Thr Pro Leu Arg Leu Trp Asp Ser Pro	Cys His Asp Arg Ser	Pro Asp
340	345	350
Val Met Leu Asn Asp Thr Ala Lys Ser	Phe Ser Gly Ala Pro	Ser Ile
355	360	365
Leu Lys Lys Arg His Arg Asp Leu Leu Ser	Pro Val Leu Asp Arg Arg	
370	375	380
Lys Asp Lys Lys Leu Lys Arg Ala Ala Thr	Ser Ser Leu Ala Asn Asp	
385	390	395
Phe Ser Arg Leu Asp Val Met Leu Asp	Glu Gly Asp Asp Cys Met Thr	
405	410	415
Ser Arg Pro Ser Glu Ser Pro Glu Asp	Lys Asn Ile Cys Ala Ser Pro	
420	425	430
Ser Ile Ala Arg Asp Asn Arg Asn Cys	Ala Ser Ser Arg Leu Tyr Gln	
435	440	445
Glu Met Ile Pro Ile Asp Glu Glu Pro Lys	Glu Thr Leu Glu Ser Gly	
450	455	460
Gly Val Thr Ser Met Gln Asn Glu Asn Gly	Cys Asn Asp Gly Gly Ala	
465	470	475
Ser Ala Lys Asn Asp Gln Glu Thr Ser Gly	Ser Phe Phe Glu Leu Arg	
485	490	495
Leu Cys Ser Pro Gly Met Thr Arg Ala Arg	Pro Asp Asn Lys Val Asn	
500	505	510
Ala Ser Ala Lys Asp Leu Ser Asn Gln His	Lys Ile Ser Leu Gly Asp	
515	520	525
Phe Pro Thr Glu Glu Met Ser Ser Glu Pro	Leu Cys Thr Val Asp Ser	
530	535	540
Ile Pro Leu Ser Ala Ile Asp Lys Thr Asn	Thr Ala Glu Thr Ser Phe	
545	550	555
Asp Ile Glu Asn Phe Asn Ile Phe Asp Gly	Thr Pro Phe Arg Lys Leu	
565	570	575
Leu Asp Thr Pro Ser Pro Trp Lys Ser Pro	Leu Leu Phe Gly Ser Phe	
580	585	590
Leu Gln Ser Pro Lys Leu Pro Pro Glu Ile	Thr Phe Glu Asp Ile Gly	
595	600	605
Cys Phe Met Ser Pro Gly Glu Arg Ser Tyr	Asp Ala Ile Gly Leu Met	
610	615	620
Lys His Leu Ser Glu His Ser Ala Thr Ala	Tyr Ala Asp Ala Leu Glu	
625	630	635
Val Leu Gly Asn Asp Thr Pro Glu Ser Ile	Leu Lys Lys Arg Gln Leu	
645	650	655
Asn Lys Ser Ile Gln Gly Lys Glu Asn Gln	His Gln Pro His Asp Gln	
660	665	670
Leu Gly Asn Arg Ser His Val Glu Cys Arg	Ala Leu Asp Phe Ser Asp	
675	680	685

Cys Gly Thr Pro Gly Lys Ala Lys Val Pro Ser Ala Ser Pro Gly Gly
690 695 700
Tyr Ser Ser Pro Ser Ser Tyr Leu Leu Lys Ser Cys Arg
705 710 715

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 645 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..645

(D) OTHER INFORMATION: / Ceres Seq. ID 1566355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Met Asp Asn Gly Gly Lys Asn Gln Ala Leu Gln Gln Asp Phe Gln Ser
1 5 10 15
Ser Val Arg Leu Ser Asp Gln Pro Phe Leu Ser Asn Ser Asp Thr Asp
20 25 30
Pro Glu Ala Gln Thr Leu Ile Thr Asp Glu Glu Cys Cys Arg Val Leu
35 40 45
Phe Pro Asp Asn Met Lys Asp Ser Ser Thr Ser Ser Gly Glu Gln Gly
50 55 60
Arg Asn Met Val Asp Pro Gln Asn Gly Lys Gly Ser Leu Cys Ser Gln
65 70 75 80
Ala Ala Glu Thr His Ala His Glu Thr Gly Lys Val Pro Ala Leu Pro
85 90 95
Trp His Pro Ser Ser Ser Glu Gly Leu Ala Gly His Asn Cys Val Pro
100 105 110
Leu Leu Asp Ser Asp Leu Lys Asp Ser Leu Leu Pro Arg Asn Asp Ser
115 120 125
Asn Ala Pro Ile Gln Gly Cys Arg Leu Phe Gly Ala Thr Glu Leu Glu
130 135 140
Cys Lys Thr Asp Thr Asn Asp Gly Phe Ile Asp Thr Tyr Gly His Val
145 150 155 160
Thr Ser His Gly Asn Asp Asp Asn Gly Gly Phe Pro Glu Gln Gln Gly
165 170 175
Leu Ser Tyr Ile Pro Lys Asp Ser Leu Lys Leu Val Pro Leu Asn Ser
180 185 190
Phe Ser Ser Pro Ser Arg Val Asn Lys Ile Tyr Phe Pro Ile Asp Asp
195 200 205
Lys Pro Ala Glu Lys Asp Lys Gly Ala Leu Cys Tyr Glu Pro Pro Arg
210 215 220
Phe Pro Ser Ala Asp Ile Pro Phe Phe Ser Cys Asp Leu Val Pro Ser
225 230 235 240
Asn Ser Asp Leu Arg Gln Glu Tyr Ser Pro Phe Gly Ile Arg Gln Leu
245 250 255
Met Ile Ser Ser Met Asn Cys Thr Thr Pro Leu Arg Leu Trp Asp Ser
260 265 270
Pro Cys His Asp Arg Ser Pro Asp Val Met Leu Asn Asp Thr Ala Lys
275 280 285
Ser Phe Ser Gly Ala Pro Ser Ile Leu Lys Lys Arg His Arg Asp Leu
290 295 300
Leu Ser Pro Val Leu Asp Arg Arg Lys Asp Lys Lys Leu Lys Arg Ala
305 310 315 320
Ala Thr Ser Ser Leu Ala Asn Asp Phe Ser Arg Leu Asp Val Met Leu
325 330 335
Asp Glu Gly Asp Asp Cys Met Thr Ser Arg Pro Ser Glu Ser Pro Glu
340 345 350
Asp Lys Asn Ile Cys Ala Ser Pro Ser Ile Ala Arg Asp Asn Arg Asn

355 360 365
Cys Ala Ser Ser Arg Leu Tyr Gln Glu Met Ile Pro Ile Asp Glu Glu
370 375 380
Pro Lys Glu Thr Leu Glu Ser Gly Gly Val Thr Ser Met Gln Asn Glu
385 390 395 400
Asn Gly Cys Asn Asp Gly Gly Ala Ser Ala Lys Asn Asp Gln Glu Thr
405 410 415
Ser Gly Ser Phe Phe Glu Leu Arg Leu Cys Ser Pro Gly Met Thr Arg
420 425 430
Ala Arg Pro Asp Asn Lys Val Asn Ala Ser Ala Lys Asp Leu Ser Asn
435 440 445
Gln His Lys Ile Ser Leu Gly Asp Phe Pro Thr Glu Glu Met Ser Ser
450 455 460
Glu Pro Leu Cys Thr Val Asp Ser Ile Pro Leu Ser Ala Ile Asp Lys
465 470 475 480
Thr Asn Thr Ala Glu Thr Ser Phe Asp Ile Glu Asn Phe Asn Ile Phe
485 490 495
Asp Gly Thr Pro Phe Arg Lys Leu Leu Asp Thr Pro Ser Pro Trp Lys
500 505 510
Ser Pro Leu Leu Phe Gly Ser Phe Leu Gln Ser Pro Lys Leu Pro Pro
515 520 525
Glu Ile Thr Phe Glu Asp Ile Gly Cys Phe Met Ser Pro Gly Glu Arg
530 535 540
Ser Tyr Asp Ala Ile Gly Leu Met Lys His Leu Ser Glu His Ser Ala
545 550 555 560
Thr Ala Tyr Ala Asp Ala Leu Glu Val Leu Gly Asn Asp Thr Pro Glu
565 570 575
Ser Ile Leu Lys Lys Arg Gln Leu Asn Lys Ser Ile Gln Gly Lys Glu
580 585 590
Asn Gln His Gln Pro His Asp Gln Leu Gly Asn Arg Ser His Val Glu
595 600 605
Cys Arg Ala Leu Asp Phe Ser Asp Cys Gly Thr Pro Gly Lys Ala Lys
610 615 620
Val Pro Ser Ala Ser Pro Gly Gly Tyr Ser Ser Pro Ser Ser Tyr Leu
625 630 635 640
Leu Lys Ser Cys Arg
645

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..593

(D) OTHER INFORMATION: / Ceres Seq. ID 1566356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Met Lys Asp Ser Ser Thr Ser Ser Gly Glu Gln Gly Arg Asn Met Val
1 5 10 15
Asp Pro Gln Asn Gly Lys Gly Ser Leu Cys Ser Gln Ala Ala Glu Thr
20 25 30
His Ala His Glu Thr Gly Lys Val Pro Ala Leu Pro Trp His Pro Ser
35 40 45
Ser Ser Glu Gly Leu Ala Gly His Asn Cys Val Pro Leu Leu Asp Ser
50 55 60
Asp Leu Lys Asp Ser Leu Leu Pro Arg Asn Asp Ser Asn Ala Pro Ile
65 70 75 80
Gln Gly Cys Arg Leu Phe Gly Ala Thr Glu Leu Glu Cys Lys Thr Asp
85 90 95

Thr	Asn	Asp	Gly	Phe	Ile	Asp	Thr	Tyr	Gly	His	Val	Thr	Ser	His	Gly	
			100						105					110		
Asn	Asp	Asp	Asn	Gly	Gly	Phe	Pro	Glu	Gln	Gln	Gly	Leu	Ser	Tyr	Ile	
		115					120					125				
Pro	Lys	Asp	Ser	Leu	Lys	Leu	Val	Pro	Leu	Asn	Ser	Phe	Ser	Ser	Pro	
		130				135						140				
Ser	Arg	Val	Asn	Lys	Ile	Tyr	Phe	Pro	Ile	Asp	Asp	Lys	Pro	Ala	Glu	
		145			150					155					160	
Lys	Asp	Lys	Gly	Ala	Leu	Cys	Tyr	Glu	Pro	Pro	Arg	Phe	Pro	Ser	Ala	
				165					170					175		
Asp	Ile	Pro	Phe	Phe	Ser	Cys	Asp	Leu	Val	Pro	Ser	Asn	Ser	Asp	Leu	
			180						185				190			
Arg	Gln	Glu	Tyr	Ser	Pro	Phe	Gly	Ile	Arg	Gln	Leu	Met	Ile	Ser	Ser	
		195					200						205			
Met	Asn	Cys	Thr	Thr	Pro	Leu	Arg	Leu	Trp	Asp	Ser	Pro	Cys	His	Asp	
		210				215					220					
Arg	Ser	Pro	Asp	Val	Met	Leu	Asn	Asp	Thr	Ala	Lys	Ser	Phe	Ser	Gly	
		225			230					235					240	
Ala	Pro	Ser	Ile	Leu	Lys	Lys	Arg	His	Arg	Asp	Leu	Leu	Ser	Pro	Val	
				245					250					255		
Leu	Asp	Arg	Arg	Lys	Asp	Lys	Lys	Leu	Lys	Arg	Ala	Ala	Thr	Ser	Ser	
		260					265						270			
Leu	Ala	Asn	Asp	Phe	Ser	Arg	Leu	Asp	Val	Met	Leu	Asp	Glu	Gly	Asp	
		275					280					285				
Asp	Cys	Met	Thr	Ser	Arg	Pro	Ser	Glu	Ser	Pro	Glu	Asp	Lys	Asn	Ile	
		290				295					300					
Cys	Ala	Ser	Pro	Ser	Ile	Ala	Arg	Asp	Asn	Arg	Asn	Cys	Ala	Ser	Ser	
		305			310					315					320	
Arg	Leu	Tyr	Gln	Glu	Met	Ile	Pro	Ile	Asp	Glu	Glu	Pro	Lys	Glu	Thr	
				325					330					335		
Leu	Glu	Ser	Gly	Gly	Val	Thr	Ser	Met	Gln	Asn	Glu	Asn	Gly	Cys	Asn	
			340					345					350			
Asp	Gly	Gly	Ala	Ser	Ala	Lys	Asn	Asp	Gln	Glu	Thr	Ser	Gly	Ser	Phe	
		355					360					365				
Phe	Glu	Leu	Arg	Leu	Cys	Ser	Pro	Gly	Met	Thr	Arg	Ala	Arg	Pro	Asp	
		370				375					380					
Asn	Lys	Val	Asn	Ala	Ser	Ala	Lys	Asp	Leu	Ser	Asn	Gln	His	Lys	Ile	
		385			390					395					400	
Ser	Leu	Gly	Asp	Phe	Pro	Thr	Glu	Glu	Met	Ser	Ser	Glu	Pro	Leu	Cys	
			405						410					415		
Thr	Val	Asp	Ser	Ile	Pro	Leu	Ser	Ala	Ile	Asp	Lys	Thr	Asn	Thr	Ala	
		420						425					430			
Glu	Thr	Ser	Phe	Asp	Ile	Glu	Asn	Phe	Asn	Ile	Phe	Asp	Gly	Thr	Pro	
		435					440					445				
Phe	Arg	Lys	Leu	Leu	Asp	Thr	Pro	Ser	Pro	Trp	Lys	Ser	Pro	Leu	Leu	
		450			455						460					
Phe	Gly	Ser	Phe	Leu	Gln	Ser	Pro	Lys	Leu	Pro	Pro	Glu	Ile	Thr	Phe	
		465			470					475					480	
Glu	Asp	Ile	Gly	Cys	Phe	Met	Ser	Pro	Gly	Glu	Arg	Ser	Tyr	Asp	Ala	
				485					490					495		
Ile	Gly	Leu	Met	Lys	His	Leu	Ser	Glu	His	Ser	Ala	Thr	Ala	Tyr	Ala	
			500					505					510			
Asp	Ala	Leu	Glu	Val	Leu	Gly	Asn	Asp	Thr	Pro	Glu	Ser	Ile	Leu	Lys	
		515					520					525				
Lys	Arg	Gln	Leu	Asn	Lys	Ser	Ile	Gln	Gly	Lys	Glu	Asn	Gln	His	Gln	
		530			535						540					
Pro	His	Asp	Gln	Leu	Gly	Asn	Arg	Ser	His	Val	Glu	Cys	Arg	Ala	Leu	
		545			550					555					560	
Asp	Phe	Ser	Asp	Cys	Gly	Thr	Pro	Gly	Lys	Ala	Lys	Val	Pro	Ser	Ala	
				565					570					575		
Ser	Pro	Gly	Gly	Tyr	Ser	Ser	Pro	Ser	Ser	Tyr	Leu	Leu	Lys	Ser	Cys	

Arg 580 585 590

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 574 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..574

(D) OTHER INFORMATION: / Ceres Seq. ID 1566364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

actagaaatt	ttgtctctct	cgccgccttg	cgaaaaagcat	tttcgatctt	actcttagga	60
taaaaaaatg	tcgacagtgt	gagagcttgc	tntGCagcta	cgctgttatg	atcctcgagg	120
acgagggtat	cgctatcacg	gctgacaaaa	tcgcgacctt	ggtgaaagct	gctggtgtta	180
gtattgagtc	atactggcca	atgctattcg	ccaagatggc	tgagaaacgt	aacgtgactg	240
atctcatcat	gaacgttggt	gctggtggtg	gaggtggtgc	tccggttgca	gctgctgctc	300
caagctgctgg	cggtggtgcg	gcaGctgctc	ctgctgctga	ggagaagaag	aaggatgagc	360
cagcagaaga	gagtgacgga	gatttggggt	tcggttttgt	tgactaaacg	caGtcaactg	420
tctttctctc	ttgtagtgtg	atattggaga	ctatattttg	tcgtatgagt	tattattact	480
tgtttgatct	ggctaaagga	ctattagtgt	gtttatgatg	cgtatgttgt	ataactcaag	540
ttctctagca	aaccaatcgg	ctcgggcttt	tggt			

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1566365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Met	Ile	Leu	Glu	Asp	Glu	Gly	Ile	Ala	Ile	Thr	Ala	Asp	Lys	Ile	Ala
1			5					10						15	
Thr	Leu	Val	Lys	Ala	Ala	Gly	Val	Ser	Ile	Glu	Ser	Tyr	Trp	Pro	Met
			20					25					30		
Leu	Phe	Ala	Lys	Met	Ala	Glu	Lys	Arg	Asn	Val	Thr	Asp	Leu	Ile	Met
			35					40				45			
Asn	Val	Gly	Ala	Gly	Gly	Gly	Gly	Ala	Pro	Val	Ala	Ala	Ala	Ala	Ala
			50				55					60			
Pro	Ala	Ala	Gly	Gly	Gly	Ala	Ala	Ala	Ala	Pro	Ala	Ala	Glu	Glu	Lys
			65				70			75			80		
Lys	Lys	Asp	Glu	Pro	Ala	Glu	Glu	Ser	Asp	Gly	Asp	Leu	Gly	Phe	Gly
			85					90				95			
Leu	Phe	Asp													

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1566366
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:
Met Leu Phe Ala Lys Met Ala Glu Lys Arg Asn Val Thr Asp Leu Ile
1 5 10 15
Met Asn Val Gly Ala Gly Gly Gly Gly Ala Pro Val Ala Ala Ala
20 25 30
Ala Pro Ala Ala Gly Gly Gly Ala Ala Ala Pro Ala Ala Glu Glu
35 40 45
Lys Lys Lys Asp Glu Pro Ala Glu Glu Ser Asp Gly Asp Leu Gly Phe
50 55 60
Gly Leu Phe Asp
65

(2) INFORMATION FOR SEQ ID NO:266:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1566367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:
Met Ala Glu Lys Arg Asn Val Thr Asp Leu Ile Met Asn Val Gly Ala
1 5 10 15
Gly Gly Gly Gly Gly Ala Pro Val Ala Ala Ala Pro Ala Ala Gly
20 25 30
Gly Gly Ala Ala Ala Ala Pro Ala Ala Glu Glu Lys Lys Lys Asp Glu
35 40 45
Pro Ala Glu Glu Ser Asp Gly Asp Leu Gly Phe Gly Leu Phe Asp
50 55 60

(2) INFORMATION FOR SEQ ID NO:267:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1582 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1582

(D) OTHER INFORMATION: / Ceres Seq. ID 1566379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:
tgagaaaaatg cctgagagaa atgcagtgct atgatacgtg ggctttgtca 60
gaacgggtgaa gtggatcgcg cggttggtgt gtttcggaaa atgcctgtga aggattcgctc 120
tcctctatgt gcactgttgg ctggtcttat taaaaacgag agactttcag aagctgcggtg 180
ggttttgggt cagtatggga gtttagtttc aggaagggaa gatttggtgt atgcttataa 240
caccttggatt gttggatatg gacagcgagg acaagtagaa gcagctcgat gtcgtgttga 300
tcagattcct gatctctgtg gtgatgatca tgggtggaga tttagagaga ggttctgtaa 360
aaatgtgtgt tcatggaatt ctatgatcaa agcttacttg aaagtgggtg atgtggtctc 420
tgctaggttg ctatttggatc agatgaaaga ccgcgataca atttcttggg acacaatgat 480
tgatggatgc gtacatgttt ccaggatgga agatgctttt gctctgtttt cggaaatgcc 540
gaaccgtgat gcacattcgt ggaacatgat ggtctcgggt tatgctagtgt ttggcgaagt 600
agagcttgct cgccactact ttgaaaaaac acctgagaaa catcacgtct cgtggaactc 660
gataatatga gcttatgaga aaaacaagga ctacaagaa gctgttgatt tgtttatccg 720
gatgaacatt gaaggagaga agcctgaccc acatacttta acctctcttc tcagtgcaatc 780
taccgggctt gtaaatctgc gtttaggaat gcagatgcac caaatcggtt tcaagactgt 840
gatcccgatc gttccagctc acaatgcctt tatcactatg tattcaagat cggttgaaat 900
aatggagtcg agggagaatc tcgatgaaat gaaactcaaa agagaagtaa tcacatggaa 960
tgcaatgata ggaggatatg catttcatgt taatgcctca gaggccttga atctgttcgg 1020

gtcgatgaaa	agcaacggga	tatatccttc	tcacataaca	ttcgtctcag	ttctgaacgc	1080
ttgtgCtca	gggggacttg	ttgatgaggc	taaagcacag	ttgtgtccca	tgatgagtgt	1140
gtacaagatc	gagccgatga	tggaaacatta	ttcttccctg	gtcaacgtta	ccagtggaca	1200
agggcagttt	gaagaggcca	tgtatatcat	aaagagtatg	ccttttgagc	cagacaaaac	1260
ggatgggggt	gcattattgg	atgctttgtg	gatataacaa	tgtaggggctt	gcacatgttg	1320
cagctgaagc	aatgtcgaga	ctcgaaccag	agagctcaac	accttatgta	ctgttataca	1380
acatgtacgc	ggatatggga	ctatggggagc	aagcttctca	agtgagaatg	aaacatggaga	1440
gtaaaagaat	caagaaggaa	agaggatcca	gttgggttga	ctctctcaacg	taaaaagcag	1500
cttttattta	tgtttactta	aacataaaaa	ttgatttggg	atcagaattg	agatagaaat	1560
tgataaggta	ctcttgaag	tt				

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..431

(D) OTHER INFORMATION: / Ceres Seq. ID 1566380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Glu	Lys	Met	Pro	Glu	Arg	Asn	Ala	Val	Ser	Trp	Ser	Ala	Met	Ile	Thr
1			5						10					15	
Gly	Leu	Cys	Gln	Asn	Gly	Glu	Val	Asp	Arg	Ala	Val	Val	Leu	Phe	Arg
			20					25					30		
Lys	Met	Pro	Val	Lys	Asp	Ser	Ser	Pro	Leu	Cys	Ala	Leu	Val	Ala	Gly
			35				40					45			
Leu	Ile	Lys	Asn	Glu	Arg	Leu	Ser	Glu	Ala	Ala	Trp	Val	Leu	Gly	Gln
			50				55				60				
Tyr	Gly	Ser	Leu	Val	Ser	Gly	Arg	Glu	Asp	Leu	Val	Tyr	Ala	Tyr	Asn
			65			70			75					80	
Thr	Leu	Ile	Val	Gly	Tyr	Gly	Gln	Arg	Gly	Gln	Val	Glu	Ala	Ala	Arg
			85						90					95	
Cys	Leu	Phe	Asp	Gln	Ile	Pro	Asp	Leu	Cys	Gly	Asp	Asp	His	Gly	Gly
			100				105						110		
Glu	Phe	Arg	Gly	Arg	Phe	Cys	Lys	Asn	Val	Val	Ser	Trp	Asn	Ser	Met
			115				120					125			
Ile	Lys	Ala	Tyr	Leu	Lys	Val	Gly	Asp	Val	Val	Ser	Ala	Arg	Leu	Leu
			130				135				140				
Phe	Asp	Gln	Met	Lys	Asp	Arg	Asp	Thr	Ile	Ser	Trp	Asn	Thr	Met	Ile
			145			150			155					160	
Asp	Gly	Tyr	Val	His	Val	Ser	Arg	Met	Glu	Asp	Ala	Phe	Ala	Leu	Phe
			165						170					175	
Ser	Glu	Met	Pro	Asn	Arg	Asp	Ala	His	Ser	Trp	Asn	Met	Met	Val	Ser
			180				185							190	
Gly	Tyr	Ala	Ser	Val	Gly	Asn	Val	Glu	Leu	Ala	Arg	His	Tyr	Phe	Glu
			195				200					205			
Lys	Thr	Pro	Glu	Lys	His	Thr	Val	Ser	Trp	Asn	Ser	Ile	Ile	Ala	Ala
			210				215				220				
Tyr	Glu	Lys	Asn	Lys	Asp	Tyr	Lys	Glu	Ala	Val	Asp	Leu	Phe	Ile	Arg
			225			230			235					240	
Met	Asn	Ile	Glu	Gly	Glu	Lys	Pro	Asp	Pro	His	Thr	Leu	Thr	Ser	Leu
			245						250					255	
Leu	Ser	Ala	Ser	Thr	Gly	Leu	Val	Asn	Leu	Arg	Leu	Gly	Met	Gln	Met
			260					265						270	
His	Gln	Ile	Val	Val	Lys	Thr	Val	Ile	Pro	Asp	Val	Pro	Val	His	Asn
			275				280					285			
Ala	Leu	Ile	Thr	Met	Tyr	Ser	Arg	Cys	Gly	Glu	Ile	Met	Glu	Ser	Arg
			290			295					300				
Arg	Ile	Phe	Asp	Glu	Met	Lys	Leu	Lys	Arg	Glu	Val	Ile	Thr	Trp	Asn

305		310		315		320
Ala Met Ile Gly	Gly Tyr Ala Phe His	Gly Asn Ala Ser	Glu Ala Leu			
	325	330	335			
Asn Leu Phe Gly	Ser Met Lys Ser Asn Gly	Ile Tyr Pro Ser	His Ile			
	340	345	350			
Thr Phe Val Ser	Val Leu Asn Ala Cys Ala His	Ala Gly Leu Val	Asp			
	355	360	365			
Glu Ala Lys Ala	Gln Phe Val Ser Met Met Ser	Val Tyr Lys Ile	Glu			
	370	375	380			
Pro Met Met Glu	His Tyr Ser Ser Leu Val Asn Val	Thr Ser Gly Gln				
	385	390	395			400
Gly Gln Phe Glu	Glu Ala Met Tyr Ile Ile Lys	Ser Met Pro Phe	Glu			
	405	410	415			
Pro Asp Lys Thr	Val Trp Gly Ala Leu Leu Asp	Ala Cys Arg Ile				
	420	425	430			

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..429

(D) OTHER INFORMATION: / Ceres Seq. ID 1566381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

Met Pro Glu Arg	Asn Ala Val Ser Trp	Ser Ala Met Ile Thr	Gly Leu
1	5	10	15
Cys Gln Asn Gly	Glu Val Asp Arg Ala	Val Val Leu Phe Arg	Lys Met
	20	25	30
Pro Val Lys Asp	Ser Ser Pro Leu Cys	Ala Leu Val Ala Gly	Leu Ile
	35	40	45
Lys Asn Glu Arg	Leu Ser Glu Ala Ala	Trp Val Leu Gly	Gln Tyr Gly
	50	55	60
Ser Leu Val Ser	Gly Arg Glu Asp Leu Val	Tyr Ala Tyr Asn Thr	Leu
	65	70	75
Ile Val Gly Tyr	Gln Arg Gly Gln Val	Glu Ala Ala Arg Cys	Leu
	85	90	95
Phe Asp Gln Ile	Pro Asp Leu Cys Gly Asp	Asp His Gly Gly	Glu Phe
	100	105	110
Arg Glu Arg Phe	Cys Lys Asn Val Val Ser Trp	Asn Ser Met Ile Lys	
	115	120	125
Ala Tyr Leu Lys	Val Gly Asp Val Val Ser Ala	Arg Leu Leu Phe Asp	
	130	135	140
Gln Met Lys Asp	Arg Asp Thr Ile Ser Trp	Asn Thr Met Ile Asp	Gly
	145	150	155
Tyr Val His Val	Ser Arg Met Glu Asp Ala	Phe Ala Leu Phe Ser	Glu
	165	170	175
Met Pro Asn Arg	Asp Ala His Ser Trp Asn	Met Met Val Ser Gly	Tyr
	180	185	190
Ala Ser Val Gly	Asn Val Glu Leu Ala Arg	His Tyr Phe Glu Lys	Thr
	195	200	205
Pro Glu Lys His	Thr Val Ser Trp Asn Ser	Ile Ile Ala Ala Tyr	Glu
	210	215	220
Lys Asn Lys Asp	Tyr Lys Glu Ala Val Asp	Phe Ile Arg Met Asn	
	225	230	235
Ile Glu Gly Glu	Lys Pro Asp Pro His Thr	Leu Thr Ser Leu Leu	Ser
	245	250	255
Ala Ser Thr Gly	Leu Val Asn Leu Arg Leu	Gly Met Gln Met His	Gln
	260	265	270

Ile	Val	Val	Lys	Thr	Val	Ile	Pro	Asp	Val	Pro	Val	His	Asn	Ala	Leu
	275						280					285			
Ile	Thr	Met	Tyr	Ser	Arg	Cys	Gly	Glu	Ile	Met	Glu	Ser	Arg	Arg	Ile
	290						295				300				
Phe	Asp	Glu	Met	Lys	Leu	Lys	Arg	Glu	Val	Ile	Thr	Trp	Asn	Ala	Met
	305				310					315				320	
Ile	Gly	Gly	Tyr	Ala	Phe	His	Gly	Asn	Ala	Ser	Glu	Ala	Leu	Asn	Leu
				325					330					335	
Phe	Gly	Ser	Met	Lys	Ser	Asn	Gly	Ile	Tyr	Pro	Ser	His	Ile	Thr	Phe
			340					345					350		
Val	Ser	Val	Leu	Asn	Ala	Cys	Ala	His	Ala	Gly	Leu	Val	Asp	Glu	Ala
			355				360					365			
Lys	Ala	Gln	Phe	Val	Ser	Met	Met	Ser	Val	Tyr	Lys	Ile	Glu	Pro	Met
	370					375					380				
Met	Glu	His	Tyr	Ser	Ser	Leu	Val	Asn	Val	Thr	Ser	Gly	Gln	Gly	Gln
	385					390				395				400	
Phe	Glu	Glu	Ala	Met	Tyr	Ile	Ile	Lys	Ser	Met	Pro	Phe	Glu	Pro	Asp
				405					410					415	
Lys	Thr	Val	Trp	Gly	Ala	Leu	Leu	Asp	Ala	Cys	Arg	Ile			
			420					425							

- (2) INFORMATION FOR SEQ ID NO:270:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 418 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..418
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1566382
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

Met	Ile	Thr	Gly	Leu	Cys	Gln	Asn	Gly	Glu	Val	Asp	Arg	Ala	Val	Val
1				5					10					15	
Leu	Phe	Arg	Lys	Met	Pro	Val	Lys	Asp	Ser	Ser	Pro	Leu	Cys	Ala	Leu
			20					25				30			
Val	Ala	Gly	Leu	Ile	Lys	Asn	Glu	Arg	Leu	Ser	Glu	Ala	Ala	Trp	Val
		35				40					45				
Leu	Gly	Gln	Tyr	Gly	Ser	Leu	Val	Ser	Gly	Arg	Glu	Asp	Leu	Val	Tyr
	50				55						60				
Ala	Tyr	Asn	Thr	Leu	Ile	Val	Gly	Tyr	Gly	Gln	Arg	Gly	Gln	Val	Glu
	65				70				75					80	
Ala	Ala	Arg	Cys	Leu	Phe	Asp	Gln	Ile	Pro	Asp	Leu	Cys	Gly	Asp	Asp
			85						90					95	
His	Gly	Gly	Glu	Phe	Arg	Glu	Arg	Phe	Cys	Lys	Asn	Val	Val	Ser	Trp
			100				105					110			
Asn	Ser	Met	Ile	Lys	Ala	Tyr	Leu	Lys	Val	Gly	Asp	Val	Val	Ser	Ala
		115					120					125			
Arg	Leu	Leu	Phe	Asp	Gln	Met	Lys	Asp	Arg	Asp	Thr	Ile	Ser	Trp	Asn
	130					135					140				
Thr	Met	Ile	Asp	Gly	Tyr	Val	His	Val	Ser	Arg	Met	Glu	Asp	Ala	Phe
	145				150					155				160	
Ala	Leu	Phe	Ser	Glu	Met	Pro	Asn	Arg	Asp	Ala	His	Ser	Trp	Asn	Met
				165					170					175	
Met	Val	Ser	Gly	Tyr	Ala	Ser	Val	Gly	Asn	Val	Glu	Leu	Ala	Arg	His
			180					185					190		
Tyr	Phe	Glu	Lys	Thr	Pro	Glu	Lys	His	Thr	Val	Ser	Trp	Asn	Ser	Ile
			195				200					205			
Ile	Ala	Ala	Tyr	Glu	Lys	Asn	Lys	Asp	Tyr	Lys	Glu	Ala	Val	Asp	Leu
	210					215					220				
Phe	Ile	Arg	Met	Asn	Ile	Glu	Gly	Glu	Lys	Pro	Asp	Pro	His	Thr	Leu

225				230				235				240
Thr	Ser	Leu	Leu	Ser	Ala	Ser	Thr	Gly	Leu	Val	Asn	Leu
				245				250				255
Met	Gln	Met	His	Gln	Ile	Val	Val	Lys	Thr	Val	Ile	Pro
			260					265			270	275
Val	His	Asn	Ala	Leu	Ile	Thr	Met	Tyr	Ser	Arg	Cys	Gly
			275				280				285	290
Glu	Ser	Arg	Arg	Ile	Phe	Asp	Glu	Met	Lys	Leu	Lys	Arg
						295					300	305
Thr	Trp	Asn	Ala	Met	Ile	Gly	Gly	Tyr	Ala	Phe	His	Gly
						310			315			320
Glu	Ala	Leu	Asn	Leu	Phe	Gly	Ser	Met	Lys	Ser	Asn	Gly
						325			330			335
Ser	His	Ile	Thr	Phe	Val	Ser	Val	Leu	Asn	Ala	Cys	Ala
			340					345				350
Leu	Val	Asp	Glu	Ala	Lys	Ala	Gln	Phe	Val	Ser	Met	Ser
			355				360				365	370
Lys	Ile	Glu	Pro	Met	Met	Glu	His	Tyr	Ser	Ser	Leu	Val
						375					380	385
Ser	Gly	Gln	Gly	Gln	Phe	Glu	Glu	Ala	Met	Tyr	Ile	Ile
						390			395			400
Pro	Phe	Glu	Pro	Asp	Lys	Thr	Val	Trp	Gly	Ala	Leu	Leu
				405					410			415
Arg	Ile											

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 974 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..974

(D) OTHER INFORMATION: / Ceres Seq. ID 1566387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

aaMcaacgaa	cgccgagagc	tctcacttca	cactttatcc	acttggagct	tcgacaaatgg	60
cgtctccttc	gcttctgcag	tcttcgcgtt	cttcggtttca	cggacgtttc	tcacattag	120
cggtctccatc	ctccgcacga	atgctctctc	cgccgcctcag	aaacgttggtg	aaagtctcgg	180
cgtctggaaac	tgtaactggc	gagaaatctg	aagccgagaa	aactcaacgc	ctcaaaacgg	240
cttacctcga	gaggattatc	cctgcgctca	aagaagagtt	caagtacgtt	aatattcacc	300
aggttccaaa	ggtacagaag	attgtagtga	attgtggtat	tggagatgcg	gcgcagaaag	360
acaagggttt	ggaggctgcg	atgaaggata	tcgcgcttat	cacaggggcag	aaacctatta	420
agacacgagc	tagagcttcc	attgctactt	tcaagatcag	ggaagatcaa	cctctgggga	480
tgtctgtcac	tctcagagga	gatgtaattg	actcctctct	ggatcgctct	atcaacttag	540
cccttcgcag	aactcgagat	ttccaagggt	tgagtccccag	tatctttgat	gggaacggaa	600
actactcgat	tgggtgtgaa	gaccaagggt	tattccctga	aatcaggttt	gatgcctgtg	660
gaaaaacgag	aggaatggat	gtatgcatca	gcacaacggc	taaaagcgat	caagaaggac	720
agaaactatt	ggctctaatg	ggaatgcctt	tcagggaagg	aggtgtgtggc	agccacggcg	780
cgatagtgcg	gaagaagaaa	ctaaagtctc	atcaactttga	tgctaaagga	aaaggaaaaga	840
gatgatgaac	atagctgcot	attgtatgta	tcgtctctcg	taaccaacca	tttcagtgtt	900
cagaaaaacc	atctcctttt	gtaatgcttt	atgagtcaat	ttgaaaataa	tatcagggat	960
cttgttgtaa	tggt					

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..280

(D) OTHER INFORMATION: / Ceres Seq. ID 1566388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Xaa Thr Asn Ala Glu Ser Ser His Phe Thr Leu Tyr Pro Leu Gly Ala
1 5 10 15
Ser Thr Met Ala Ser Pro Ser Leu Leu Gln Ser Ser Ala Ser Ser Phe
20 25 30
His Gly Arg Phe Ser Pro Leu Ala Ala Pro Ser Ser Ala Arg Met Leu
35 40 45
Ser Pro Pro Leu Arg Asn Val Val Lys Val Ser Ala Ser Gly Thr Val
50 55 60
Leu Val Glu Lys Ser Glu Ala Glu Lys Thr Gln Arg Leu Lys Thr Ala
65 70 75 80
Tyr Leu Glu Arg Ile Ile Pro Ala Leu Lys Glu Glu Phe Lys Tyr Val
85 90 95
Asn Ile His Gln Val Pro Lys Val Gln Lys Ile Val Val Asn Cys Gly
100 105 110
Ile Gly Asp Ala Ala Gln Asn Asp Lys Gly Leu Glu Ala Ala Met Lys
115 120 125
Asp Ile Ala Leu Ile Thr Gly Gln Lys Pro Ile Lys Thr Arg Ala Arg
130 135 140
Ala Ser Ile Ala Thr Phe Lys Ile Arg Glu Asp Gln Pro Leu Gly Ile
145 150 155 160
Ala Val Thr Leu Arg Gly Asp Val Met Tyr Ser Phe Leu Asp Arg Leu
165 170 175
Ile Asn Leu Ala Leu Pro Arg Thr Arg Asp Phe Gln Gly Val Ser Pro
180 185 190
Ser Ser Phe Asp Gly Asn Gly Asn Tyr Ser Ile Gly Val Lys Asp Gln
195 200 205
Gly Val Phe Pro Glu Ile Arg Phe Asp Ala Val Gly Lys Thr Arg Gly
210 215 220
Met Asp Val Cys Ile Ser Thr Thr Ala Lys Ser Asp Gln Glu Gly Gln
225 230 235 240
Lys Leu Leu Ala Leu Met Gly Met Pro Phe Arg Glu Gly Gly Gly Gly
245 250 255
Ser Thr Gly Ala Ile Val Arg Lys Lys Lys Leu Lys Ser His His Phe
260 265 270
Asp Ala Lys Gly Lys Gly Lys Arg
275 280

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..262

(D) OTHER INFORMATION: / Ceres Seq. ID 1566389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Met Ala Ser Pro Ser Leu Leu Gln Ser Ser Ala Ser Ser Phe His Gly
1 5 10 15
Arg Phe Ser Pro Leu Ala Ala Pro Ser Ser Ala Arg Met Leu Ser Pro
20 25 30
Pro Leu Arg Asn Val Val Lys Val Ser Ala Ser Gly Thr Val Leu Val
35 40 45
Glu Lys Ser Glu Ala Glu Lys Thr Gln Arg Leu Lys Thr Ala Tyr Leu
50 55 60

Glu Arg Ile Ile Pro Ala Leu Lys Glu Glu Phe Lys Tyr Val Asn Ile
65 70 75 80
His Gln Val Pro Lys Val Gln Lys Ile Val Val Asn Cys Gly Ile Gly
85 90 95
Asp Ala Ala Gln Asn Asp Lys Gly Leu Glu Ala Ala Met Lys Asp Ile
100 105 110
Ala Leu Ile Thr Gly Gln Lys Pro Ile Lys Thr Arg Ala Arg Ala Ser
115 120 125
Ile Ala Thr Phe Lys Ile Arg Glu Asp Gln Pro Leu Gly Ile Ala Val
130 135 140
Thr Leu Arg Gly Asp Val Met Tyr Ser Phe Leu Asp Arg Leu Ile Asn
145 150 155 160
Leu Ala Leu Pro Arg Thr Arg Asp Phe Gln Gly Val Ser Pro Ser Ser
165 170 175
Phe Asp Gly Asn Gly Asn Tyr Ser Ile Gly Val Lys Asp Gln Gly Val
180 185 190
Phe Pro Glu Ile Arg Phe Asp Ala Val Gly Lys Thr Arg Gly Met Asp
195 200 205
Val Cys Ile Ser Thr Thr Ala Lys Ser Asp Gln Glu Gly Gln Lys Leu
210 215 220
Leu Ala Leu Met Gly Met Pro Phe Arg Glu Gly Gly Gly Ser Thr
225 230 235 240
Gly Ala Ile Val Arg Lys Lys Leu Lys Ser His His Phe Asp Ala
245 250 255
Lys Gly Lys Gly Lys Arg
260

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..234

(D) OTHER INFORMATION: / Ceres Seq. ID 1566390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Met Leu Ser Pro Pro Leu Arg Asn Val Val Lys Val Ser Ala Ser Gly
1 5 10 15
Thr Val Leu Val Glu Lys Ser Glu Ala Glu Lys Thr Gln Arg Leu Lys
20 25 30
Thr Ala Tyr Leu Glu Arg Ile Ile Pro Ala Leu Lys Glu Phe Lys
35 40 45
Tyr Val Asn Ile His Gln Val Pro Lys Val Gln Lys Ile Val Val Asn
50 55 60
Cys Gly Ile Gly Asp Ala Ala Gln Asn Asp Lys Gly Leu Glu Ala Ala
65 70 75 80
Met Lys Asp Ile Ala Leu Ile Thr Gly Gln Lys Pro Ile Lys Thr Arg
85 90 95
Ala Arg Ala Ser Ile Ala Thr Phe Lys Ile Arg Glu Asp Gln Pro Leu
100 105 110
Gly Ile Ala Val Thr Leu Arg Gly Asp Val Met Tyr Ser Phe Leu Asp
115 120 125
Arg Leu Ile Asn Leu Ala Leu Pro Arg Thr Arg Asp Phe Gln Gly Val
130 135 140
Ser Pro Ser Ser Phe Asp Gly Asn Gly Asn Tyr Ser Ile Gly Val Lys
145 150 155 160
Asp Gln Gly Val Phe Pro Glu Ile Arg Phe Asp Ala Val Gly Lys Thr
165 170 175
Arg Gly Met Asp Val Cys Ile Ser Thr Thr Ala Lys Ser Asp Gln Glu

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..103
(D) OTHER INFORMATION: / Ceres Seq. ID 1566397
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:
Met Ala Gln Lys Val Val Leu Lys Val Leu Thr Met Thr Asp Asp Lys
1 5 10 15
Thr Lys Gln Lys Ala Ile Glu Ala Ala Asp Ile Phe Gly Val Asp
20 25 30
Ser Ile Ala Ala Asp Met Lys Asp Gln Lys Leu Thr Val Ile Gly Leu
35 40 45
Met Asp Ala Val Ala Val Val Lys Lys Leu Lys Lys Val Gly Lys Val
50 55 60
Asp Leu Ile Ser Val Gly Pro Ala Lys Glu Glu Lys Lys Glu Glu Lys
65 70 75 80
Lys Glu Glu Lys Lys Lys Glu Lys Lys Glu Glu Lys Lys Glu Glu Lys
85 90 95
Lys Glu Glu Glu Pro Lys Lys
100

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..92
(D) OTHER INFORMATION: / Ceres Seq. ID 1566398
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:
Met Thr Asp Asp Lys Thr Lys Gln Lys Ala Ile Glu Ala Ala Asp
1 5 10 15
Ile Phe Gly Val Asp Ser Ile Ala Ala Asp Met Lys Asp Gln Lys Leu
20 25 30
Thr Val Ile Gly Leu Met Asp Ala Val Ala Val Lys Lys Lys Leu Lys
35 40 45
Lys Val Gly Lys Val Asp Leu Ile Ser Val Gly Pro Ala Lys Glu Glu
50 55 60
Lys Lys Glu Glu Lys Lys Glu Glu Lys Lys Lys Glu Lys Lys Glu Glu
65 70 75 80
Lys Lys Glu Glu Lys Lys Glu Glu Glu Pro Lys Lys
85 90

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1221
(D) OTHER INFORMATION: / Ceres Seq. ID 1566423
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:
aatcaacaca cacaaacaca cacacacaca gcctttttcc ttcgttgatc gattgttaag

二、三、四、五、六、七、八、九、十、十一、十二、十三、十四、十五、十六、十七、十八、十九、二十、二十一、二十二、二十三、二十四、二十五、二十六、二十七、二十八、二十九、三十、三十一、三十二、三十三、三十四、三十五、三十六、三十七、三十八、三十九、四十、四十一、四十二、四十三、四十四、四十五、四十六、四十七、四十八、四十九、五十、五十一、五十二、五十三、五十四、五十五、五十六、五十七、五十八、五十九、六十、六十一、六十二、六十三、六十四、六十五、六十六、六十七、六十八、六十九、七十、七十一、七十二、七十三、七十四、七十五、七十六、七十七、七十八、七十九、八十、八十一、八十二、八十三、八十四、八十五、八十六、八十七、八十八、八十九、九十、九十一、九十二、九十三、九十四、九十五、九十六、九十七、九十八、九十九、一百

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..257

SEQUENCE DESCRIPTION: SEQ ID NO:280:

	1	5	10	15
--	---	---	----	----

20 25 30

35 40 45

50 55 60

65 70 75 80

85 90 95

100 105 110

115 120 125

Mid	Sci	City	Pop	State	Area	Pop	Mid	Sci	City	Pop	State	Area	Pop	Mid	Sci	City	Pop	State	Area	Pop
130						135							140							

Set	City	Inc	Mid	Inc	Mid	Val	City	Inc	Inc	City	Inc	Mid	Mid	City	City
145					150					155					160

110 var the var Ala var Tyr Sin 110 var Sin Thr Leu var var Ala
165 170 175

180 185 190

11e Gly Ala Val Leu 11e 11e Ala Gly Leu Tyr 11e Val Leu Tyr Gly
195 300 305

Lys Ser Glu Glu Arg Lys Phe Ala Ala Leu Glu Lys Ala Glu Ile Gln
210 215 220

Ser Ser Ala Glu His Gly Ile Glu Arg Ala Pro Val Ser Arg Asn Ser

225		230		235		240
Ile	Lys	Ser	Ser	Ile	Thr	Thr
				Pro	Leu	Leu
		245			250	
				His	Gln	Ser
				Thr	Asp	Asn
					255	

Val

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..234
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Met	Leu	Thr	Leu	Gln	Phe	Gly	Tyr	Ala	Gly	Phe	His	Val	Val	Ser	Arg
1			5						10					15	
Ala	Ala	Leu	Asn	Met	Gly	Ile	Ser	Lys	Leu	Val	Phe	Pro	Val	Tyr	Arg
			20					25					30		
Asn	Ile	Ile	Ala	Leu	Leu	Leu	Leu	Pro	Phe	Ala	Tyr	Phe	Leu	Glu	
		35					40				45				
Lys	Lys	Glu	Arg	Pro	Ala	Ile	Thr	Leu	Asn	Phe	Leu	Ile	Gln	Phe	Phe
	50					55				60					
Phe	Leu	Ala	Leu	Ile	Gly	Ile	Thr	Ala	Arg	Leu	Ser	Val	Thr	Ser	Tyr
	65				70				75				80		
Thr	Cys	Phe	Phe	Gly	Ile	Ile	Gln	Phe	Leu	Ile	Ile	Ala	Ala	Phe	Cys
			85					90					95		
Glu	Arg	Asp	Ser	Gln	Ala	Trp	Val	Phe	His	Ser	Gly	Trp	Glu	Leu	Phe
			100					105				110			
Thr	Ile	Leu	Tyr	Ala	Gly	Ile	Val	Ala	Ser	Gly	Ile	Ala	Phe	Ala	Val
		115				120					125				
Gln	Ile	Trp	Cys	Ile	Asp	Arg	Gly	Gly	Pro	Val	Phe	Val	Ala	Val	Tyr
	130				135					140					
Gln	Pro	Val	Gln	Thr	Leu	Val	Val	Ala	Ile	Met	Ala	Ser	Ile	Ala	Leu
	145				150				155					160	
Gly	Glu	Glu	Phe	Tyr	Leu	Gly	Gly	Ile	Ile	Gly	Ala	Val	Leu	Ile	Ile
			165					170					175		
Ala	Gly	Leu	Tyr	Phe	Val	Leu	Tyr	Gly	Lys	Ser	Glu	Glu	Arg	Lys	Phe
		180					185					190			
Ala	Ala	Leu	Glu	Lys	Ala	Glu	Ile	Gln	Ser	Ser	Ala	Glu	His	Gly	Ile
		195				200						205			
Glu	Arg	Ala	Pro	Val	Ser	Arg	Asn	Ser	Ile	Lys	Ser	Ser	Ile	Thr	Thr
	210					215				220					
Pro	Leu	Leu	His	Gln	Ser	Thr	Asp	Asn	Val						
	225				230										

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..214
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Met	Gly	Ile	Ser	Lys	Leu	Val	Phe	Pro	Val	Tyr	Arg	Asn	Ile	Ile	Ala
1			5						10				15		

Leu Leu Leu Leu Leu Pro Phe Ala Tyr Phe Leu Glu Lys Lys Glu Arg
20 25 30
Pro Ala Ile Thr Leu Asn Phe Leu Ile Gln Phe Phe Phe Leu Ala Leu
35 40 45
Ile Gly Ile Thr Ala Arg Leu Ser Val Thr Ser Tyr Thr Cys Phe Phe
50 55 60
Gly Ile Ile Gln Phe Leu Ile Ile Ala Ala Phe Cys Glu Arg Asp Ser
65 70 75 80
Gln Ala Trp Val Phe His Ser Gly Trp Glu Leu Phe Thr Ile Leu Tyr
85 90 95
Ala Gly Ile Val Ala Ser Gly Ile Ala Phe Ala Val Gln Ile Trp Cys
100 105 110
Ile Asp Arg Gly Gly Pro Val Phe Val Ala Val Tyr Gln Pro Val Gln
115 120 125
Thr Leu Val Val Ala Ile Met Ala Ser Ile Ala Leu Gly Glu Glu Phe
130 135 140
Tyr Leu Gly Gly Ile Ile Gly Ala Val Leu Ile Ile Ala Gly Leu Tyr
145 150 155 160
Phe Val Leu Tyr Gly Lys Ser Glu Glu Arg Lys Phe Ala Ala Leu Glu
165 170 175
Lys Ala Glu Ile Gln Ser Ser Ala Glu His Gly Ile Glu Arg Ala Pro
180 185 190
Val Ser Arg Asn Ser Ile Lys Ser Ser Ile Thr Thr Pro Leu Leu His
195 200 205
Gln Ser Thr Asp Asn Val
210

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..604
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

aattcgaaga	gagttcttagc	aaaacaaaac	aaaacagagc	aaacagagta	agtgaacacgA	60
tgtctctagt	tccgagcttt	tttgaggccc	gaagaacaaa	cgtgttcgac	ccattttcac	120
tagacgtatg	ggatccgttc	gaaggattct	tgacgcccg	gttgacaaaac	gcacctgccA	180
aggacgtgtg	agcggttcaca	aacgctaagg	tggactggag	ggagacacct	gaagcgcgatg	240
tgttcaaggg	ggacgtgcct	gggcttaaga	aggaagaggt	gaaggtggag	gttgaagatg	300
gtaacatact	tcagataagc	ggtgagagga	gcagtgagaa	tgaagagaag	agtgacacct	360
ggcaccgtgt	ggagcgggtca	agtggaagat	tcatgaggag	gtttaggttg	ccagacaagt	420
caaaagtgga	ggaagtaaa	gcgagtatgg	agaatggtgt	gtgtcggtt	acggtgccga	480
aagttcagga	gagtaagccg	gaggtcaagt	ccattgatat	ctctggttaa	gaggaaactct	540
gaagttggaa	agcttaagac	agtaatatgt	gatagtgtga	aataaatggt	gcgactttcc	600
ttcc						

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Phe Glu Glu Ser Ser Ser Lys Thr Lys Gln Asn Arg Ala Asn Arg Val
1 5 10 15
Ser Glu Thr Met Ser Leu Val Pro Ser Phe Phe Gly Gly Arg Arg Thr
20 25 30
Asn Val Phe Asp Pro Phe Ser Leu Asp Val Trp Asp Pro Phe Glu Gly
35 40 45
Phe Leu Thr Pro Gly Leu Thr Asn Ala Pro Ala Lys Asp Val Ala Ala
50 55 60
Phe Thr Asn Ala Lys Val Asp Trp Arg Glu Thr Pro Glu Ala His Val
65 70 75 80
Phe Lys Ala Asp Val Pro Gly Leu Lys Lys Glu Glu Val Lys Val Glu
85 90 95
Val Glu Asp Gly Asn Ile Leu Gln Ile Ser Gly Glu Arg Ser Ser Glu
100 105 110
Asn Glu Glu Lys Ser Asp Thr Trp His Arg Val Glu Arg Ser Ser Gly
115 120 125
Lys Phe Met Arg Arg Phe Arg Leu Pro Asp Asn Ala Lys Val Glu Glu
130 135 140
Val Lys Ala Ser Met Glu Asn Gly Val Leu Ser Val Thr Val Pro Lys
145 150 155 160
Val Gln Glu Ser Lys Pro Glu Val Lys Ser Ile Asp Ile Ser Gly
165 170 175

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Met Ser Leu Val Pro Ser Phe Phe Gly Gly Arg Arg Thr Asn Val Phe
1 5 10 15
Asp Pro Phe Ser Leu Asp Val Trp Asp Pro Phe Glu Gly Phe Leu Thr
20 25 30
Pro Gly Leu Thr Asn Ala Pro Ala Lys Asp Val Ala Ala Phe Thr Asn
35 40 45
Ala Lys Val Asp Trp Arg Glu Thr Pro Glu Ala His Val Phe Lys Ala
50 55 60
Asp Val Pro Gly Leu Lys Lys Glu Glu Val Lys Val Glu Val Glu Asp
65 70 75 80
Gly Asn Ile Leu Gln Ile Ser Gly Glu Arg Ser Ser Glu Asn Glu Glu
85 90 95
Lys Ser Asp Thr Trp His Arg Val Glu Arg Ser Ser Gly Lys Phe Met
100 105 110
Arg Arg Phe Arg Leu Pro Asp Asn Ala Lys Val Glu Glu Val Lys Ala
115 120 125
Ser Met Glu Asn Gly Val Leu Ser Val Thr Val Pro Lys Val Gln Glu
130 135 140
Ser Lys Pro Glu Val Lys Ser Ile Asp Ile Ser Gly
145 150 155

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1325

(D) OTHER INFORMATION: / Ceres Seq. ID 1566453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```

aaCttctcct cggatgcact attgtccgtg agatcagaga ttccacctct ttagatatttg      60
cgcagaaaact tttgccacaca attttgtttt ctacaaaactt gagctgagat ctctagagtg      120
agaaaaatgag catcactaat gaagaagcag tgaagcaatt gcgtgcttta atggaagatg      180
ttgatgattc actcagagag tcgtatcggg acattcatca agggatattcc acagagaatt      240
tgttactgctt tcttaaagcc agggatggga atgtccagaa agctcataaa attgttgctg      300
ctgtgtttgga atggaggagt caaaacgaga ttgacaagat actaactaaa cccattgttc      360
ctgttgacct gtacagagag atcagagaca cacaacttgt cgggtgtgct ggttactcta      420
aagaggggtct cctgtcatt gccattggtg tggggccttag cacatatgat aaagcctccg      480
ttcactacta tgtacagtct cacattcaaa tgaatgagta ccgggatcgt gttgtattgc      540
catctgcttc aaagaaacag ggacgaccaa ttgacacttg ttgaaaaatt ttggatatgt      600
ctggttttaaa gctttcagct ttaagtcaaa ttaagttaat gactgctata acaacaatag      660
atgatttgaa ctatccagag aagacagaga catactatgt tgtcaatgct ccgtacatat      720
tctctgctgt ttggaaaacc ataaagcctc tgttgcaaga gagaacaaag aagaagatc      780
aagttctgaa aggttgccgg aaagatgagt tgctaaagat aatggactat gactctctcc      840
cacattctgt tagaagagaa gggctctggat ctggtaggca tatctcaaat ggaacagtag      900
acaattgttt ctctctggat cactctttcc accaagacct ttatgattat gtcaagcagc      960
aggtctctgg taaaggatca ggtgcaccga tcagacatgg ttccagtcac gttaatgttc      1020
ctgagccaag caccgaagcg aacaagatct tgcatacctt agaaaatgag ttccagaagc      1080
ttggaatatg ccagaagatc tgagtgatct acaaccctta taacacgaat tgcccataag      1140
aaaccggaaat ttgtctctgg ttgatgagca gtatttaaga taagaatcaa tcacctttac      1200
ttgtattact agtttcgctt gcatacgtc gatgcaggtt ttttttaaaa agaagatgga      1260
acacaatttc ctccgaatg atcttttgat ctagtaccat tatatatata gaactcattt      1320
ctatc

```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..325

(D) OTHER INFORMATION: / Ceres Seq. ID 1566454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```

Met Ser Ile Thr Asn Glu Glu Ala Val Lys Gln Leu Arg Ala Leu Met
1           5           10           15
Glu Asp Val Asp Ser Leu Arg Glu Ser Tyr Arg Asn Ile His Gln
20           25           30
Gly Tyr Pro Thr Glu Asn Leu Leu Arg Phe Leu Lys Ala Arg Asp Gly
35           40           45
Asn Val Gln Lys Ala His Lys Met Leu Leu Glu Cys Leu Glu Trp Arg
50           55           60
Thr Gln Asn Glu Ile Asp Lys Ile Leu Thr Lys Pro Ile Val Pro Val
65           70           75           80
Asp Leu Tyr Arg Gly Ile Arg Asp Thr Gln Leu Val Gly Val Ser Gly
85           90           95
Tyr Ser Lys Glu Gly Leu Pro Val Ile Ala Ile Gly Val Gly Leu Ser
100          105          110
Thr Tyr Asp Lys Ala Ser Val His Tyr Tyr Val Gln Ser His Ile Gln
115          120          125
Met Asn Glu Tyr Arg Asp Arg Val Val Leu Pro Ser Ala Ser Lys Lys
130          135          140
Gln Gly Arg Pro Ile Cys Thr Cys Leu Lys Ile Leu Asp Met Ser Gly
145          150          155          160
Leu Lys Leu Ser Ala Leu Ser Gln Ile Lys Leu Met Thr Ala Ile Thr

```

```

(2) INFORMATION FOR SEQ ID NO:288:
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 310 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: peptide
  (ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..310
      (D) OTHER INFORMATION: / Ceres Seq. ID 1566455
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:
Met Glu Asp Val Asp Asp Ser Leu Arg Glu Ser Tyr Arg Asn Ile His
1          5          10          15
Gln Gly Tyr Pro Thr Glu Asn Leu Leu Arg Phe Leu Cys Ala Arg Asp
          20          25          30
Gly Asn Val Gln Lys Ala His Lys Met Leu Leu Glu Cys Leu Glu Trp
          35          40          45
Arg Thr Gln Asn Glu Ile Asp Lys Ile Leu Thr Lys Pro Ile Val Pro
50          55          60
Val Asp Leu Tyr Arg Gly Ile Arg Asp Thr Gln Leu Val Gly Val Ser
65          70          75          80
Gly Tyr Ser Lys Glu Gly Leu Pro Val Ile Ala Ile Gly Val Gly Leu
          85          90          95
Ser Thr Tyr Asp Lys Ala Ser Val His Tyr Tyr Val Gln Ser His Ile
          100          105          110
Gln Met Asn Glu Tyr Arg Asp Arg Val Val Leu Pro Ser Ala Ser Lys
          115          120          125
Lys Gln Gly Arg Pro Ile Cys Thr Cys Leu Lys Ile Leu Asp Met Ser
130          135          140
Gly Leu Lys Leu Ser Ala Leu Ser Gln Ile Lys Leu Met Thr Ala Ile
145          150          155          160
Thr Thr Ile Asp Asp Leu Asn Tyr Pro Glu Lys Thr Glu Thr Tyr Tyr
          165          170          175
Val Val Asn Val Pro Tyr Ile Phe Ser Ala Cys Trp Lys Thr Ile Lys
          180          185          190
Pro Leu Leu Gln Glu Arg Thr Lys Lys Lys Ile Gln Val Leu Lys Gly
          195          200          205
Cys Gly Lys Asp Glu Leu Leu Lys Ile Met Asp Tyr Glu Ser Leu Pro
210          215          220

```

His Phe Cys Arg Arg Glu Gly Ser Gly Ser Gly Arg His Ile Ser Asn
225 230 235 240
Gly Thr Val Asp Asn Cys Phe Ser Leu Asp His Ser Phe His Gln Asp
245 250 255
Leu Tyr Asp Tyr Val Lys Gln Gln Ala Leu Val Lys Gly Ser Gly Ala
260 265 270
Pro Ile Arg His Gly Ser Val His Val Lys Phe Pro Glu Pro Asp Thr
275 280 285
Glu Gly Asn Lys Ile Phe Asp Thr Leu Glu Asn Glu Phe Gln Lys Leu
290 295 300
Gly Asn Asp Gln Lys Ile
305 310

(2) INFORMATION FOR SEQ ID NO:289:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..270
(D) OTHER INFORMATION: / Ceres Seq. ID 1566456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Met Leu Leu Glu Cys Leu Glu Trp Arg Thr Gln Asn Glu Ile Asp Lys
1 5 10 15
Ile Leu Thr Lys Pro Ile Val Pro Val Asp Leu Tyr Arg Gly Ile Arg
20 25 30
Asp Thr Gln Leu Val Gly Val Ser Gly Tyr Ser Lys Glu Gly Leu Pro
35 40 45
Val Ile Ala Ile Gly Val Gly Leu Ser Thr Tyr Asp Lys Ala Ser Val
50 55 60
His Tyr Tyr Val Gln Ser His Ile Gln Met Asn Glu Tyr Arg Asp Arg
65 70 75 80
Val Val Leu Pro Ser Ala Ser Lys Lys Gln Gly Arg Pro Ile Cys Thr
85 90 95
Cys Leu Lys Ile Leu Asp Met Ser Gly Leu Lys Leu Ser Ala Leu Ser
100 105 110
Gln Ile Lys Leu Met Thr Ala Ile Thr Thr Ile Asp Asp Leu Asn Tyr
115 120 125
Pro Glu Lys Thr Glu Thr Tyr Tyr Val Val Asn Val Pro Tyr Ile Phe
130 135 140
Ser Ala Cys Trp Lys Thr Ile Lys Pro Leu Leu Gln Glu Arg Thr Lys
145 150 155 160
Lys Lys Ile Gln Val Leu Lys Gly Cys Gly Lys Asp Glu Leu Leu Lys
165 170 175
Ile Met Asp Tyr Glu Ser Leu Pro His Phe Cys Arg Arg Glu Gly Ser
180 185 190
Gly Ser Gly Arg His Ile Ser Asn Gly Thr Val Asp Asn Cys Phe Ser
195 200 205
Leu Asp His Ser Phe His Gln Asp Leu Tyr Asp Tyr Val Lys Gln Gln
210 215 220
Ala Leu Val Lys Gly Ser Gly Ala Pro Ile Arg His Gly Ser Val His
225 230 235 240
Val Lys Phe Pro Glu Pro Asp Thr Glu Gly Asn Lys Ile Phe Asp Thr
245 250 255
Leu Glu Asn Glu Phe Gln Lys Leu Gly Asn Asp Gln Lys Ile
260 265 270

(2) INFORMATION FOR SEQ ID NO:290:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1767 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1767
(D) OTHER INFORMATION: / Ceres Seq. ID 1566468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

```
catcttttct tctccctctt gctcttctgc aactgtatcc ctcagctctc 60
catctccgtc ttccaaggtg gaagaatcca tgtcgattta cgtcgcgctg cgaCgGnctc 120
tcggcgagaa caactgtgac ggcgcgtcgt tatgccacct ctctgagatc ttattcgacc 180
tcgtttTagg gaggagaggg acaccttcgg gccgattcaa gtctctcccg ataatgtgtg 240
gggagccagg acgcagagat cgctgcagaa cttcgaaatc ggtggtgagc gcgagCGaNa 300
tgccctgaacc aattgtccgc gcttttggcg tcttgaagaa atgcgctcgc aaggttaaca 360
tggaatcagg tcttgatccg acgattggga aagcaattat gcaagctgct cagggaagtag 420
ctgaggggaa gctcaatgat catctccccc ttgttgtctg gcaaaactgg agtggtactc 480
agagtataat gaatgctaatt gaggtcattg ctaatatagc agctgagatt cttggtcgca 540
aacgtgttga gaaatgtgtg caccacaagt accatgtgaa cagatcacaa tcttctaacc 600
acacttttcc taccgtctat cacattgcag ctgcaaccga gattaattgc aggctcatcc 660
ctagttttaa aactttgcat agcacttttg aatctaagtc cttcgagttc aaagatattg 720
tgaaaattgg aagaactcac actcaaatgt ctacaccttt gacactagga caagaatttg 780
gtgctatctg tactcaagtt aagtatggac taaatatagc cacctgcaact cttcctgcgc 840
tctatcagct tgcacaaggt ggaactcggg ttgggacagg attaaacact aagaaaaggt 900
ttgatgtaaa gatagctgct gcagtagctg aagaaacaaa cttgccaatt gtcactcagg 960
aaaaaagttt tgaagctctg gctgcacacg atgctttgtg tgaaccacgt ggttcaacta 1020
acacaatcgc cactcgtctg atgaagatcg ccaatgatat agcttttctt ggaagtggcc 1080
caagatgtgg tcttgggtgaa cttgtactac ctgaaaatga gccagggaagc agtatcatgc 1140
ctgggaaggt aatccttaca cagtgtgagg ccttgactat ggtttgtgca caggttatgg 1200
gaacacatgt agctgtgaca gttgtgggtt caaatgggtc attcgatgca atgtattca 1260
agccggtgat cgcgagtgct cttttacatt ccgtcaagatt aatagcagat gcttcagttg 1320
cgttcgagaa aaactgtgtg agggcgattg agggccaacg agaaaagatc tcaaaagctat 1380
tgcaacgagtc tcttatgctt gtgacatcat tgaatccgaa aatcgggtag gacaatgctg 1440
cagcagttgc caagaaagct cacaagaagc gatgtacatt gaagggaagc gctctgaatt 1500
taggcgtgct tactcgggaa gagtttgata cttgttgtt tcttgagaag atgattggtc 1560
cttcgcgattg atagtgtttt ttggagccaa agcttcaagt accattatc tcttgatgct 1620
tttatttagg ttataataaa aatgagcaaa tccagaaaaa attcaaatc tcttgggagg 1680
gcaacattgt tcttcatctt accgctaaac tatgatctc tttatgtatc aatttttttt 1740
```

(2) INFORMATION FOR SEQ ID NO:291:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 522 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..522
(D) OTHER INFORMATION: / Ceres Seq. ID 1566469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

```
Ile Phe Leu Ser Pro Ser Ala Leu Val Gln Leu Asp Pro Ser Ser Ser
1 5 10 15
Leu Ser Ser Pro Ser Pro Ser Ser Lys Val Glu Glu Ser Met Ser Ile
20 25 30
Tyr Val Ala Ser Arg Arg Xaa Leu Arg Arg Asn Asn Cys Asp Gly Ala
35 40 45
Ala Leu Cys His Leu Ser Glu Ile Leu Phe Asp Leu Val Leu Gly Arg
50 55 60
Arg Gly Thr Pro Ser Glu Arg Phe Lys Phe Leu Pro Ile Asn Cys Gly
65 70 75 80
```

Glu	Pro	Arg	Arg	Arg	Asp	Arg	Cys	Arg	Thr	Ser	Lys	Ser	Val	Val	Ser
				85					90					95	
Ala	Ser	Xaa	Met	Pro	Glu	Pro	Ile	Val	Arg	Ala	Phe	Gly	Val	Leu	Lys
			100					105					110		
Lys	Cys	Ala	Ala	Lys	Val	Asn	Met	Glu	Tyr	Gly	Leu	Asp	Pro	Thr	Ile
		115				120						125			
Gly	Lys	Ala	Ile	Met	Gln	Ala	Ala	Gln	Glu	Val	Ala	Glu	Gly	Lys	Leu
		130				135					140				
Asn	Asp	His	Phe	Pro	Leu	Val	Val	Trp	Gln	Thr	Gly	Ser	Gly	Thr	Gln
145				150					155					160	
Ser	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Arg	Ala	Ala	Glu	Ile
			165						170					175	
Leu	Gly	Arg	Lys	Arg	Gly	Glu	Lys	Cys	Val	His	Pro	Asn	Asp	His	Val
			180						185					190	
Asn	Arg	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Val	Met	His	Ile
			195				200					205			
Ala	Ala	Ala	Thr	Glu	Ile	Asn	Ser	Arg	Leu	Ile	Pro	Ser	Leu	Lys	Thr
			210			215					220				
Leu	His	Ser	Thr	Leu	Glu	Ser	Lys	Ser	Phe	Glu	Phe	Lys	Asp	Ile	Val
225				230					235					240	
Lys	Ile	Gly	Arg	Thr	His	Thr	Gln	Asp	Ala	Thr	Pro	Leu	Thr	Leu	Gly
			245						250					255	
Gln	Glu	Phe	Gly	Gly	Tyr	Ala	Thr	Gln	Val	Lys	Tyr	Gly	Leu	Asn	Arg
			260					265						270	
Val	Thr	Cys	Thr	Leu	Pro	Arg	Leu	Tyr	Gln	Leu	Ala	Gln	Gly	Gly	Thr
			275				280					285			
Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	Lys	Lys	Gly	Phe	Asp	Val	Lys	Ile
			290			295					300				
Ala	Ala	Ala	Val	Ala	Glu	Glu	Thr	Asn	Leu	Pro	Phe	Val	Thr	Ala	Glu
305				310					315					320	
Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Cys	Val	Glu	Thr	Ser
			325						330					335	
Gly	Ser	Leu	Asn	Thr	Ile	Ala	Thr	Ser	Leu	Met	Lys	Ile	Ala	Asn	Asp
			340					345					350		
Ile	Arg	Phe	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu	Gly	Glu	Leu	Val
			355				360					365			
Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn
			370			375					380				
Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	Met	Val	Cys	Ala	Gln	Val	Met	Gly
385				390						395				400	
Asn	His	Val	Ala	Val	Thr	Val	Gly	Gly	Ser	Asn	Gly	His	Phe	Glu	Leu
			405						410					415	
Asn	Val	Phe	Lys	Pro	Val	Ile	Ala	Ser	Ala	Leu	Leu	His	Ser	Val	Arg
			420					425				430			
Leu	Ile	Ala	Asp	Ala	Ser	Ala	Ser	Phe	Glu	Lys	Asn	Cys	Val	Arg	Gly
			435				440					445			
Ile	Glu	Ala	Asn	Arg	Glu	Arg	Ile	Ser	Lys	Leu	Leu	His	Glu	Ser	Leu
450				455							460				
Met	Leu	Val	Thr	Ser	Leu	Asn	Pro	Lys	Ile	Gly	Tyr	Asp	Asn	Ala	Ala
465				470					475					480	
Ala	Val	Ala	Lys	Lys	Ala	His	Lys	Glu	Gly	Cys	Thr	Leu	Lys	Glu	Ala
			485						490					495	
Ala	Leu	Asn	Leu	Gly	Val	Leu	Thr	Ala	Glu	Glu	Phe	Asp	Thr	Leu	Val
			500					505						510	
Val	Pro	Glu	Lys	Met	Ile	Gly	Pro	Ser	Asp						
			515			520									

(2) INFORMATION FOR SEQ ID NO:292:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 493 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..493
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Met	Ser	Ile	Tyr	Val	Ala	Ser	Arg	Arg	Xaa	Leu	Arg	Arg	Asn	Asn	Cys
1				5					10					15	
Asp	Gly	Ala	Ala	Leu	Cys	His	Leu	Ser	Glu	Ile	Leu	Phe	Asp	Leu	Val
			20					25					30		
Leu	Gly	Arg	Arg	Gly	Thr	Pro	Ser	Gly	Arg	Phe	Lys	Phe	Leu	Pro	Ile
			35				40					45			
Asn	Cys	Gly	Glu	Pro	Arg	Arg	Arg	Asp	Arg	Cys	Arg	Thr	Ser	Lys	Ser
			50			55					60				
Val	Val	Ser	Ala	Ser	Xaa	Met	Pro	Glu	Pro	Ile	Val	Arg	Ala	Phe	Gly
65					70					75				80	
Val	Leu	Lys	Lys	Cys	Ala	Ala	Lys	Val	Asn	Met	Glu	Tyr	Gly	Leu	Asp
				85					90					95	
Pro	Thr	Ile	Gly	Lys	Ala	Ile	Met	Gln	Ala	Ala	Gln	Glu	Val	Ala	Glu
			100					105					110		
Gly	Lys	Leu	Asn	Asp	His	Phe	Pro	Leu	Val	Val	Trp	Gln	Thr	Gly	Ser
			115				120					125			
Gly	Thr	Gln	Ser	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Arg	Ala
			130				135					140			
Ala	Glu	Ile	Leu	Gly	Arg	Lys	Arg	Gly	Glu	Lys	Cys	Val	His	Pro	Asn
145					150					155				160	
Asp	His	Val	Asn	Arg	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Val
				165					170					175	
Met	His	Ile	Ala	Ala	Ala	Thr	Glu	Ile	Asn	Ser	Arg	Leu	Ile	Pro	Ser
			180					185					190		
Leu	Lys	Thr	Leu	His	Ser	Thr	Leu	Glu	Ser	Lys	Ser	Phe	Glu	Phe	Lys
			195				200					205			
Asp	Ile	Val	Lys	Ile	Gly	Arg	Thr	His	Thr	Gln	Asp	Ala	Thr	Pro	Leu
						215					220				
Thr	Leu	Gly	Gln	Glu	Phe	Gly	Gly	Tyr	Ala	Thr	Gln	Val	Lys	Tyr	Gly
225					230					235				240	
Leu	Asn	Arg	Val	Thr	Cys	Thr	Leu	Pro	Arg	Leu	Tyr	Gln	Leu	Ala	Gln
				245					250					255	
Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	Lys	Lys	Gly	Phe	Asp
			260					265					270		
Val	Lys	Ile	Ala	Ala	Ala	Val	Ala	Glu	Glu	Thr	Asn	Leu	Pro	Phe	Val
			275				280					285			
Thr	Ala	Glu	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Cys	Val
			290			295					300				
Glu	Thr	Ser	Gly	Ser	Leu	Asn	Thr	Ile	Ala	Thr	Ser	Leu	Met	Lys	Ile
305					310					315				320	
Ala	Asn	Asp	Ile	Arg	Phe	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu	Gly
			325						330					335	
Glu	Leu	Val	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly
			340					345					350		
Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	Met	Val	Cys	Ala	Gln
			355				360					365			
Val	Met	Gly	Asn	His	Val	Ala	Val	Thr	Val	Gly	Gly	Ser	Asn	Gly	His
			370			375					380				
Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Val	Ile	Ala	Ser	Ala	Leu	Leu	His
385					390					395				400	
Ser	Val	Arg	Leu	Ile	Ala	Asp	Ala	Ser	Ala	Ser	Phe	Glu	Lys	Asn	Cys
			405					410						415	
Val	Arg	Gly	Ile	Glu	Ala	Asn	Arg	Glu	Arg	Ile	Ser	Lys	Leu	Leu	His
			420				425						430		

Glu	Ser	Leu	Met	Leu	Val	Thr	Ser	Leu	Asn	Pro	Lys	Ile	Gly	Tyr	Asp	
	435						440					445				
Asn	Ala	Ala	Ala	Val	Ala	Lys	Lys	Ala	His	Lys	Glu	Gly	Cys	Thr	Leu	
	450					455					460					
Lys	Glu	Ala	Ala	Leu	Asn	Leu	Gly	Val	Leu	Thr	Ala	Glu	Glu	Phe	Asp	
465				470					475						480	
Thr	Leu	Val	Val	Pro	Glu	Lys	Met	Ile	Gly	Pro	Ser	Asp				
			485					490								

(2) INFORMATION FOR SEQ ID NO:293:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 423 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..423

(D) OTHER INFORMATION: / Ceres Seq. ID 1566471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

Met	Pro	Glu	Pro	Ile	Val	Arg	Ala	Phe	Gly	Val	Leu	Lys	Lys	Cys	Ala	
1			5						10					15		
Ala	Lys	Val	Asn	Met	Glu	Tyr	Gly	Leu	Asp	Pro	Thr	Ile	Gly	Lys	Ala	
		20					25						30			
Ile	Met	Gln	Ala	Ala	Gln	Glu	Val	Ala	Glu	Gly	Lys	Leu	Asn	Asp	His	
		35				40					45					
Phe	Pro	Leu	Val	Val	Trp	Gln	Thr	Gly	Ser	Gly	Thr	Gln	Ser	Asn	Met	
	50				55					60						
Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Arg	Ala	Ala	Glu	Ile	Leu	Gly	Arg	
65				70				75						80		
Lys	Arg	Gly	Glu	Lys	Cys	Val	His	Pro	Asn	Asp	His	Val	Asn	Arg	Ser	
				85				90						95		
Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Val	Met	His	Ile	Ala	Ala	Ala	
			100					105				110				
Thr	Glu	Ile	Asn	Ser	Arg	Leu	Ile	Pro	Ser	Leu	Lys	Thr	Leu	His	Ser	
	115				120						125					
Thr	Leu	Glu	Ser	Lys	Ser	Phe	Glu	Phe	Lys	Asp	Ile	Val	Lys	Ile	Gly	
	130				135					140						
Arg	Thr	His	Thr	Gln	Asp	Ala	Thr	Pro	Leu	Thr	Leu	Gly	Gln	Glu	Phe	
145				150					155					160		
Gly	Gly	Tyr	Ala	Thr	Gln	Val	Lys	Tyr	Gly	Leu	Asn	Arg	Val	Thr	Cys	
			165					170					175			
Thr	Leu	Pro	Arg	Leu	Tyr	Gln	Leu	Ala	Gln	Gly	Gly	Thr	Ala	Val	Gly	
	180						185					190				
Thr	Gly	Leu	Asn	Thr	Lys	Lys	Gly	Phe	Asp	Val	Lys	Ile	Ala	Ala	Ala	
	195				200						205					
Val	Ala	Glu	Glu	Thr	Asn	Leu	Pro	Phe	Val	Thr	Ala	Glu	Asn	Lys	Phe	
	210				215					220						
Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Cys	Val	Glu	Thr	Ser	Gly	Ser	Leu	
225					230					235					240	
Asn	Thr	Ile	Ala	Thr	Ser	Leu	Met	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Phe	
			245					250						255		
Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu	Gly	Glu	Leu	Val	Leu	Pro	Glu	
		260					265					270				
Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	
	275					280						285				
Cys	Glu	Ala	Leu	Thr	Met	Val	Cys	Ala	Gln	Val	Met	Gly	Asn	His	Val	
	290				295						300					
Ala	Val	Thr	Val	Gly	Gly	Ser	Asn	Gly	His	Phe	Glu	Leu	Asn	Val	Phe	
305					310					315						
Lys	Pro	Val	Ile	Ala	Ser	Ala	Leu	Leu	His	Ser	Val	Arg	Leu	Ile	Ala	

325 330 335
Asp Ala Ser Ala Ser Phe Glu Lys Asn Cys Val Arg Gly Ile Glu Ala
340 345 350
Asn Arg Glu Arg Ile Ser Lys Leu Leu His Glu Ser Leu Met Leu Val
355 360 365
Thr Ser Leu Asn Pro Lys Ile Gly Tyr Asp Asn Ala Ala Val Ala
370 375 380
Lys Lys Ala His Lys Glu Gly Cys Thr Leu Lys Glu Ala Ala Leu Asn
385 390 395 400
Leu Gly Val Leu Thr Ala Glu Glu Phe Asp Thr Leu Val Val Pro Glu
405 410 415
Lys Met Ile Gly Pro Ser Asp
420

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

aacaattcag	atttcaattt	ctcaaaatct	taaaaacttt	ctctcaattc	tctctacogt	60
gatcaagatg	cagatctttg	ttaagactct	cacccgaaag	acaatcaccc	togaggtgga	120
aagctccgac	accatcgaca	acgttaaggc	caagatccag	gataaggagg	gcattctctc	180
ggatcgcagc	aggcttattt	tgcgcggcaa	gcagctagag	gatggccgta	cgttggctga	240
ttacaatatc	cagaaggaat	ccaccctcca	cttggtcctc	aggctccgtg	gtgggtatga	300
gattttcggt	aaaaccctaa	cgggaaagac	gattactctt	gaggtggaga	gttctgacac	360
catcgacaac	gtcaaaggcca	agatccaaga	caaagagggt	attcctccgg	accagcagag	420
gctgatcttc	gccggaaagc	agttggagga	tggcagaact	cttGgctgac	tacaayatyc	480
agaaggagtc	cacmcttcaT	cttgkcttTG	cAgkctscgt	gwggtatgc	agatyttcgt	540
kaagactctc	acyggaaaaga	ccatcacttt	ggaggtggag	agttctgaca	ccattgataa	600
cgtgaaagcc	aagatccagg	acaaagaggg	tatycctccg	taccacagca	gattgatctt	660
cgccggaaag	caacttgarg	atgghagaac	tttggcbgac	tacaacattc	agaaggagtc	720
cacmcttcac	ttggtcttgc	gtctgcgtgg	aggatgacag	attcttgtsa	agactytbac	780
cggaagagacy	atcacyytkg	argtrgarag	ctcygacacc	attgacaacg	tcaaggccaa	840
gatccaggac	aaggaaggtta	tctctccgga	ccagcagcgt	ctcatcttgg	ctggaaagca	900
gcttgaggat	ggagctactt	tggccgacta	caacatccag	aaggagctcta	ctcttcaactt	960
ggctcctgct	cttcgttggtg	gttttcaaat	ctcgtctctg	ttatgcttaa	gaagttcaat	1020
gtttcggttt	atgtaaaact	tgtgtgtggt	gtgttttggg	gcctgtgata	atccctgatg	1080
aataagtggt	ctactatggt	tccggt				

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Thr	Ile	Gln	Ile	Ser	Ile	Ser	Gln	Asn	Leu	Lys	Asn	Phe	Leu	Ser	Ile	
1			5					10				15				
Leu	Ser	Thr	Val	Ile	Lys	Met	Gln	Ile	Phe	Val	Lys	Thr	Leu	Thr	Gly	
			20					25				30				
Lys	Thr	Ile	Thr	Leu	Glu	Val	Glu	Ser	Ser	Asp	Thr	Ile	Asp	Asn	Val	

35 40 45
Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg
50 55 60
Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp
65 70 75 80
Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg
85 90 95
Gly Gly Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr
100 105 110
Leu Glu Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile
115 120 125
Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala
130 135 140
Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Gly
145 150 155

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..133

- (D) OTHER INFORMATION: / Ceres Seq. ID 1566507
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
1 5 10 15
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp
20 25 30
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35 40 45
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu
50 55 60
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe
65 70 75 80
Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser
85 90 95
Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile
100 105 110
Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
115 120 125
Gly Arg Thr Leu Gly
130

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

- (D) OTHER INFORMATION: / Ceres Seq. ID 1566508
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

Met Gln Xaa Phe Xaa Lys Thr Leu Xaa Gly Lys Thr Ile Thr Leu Glu
1 5 10 15
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp
20 25 30

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Lys Glu Gly Xaa Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
      35              40              45
Gln Leu Xaa Asp Xaa Arg Thr Leu Xaa Asp Tyr Asn Ile Gln Lys Glu
      50              55              60
Ser Xaa Leu His Leu Val Leu Arg Leu Arg Gly Met Gln Ile Phe
      65              70              75              80
Xaa Lys Thr Xaa Thr Gly Lys Xaa Ile Xaa Xaa Xaa Xaa Ser Xaa
      85              90              95
Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile
      100             105             110
Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
      115             120             125
Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His
      130             135             140
Leu Val Leu Arg Leu Arg Gly Gly Phe
      145             150

```

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1217
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

```

atcttatctc aactctcaaa atcatcttct tcacccaaaa acccctaataa gccttatccc
120
ttcttctctc catgctgtct tcagctctct tctcgtctct tcttctctca accctaataat
180
tcttctctct ggcgtctcca gacctgcctc cgtttccctc ttatctcctt cctctctcctt
240
taaaactcaat tccgactccg ttctctctc catcgccgcc aaatggaact cctccgcttc
300
tcgcttcgtc cgtaacgttg cgattacctc agagtccgag gtggaagaag atggtttcgc
360
tgacgtcgtc ccgcaaaaag agcaatcttt ctctgctgac cttaaaactc tcgtttggtaa
420
ccttctcttc aacgttgaca gtgctcagct cgctcagctc ttgagagtg ccggaatagt
480
tgagatggtt gaggttaact atgacaaaat tacaggaaga agcagaggtt ttgattcgt
540
gactatgtct tcagtttctg aagttgaggc agctgctcag cagttcaatg gctatgagtt
600
ggatggtaga cctttgagag tcaatgctgg tccccacca ccaagagggg aagatgggtt
660
ctccaggaga cctaggagca gctttggaag ctacaggttct ggataggag gaggtgggtg
720
ttctggtgct ggttcaggaa accgtgttta tgtgggtaac ctctcttggg gagttgatga
780
catggctctt gagagtttgt tctcggagca agaaaaggtt gttgaggcca gactcatcta
840
cgacagggac agtggctgat ccaagggttt tggatttggt acatacgact ctctccaaga
900
ggctcaaaat gccatcaagt ccttggatgg tgctgatttg gacggtagac aaatagagt
960
ctcggaagct gaggctaggg ctccaaggcg ccaatatgga gcaccaatct atgacttctc
1020
attctcaaaa acgcatattc tggaggggcg ttogaagtaa agagggtttg tgagatgatg
1080
gcagtttcag acggtactcaa gctcttagct tcgcctatgt ttgttccttt ggatgcaaga
1140
aggtcgtaaa ggaatggctt tttttttttt gagaacgta taattaagat agaactgga
1200
ggagccatgt tcttgtctgt ctgaatgctg ccattgactg Cctcgtttg gttttgattc

```

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

Ser Tyr Leu Asn Ser Gln Asn His Leu Leu His Pro Lys Thr Pro Lys
1 5 10 15
Ser Leu Ile Pro Ser Ser Ser His Gly Cys Phe Ser Ser Ser Leu Ala
20 25 30
Leu Ser Ser Phe Asn Pro Lys Ser Leu Pro Phe Gly Val Ser Arg Pro
35 40 45
Ala Ser Val Ser Leu Leu Ser Pro Ser Leu Ser Phe Lys Leu Asn Ser
50 55 60
Asp Ser Val Ser Phe Ser Ile Ala Ala Lys Trp Asn Ser Pro Ala Ser
65 70 75 80
Arg Phe Val Arg Asn Val Ala Ile Thr Ser Glu Phe Glu Val Glu Glu
85 90 95
Asp Gly Phe Ala Asp Val Ala Pro Pro Lys Glu Gln Ser Phe Ser Ala
100 105 110
Asp Leu Lys Leu Phe Val Gly Asn Leu Pro Phe Asn Val Asp Ser Ala
115 120 125
Gln Leu Ala Gln Leu Phe Glu Ser Ala Gly Asn Val Glu Met Val Glu
130 135 140
Val Ile Tyr Asp Lys Ile Thr Gly Arg Ser Arg Gly Phe Gly Phe Val
145 150 155 160
Thr Met Ser Ser Val Ser Glu Val Glu Ala Ala Gln Gln Phe Asn
165 170 175
Gly Tyr Glu Leu Asp Gly Arg Pro Leu Arg Val Asn Ala Gly Pro Pro
180 185 190
Pro Pro Lys Arg Glu Asp Gly Phe Ser Arg Gly Pro Arg Ser Ser Phe
195 200 205
Gly Ser Ser Gly Ser Gly Tyr Gly Gly Gly Gly Ser Gly Ala Gly
210 215 220
Ser Gly Asn Arg Val Tyr Val Gly Asn Leu Ser Trp Gly Val Asp Asp
225 230 235 240
Met Ala Leu Glu Ser Leu Phe Ser Glu Gln Gly Lys Val Val Glu Ala
245 250 255
Arg Val Ile Tyr Asp Arg Asp Ser Gly Arg Ser Lys Gly Phe Gly Phe
260 265 270
Val Thr Tyr Asp Ser Ser Gln Glu Val Gln Asn Ala Ile Lys Ser Leu
275 280 285
Asp Gly Ala Asp Leu Asp Gly Arg Gln Ile Arg Val Ser Glu Ala Glu
290 295 300
Ala Arg Pro Pro Arg Arg Gln Tyr
305 310

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1566519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Met Val Glu Val Ile Tyr Asp Lys Ile Thr Gly Arg Ser Arg Gly Phe
1 5 10 15
Gly Phe Val Thr Met Ser Ser Val Ser Glu Val Glu Ala Ala Gln
20 25 30
Gln Phe Asn Gly Tyr Glu Leu Asp Gly Arg Pro Leu Arg Val Asn Ala
35 40 45
Gly Pro Pro Pro Pro Lys Arg Glu Asp Gly Phe Ser Arg Gly Pro Arg
50 55 60
Ser Ser Phe Gly Ser Ser Gly Ser Gly Tyr Gly Gly Gly Gly Ser

65		70		75		80
Gly	Ala	Gly	Ser	Gly	Asn	Arg
				85		
Val	Asp	Asp	Met	Ala	Leu	Glu
				100		
Val	Glu	Ala	Arg	Val	Ile	Tyr
				115		
Phe	Gly	Phe	Val	Thr	Tyr	Asp
				130		
Lys	Ser	Leu	Asp	Gly	Ala	Asp
				145		
Glu	Ala	Glu	Ala	Arg	Pro	Arg
				165		

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1082
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

atttttaagg	tttcagatat	aggcagattc	tcacatttgc	aaacatgacg	actcagatca	60
gcaagaagag	aaagtttgtg	gcggcaggtg	tgggaaccatt	tgtatgttgc	aaatgttggg	120
gactcgagga	caatagtttc	taaaagctgg	aaagcgatcg	cgctatctga	tgaccataag	180
ccaaatagaa	gcgatgaaag	aaagcgcaatt	gaaagtgtcg	gtggtgttat	catgtgggca	240
ggaacatgga	gagtaggtgg	gggtgttgct	atgtcccggg	cccttggtaa	cagaatgctg	300
aagcaattcg	ttgtgtgtga	accgcagata	caagatctag	agatagatca	tgaggccgag	360
ttgcttggcg	ttgcaagtga	cggttttatg	gatgtggtag	caaagtggga	tgcggtaGcc	420
ctgtctcaga	gcgagggaag	gcccgaggca	gctgcccgca	agttaaactg	cactgccttc	480
agccgtggca	gtgcagacaa	catcacgtgc	attgtttgta	aattccgcca	tgataagaca	540
gaatctccta	aaatcgaaac	aaacgccatg	gctgaatcgg	aaactgaaat	gaacccccca	600
actgaactgg	aaccggaaat	aaaccccgat	actgaaatgg	aaactgaaat	aatccccaaa	660
gctgaaactg	aatccgaacc	tgatgtcata	cctgatccaa	aaactgaaac	cgaaccagag	720
accaagggtg	agaaagctgg	tgagtaaggt	agcagccggg	gaaagggtgc	catactgttg	780
gggacatgtg	gaaacagatg	aatataaaat	tgtttagtaa	gttggtgtgg	ttgtggctac	840
ctgtaaactg	tgaggatttg	tgtttttttg	ttttgtgttg	catctcatga	catgacctat	900
cctgccttga	ggacgacgac	gacccttttg	acatgtcccc	gatttttttg	tattcatattt	960
accctatttt	gtttttgttg	gtgctactca	caccaaaacc	agcacatttg	ttctctgttt	1020
ctctactttt	ttttctatct	ttatttaaaa	caccgtccat	tccaataaac	aatgtttttg	1080

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Met	Trp	Ala	Gly	Thr	Trp	Arg	Val	Gly	Gly	Val	Leu	Ala	Met	Ser	Arg
1			5					10					15		
Ala	Phe	Gly	Asn	Arg	Met	Leu	Lys	Gln	Phe	Val	Val	Ala	Glu	Pro	Glu
								20					25		
Ile	Gln	Asp	Leu	Glu	Ile	Asp	His	Glu	Ala	Glu	Leu	Leu	Val	Leu	Ala

35 40 45
Ser Asp Gly Leu Trp Asp Val Pro Asn Glu Asp Ala Val Ala Leu
50 55 60
Ala Gln Ser Glu Glu Glu Pro Glu Ala Ala Arg Lys Leu Thr Asp
65 70 75 80
Thr Ala Phe Ser Arg Gly Ser Ala Asp Asn Ile Thr Cys Ile Val Val
85 90
Lys Phe Arg His Asp Lys Thr Glu Ser Pro Lys Ile Glu Thr Asn Ala
100 105 110
Met Ala Glu Ser Glu Pro Glu Met Asn Pro Thr Thr Glu Leu Glu Pro
115 120 125
Glu Ser Asn Pro Ser Thr Glu Met Glu Thr Glu Ser Ile Pro Lys Ala
130 135 140
Glu Leu Glu Ser Glu Pro Asp Ala Ile Pro Asp Pro Lys Pro Glu Thr
145 150 155 160
Glu Pro Glu Thr Lys Gly Glu Lys Ala Gly Glu
165 170

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

Met Ser Arg Ala Phe Gly Asn Arg Met Leu Lys Gln Phe Val Val Ala
1 5 10 15
Glu Pro Glu Ile Gln Asp Leu Glu Ile Asp His Glu Ala Glu Leu Leu
20 25 30
Val Leu Ala Ser Asp Gly Leu Trp Asp Val Val Pro Asn Glu Asp Ala
35 40 45
Val Ala Leu Ala Gln Ser Glu Glu Glu Pro Glu Ala Ala Arg Lys
50 55 60
Leu Thr Asp Thr Ala Phe Ser Arg Gly Ser Ala Asp Asn Ile Thr Cys
65 70 75 80
Ile Val Val Lys Phe Arg His Asp Lys Thr Glu Ser Pro Lys Ile Glu
85 90 95
Thr Asn Ala Met Ala Glu Ser Glu Pro Glu Met Asn Pro Thr Thr Glu
100 105 110
Leu Glu Pro Glu Ser Asn Pro Ser Thr Glu Met Glu Thr Glu Ser Ile
115 120 125
Pro Lys Ala Glu Leu Glu Ser Glu Pro Asp Ala Ile Pro Asp Pro Lys
130 135 140
Pro Glu Thr Glu Pro Glu Thr Lys Gly Glu Lys Ala Gly Glu
145 150 155

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Met Leu Lys Gln Phe Val Val Ala Glu Pro Glu Ile Gln Asp Leu Glu
1 5 10 15
Ile Asp His Glu Ala Glu Leu Leu Val Leu Ala Ser Asp Gly Leu Trp
20 25 30
Asp Val Val Pro Asn Glu Asp Ala Val Ala Leu Ala Gln Ser Glu Glu
35 40 45
Glu Pro Glu Ala Ala Ala Arg Lys Leu Thr Asp Thr Ala Phe Ser Arg
50 55 60
Gly Ser Ala Asp Asn Ile Thr Cys Ile Val Val Lys Phe Arg His Asp
65 70 75 80
Lys Thr Glu Ser Pro Lys Ile Glu Thr Asn Ala Met Ala Glu Ser Glu
85 90 95
Pro Glu Met Asn Pro Thr Thr Glu Leu Glu Pro Glu Ser Asn Pro Ser
100 105 110
Thr Glu Met Glu Thr Glu Ser Ile Pro Lys Ala Glu Leu Glu Ser Glu
115 120 125
Pro Asp Ala Ile Pro Asp Pro Lys Pro Glu Thr Glu Pro Glu Thr Lys
130 135 140
Gly Glu Lys Ala Gly Glu
145 150

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..719
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

aaaaaaaaat catttcttct ctgaaacgaa aaaccaaaga aacgagaaga agaagctatg	60
goggatcagc taactgatga acagatctct gagtttaagg aagctttag cctcttcgac	120
aaagatggag atggtttgcat caccacaaag gagctgggaa cagtgtatgag gtcactaggg	180
cagaacccaa cagaagctga gctacaagac atgatcaacg aggttgacgc tgatggaaac	240
ggaaccattg acctccctga gttcttaaac ctaatggcta aaaagatgaa ggacacagac	300
tccgaggaag agctgaaaga agctttcagg gtgttcgaca aagaccagaa cgttttcata	360
tccgtcgagc aGcttcgcca tgtgatgacg aatctagggt agaaactgac tgatgaagag	420
gtcagaggaga tgatttcgtga agcagatgtt gatggagatg gtcagataaa ctacgaggag	480
tttgtaaga ttatgatggc taagtgatga tgataagaaa aaaatgaaga ataaaagtgg	540
tgatgtgatg accttttagc cttttactat ctacaaaaga atgattcgac ctttaattgc	600
ttgggtttga tttagacctg gtatgtttctt aaggttttaa cagactgaat ttgtgactca	660
tcctttttta tttttgttgt ttctttctcg ttggcataat ggcagtgtta gatttcggc	

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Met Ala Asp Gln Leu Thr Asp Glu Gln Ile Ser Glu Phe Lys Glu Ala
1 5 10 15
Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys Glu
20 25 30
Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu

Met	Ile	Asn	Glu	Val	Asp	Ala	Asp	Gly	Asn	Gly	Thr	Ile	Asp	Phe	Pro
1				5				10						15	
Glu	Phe	Leu	Asn	Leu	Met	Ala	Lys	Lys	Met	Lys	Asp	Thr	Asp	Ser	Glu
			20					25					30		
Glu	Glu	Leu	Lys	Glu	Ala	Phe	Arg	Val	Phe	Asp	Lys	Asp	Gln	Asn	Gly
		35					40					45			

Phe Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu Gly Glu
50 55 60
Lys Leu Thr Asp Glu Glu Val Glu Glu Met Ile Arg Glu Ala Asp Val
65 70 75 80
Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu Phe Val Lys Ile Met Met
85 90 95
Ala Lys

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1651

(D) OTHER INFORMATION: / Ceres Seq. ID 1566580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

aagctaaagct	ctagaaacac	cgcctttaac	gtctcgctgc	accatttttc	atcggtgatc	60
agtcgtcgat	cctcttgagt	gatttgattt	tagactttct	agttatcaaa	ctcgaaagat	120
ggattctgtc	cttgtagtgg	gcattgcato	ggttattctc	ggtgcgttga	tcgctgtact	180
ctttctcggt	agctacttcc	ggaagcggac	atcggaggtg	caatccatgg	ccaaaagcga	240
gcctcaggat	ccgatccgga	atccaaagtc	gaatcatcct	gctccgaaga	agaattcatc	300
caaatctcaa	gcgtccgata	agaatcagaa	caaacggcat	catcctttag	atttaaacac	360
gttgaaagcc	caagggtgat	ctgttactgg	actctgtttc	tcgtccgatg	gaaagagctt	420
ggccacagct	tgccgctgat	gtttaactca	gggtgttcaa	ctagatgatg	catcaagcaa	480
aagcttcaaa	tttttaagga	taaatctctc	tgctggagga	catccaaacc	ccgtggcatt	540
tgctgacgat	gcctcatcta	ttgttggg	ttgtcatcat	atgtctggtt	catcttttga	600
catgtacggc	gaagataagc	aaaaggatca	gcaagggaag	cttctctctc	ctagtatcaa	660
atgggaccac	catcatattc	atgagaagag	atcagtgctt	accatctctg	gagctactgc	720
aacttacggt	actgctgatg	gaagtgttgt	catgtcctct	tgttctgaag	ggactgatat	780
cgtcctttgg	catgggaaaa	cgtggaggaa	tttgggacat	gttgatacaa	accagtgtga	840
gaaccacatg	gcagctgtat	caccaaatgg	acgttttttg	gcagctgca	catttactgc	900
agatgtgaaa	gtgtgggaaa	ttgtgtatca	gaaagatggt	tctgtgaaag	aggtttcaag	960
agttatgcaa	cttaaaaggcc	acaagagtgc	agtgaacttg	ttatgctttt	ctccaaactc	1020
agagaaaatc	atcaccgctt	caaaagatgg	ttcaataaga	gtctggaaca	tcaatgtccg	1080
ttatcatctt	gatgaggatc	caaagacttt	gaagggtgtc	ccgatccac	tttgcgactc	1140
aggaggcaat	ccggtgcact	atgatcgtct	cagcttatgc	ccagagggaa	agatattggc	1200
agcaagcatg	ggttccacat	gtcagtggtt	atgtgctgaa	actggaaaatg	tcttgggacac	1260
agctgagaaa	gcccacgaag	gggatatcac	atgcatatct	tgggcaccca	aggctattac	1320
acttggggaa	agacatgcga	tggttttggg	gacatcaggc	Ngatgacaag	aaagtgaagc	1380
tgtgggaagc	tccaaagctg	caatctttgt	aggctctcgc	atcacagtag	tcctttgatg	1440
acatgaggcg	tatttaaacc	gtacaacttg	cgaggaaaaa	aactcttaata	ggttttgttt	1500
cgagtcccaa	gttgggatca	aatgaagggt	ggtttaaagt	ccttcttggt	accaggtgtc	1560
ttttaacttc	tgaagttttg	aattttgtct	ataggactag	tacaacactc	acagtcttct	1620
atgttttcca	aattaaaggaa	attttaaaga	c			

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..261
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Met Ser Gly Ser Ser Leu Tyr Met Tyr Gly Glu Asp Lys Lys Asp

1	5	10	15
Gln Gln Gly Lys Leu Pro Leu Pro Ser Ile Lys Trp Asp His His His	20	25	30
Ile His Glu Lys Arg Ser Val Leu Thr Ile Ser Gly Ala Thr Ala Thr	35	40	45
Tyr Gly Thr Ala Asp Gly Ser Val Val Ile Ala Ser Cys Ser Glu Gly	50	55	60
Thr Asp Ile Val Leu Trp His Gly Lys Thr Gly Arg Asn Leu Gly His	65	70	75
Val Asp Thr Asn Gln Leu Lys Asn His Met Ala Ala Val Ser Pro Asn	80	85	90
Gly Arg Phe Leu Ala Ala Ala Phe Thr Ala Asp Val Lys Val Trp	95	100	105
Glu Ile Val Tyr Gln Lys Asp Gly Ser Val Lys Glu Val Ser Arg Val	110	115	120
Met Gln Leu Lys Gly His Lys Ser Ala Val Thr Trp Leu Cys Phe Ser	125	130	135
Pro Asn Ser Glu Lys Ile Ile Thr Ala Ser Lys Asp Gly Ser Ile Arg	140	145	150
Val Trp Asn Ile Asn Val Arg Tyr His Leu Asp Glu Asp Pro Lys Thr	155	160	165
Leu Lys Val Phe Pro Ile Pro Leu Cys Asp Ser Gly Gly Asn Pro Xaa	170	175	180
His Tyr Asp Arg Leu Ser Leu Cys Pro Glu Gly Lys Ile Leu Ala Ala	185	190	195
Ser His Gly Ser Thr Leu Gln Trp Leu Cys Ala Glu Thr Gly Asn Val	200	205	210
Leu Asp Thr Ala Glu Lys Ala His Glu Gly Asp Ile Thr Cys Ile Ser	215	220	225
Trp Ala Pro Lys Ala Ile Thr Val Gly Glu Arg His Ala Met Val Leu	230	235	240
Gly Thr Ser Gly Xaa	245	250	255
	260		

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..254
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Met Tyr Gly Glu Asp Lys Gln Lys Asp Gln Gln Gly Lys Leu Pro Leu	1	5	10	15
Pro Ser Ile Lys Trp Asp His His His Ile His Glu Lys Arg Ser Val	20	25	30	35
Leu Thr Ile Ser Gly Ala Thr Ala Thr Tyr Gly Thr Ala Asp Gly Ser	40	45	50	55
Val Val Ile Ala Ser Cys Ser Glu Gly Thr Asp Ile Val Leu Trp His	60	65	70	75
Gly Lys Thr Gly Arg Asn Leu Gly His Val Asp Thr Asn Gln Leu Lys	80	85	90	95
Asn His Met Ala Ala Val Ser Pro Asn Gly Arg Phe Leu Ala Ala Ala	100	105	110	115
Ala Phe Thr Ala Asp Val Lys Val Trp Glu Ile Val Tyr Gln Lys Asp	120	125	130	135
Gly Ser Val Lys Glu Val Ser Arg Val Met Gln Leu Lys Gly His Lys	140	145	150	155

Ser Ala Val Thr Trp Leu Cys Phe Ser Pro Asn Ser Glu Lys Ile Ile
130 135 140
Thr Ala Ser Lys Asp Gly Ser Ile Arg Val Trp Asn Ile Asn Val Arg
145 150 155 160
Tyr His Leu Asp Glu Asp Pro Lys Thr Leu Lys Val Phe Pro Ile Pro
165 170 175
Leu Cys Asp Ser Ser Gly Gly Asn Pro Xaa His Tyr Asp Arg Leu Ser Leu
180 185 190
Cys Pro Glu Gly Lys Ile Leu Ala Ala Ser His Gly Ser Thr Leu Gln
195 200 205
Trp Leu Cys Ala Glu Thr Gly Asn Val Leu Asp Thr Ala Glu Lys Ala
210 215 220
His Glu Gly Asp Ile Thr Cys Ile Ser Trp Ala Pro Lys Ala Ile Thr
225 230 235 240
Val Gly Glu Arg His Ala Met Val Leu Gly Thr Ser Gly Xaa
245 250

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..172
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Met Ala Ala Val Ser Pro Asn Gly Arg Phe Leu Ala Ala Ala Ala Phe
1 5 10 15
Thr Ala Asp Val Lys Val Trp Glu Ile Val Tyr Gln Lys Asp Gly Ser
20 25 30
Val Lys Glu Val Ser Arg Val Met Gln Leu Lys Gly His Lys Ser Ala
35 40 45
Val Thr Trp Leu Cys Phe Ser Pro Asn Ser Glu Lys Ile Ile Thr Ala
50 55 60
Ser Lys Asp Gly Ser Ile Arg Val Trp Asn Ile Asn Val Arg Tyr His
65 70 75 80
Leu Asp Glu Asp Pro Lys Thr Leu Lys Val Phe Pro Ile Pro Leu Cys
85 90 95
Asp Ser Gly Gly Asn Pro Xaa His Tyr Asp Arg Leu Ser Leu Cys Pro
100 105 110
Glu Gly Lys Ile Leu Ala Ala Ser His Gly Ser Thr Leu Gln Trp Leu
115 120 125
Cys Ala Glu Thr Gly Asn Val Leu Asp Thr Ala Glu Lys Ala His Glu
130 135 140
Gly Asp Ile Thr Cys Ile Ser Trp Ala Pro Lys Ala Ile Thr Val Gly
145 150 155 160
Glu Arg His Ala Met Val Leu Gly Thr Ser Gly Xaa
165 170

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..781
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

atagttttat	atcatatcaa	tcgacatggc	gaatgtggac	cgtgatcgcc	gtgtgcatgt	60
agaccgttact	gacaaacgtg	ttcatcagcc	aaactacgaa	gatgatgtcg	gttttgggtg	120
ctatggcgggt	tatgggtcgt	gtttctgatta	taagagtctg	ggccctccca	ctaaccaaat	180
cttggcactt	atagcaggag	ttcccatctg	tggcacactg	ctaaccctag	ctggactcac	240
tctagccgggt	tcgggtgatcg	Cgcttgctag	tctccatacc	cctcttctct	ctcttcagtc	300
cggtgatagt	cccgccggct	ctcactattg	ggcttgctgt	gacgggaatc	ttggccttct	360
gtttgttttg	gttgacgggt	ctgagctcgg	tctcgtgggt	cctcaactac	ctccgtggga	420
cgagtgtac	agtgccagag	caattggact	acgctaaacg	gcgtatggct	gatgcggtaa	480
gctatgctgg	tatgaaggga	aaagaSATgg	gtcagtatgt	gcaagataag	gcgcagtagg	540
ctcgtgagac	tgagttcatc	actgagacc	atgagccggg	taaggccagg	agaggctcat	600
aagctaatat	aaatttgcgg	agtcagttgg	aaaggcgata	aatgtagtgt	tacttttatg	660
ttccagtttc	tttctctctt	taagaatatc	tttgtctata	tgtgtacggt	cgttttgtct	720
gtcccaaata	aaaatccttg	ttagtgaat	aagaaatgaa	ataaatatgt	tttctttttt	780

g

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1566589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Met	Ala	Asn	Val	Asp	Arg	Asp	Arg	Arg	Val	His	Val	Asp	Arg	Thr	Asp
1			5					10				15			
Lys	Arg	Val	His	Gln	Pro	Asn	Tyr	Glu	Asp	Asp	Val	Gly	Phe	Gly	Gly
		20					25				30				
Tyr	Gly	Gly	Tyr	Gly	Ala	Gly	Ser	Asp	Tyr	Lys	Ser	Arg	Gly	Pro	Ser
		35				40					45				
Thr	Asn	Gln	Ile	Leu	Ala	Leu	Ile	Ala	Gly	Val	Pro	Ile	Gly	Gly	Thr
		50				55					60				
Leu	Leu	Thr	Leu	Ala	Gly	Leu	Thr	Leu	Ala	Gly	Ser	Val	Ile	Ala	Leu
		65				70				75				80	
Ala	Ser	Leu	His	Thr	Pro	Leu	Pro	Pro	Leu	Gln	Ser	Gly	Asp	Ser	Pro
			85						90				95		
Gly	Gly	Ser	His	Tyr	Trp	Ala	Cys	Cys	Asp	Gly	Asn	Leu	Gly	Phe	Trp
			100					105					110		
Phe	Val	Trp	Val	Asp	Gly	Ser	Glu	Leu	Gly	Leu	Val	Gly	Pro	Gln	Leu
		115					120					125			
Pro	Pro	Trp	Asp	Glu											
			130												

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 717 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..717

(D) OTHER INFORMATION: / Ceres Seq. ID 1566597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

aacacatctc	actgctcaact	actctcactg	taatccctta	gatcttcttt	tcaaatttca	60
atggcgctccg	gtgatgttga	gtatcggtgc	ttctgttggag	gtctagcatg	ggccactgat	120
gacagagctc	ttgagactgc	cttcgctcaa	tacggcgacg	ttattgattc	caagatcatt	180
aacgatcgtg	agactggaag	atcaaagggga	ttcggattcc	tcaccttcaa	ggatgagaaa	240

gccatgaagg atgcgattga gggaatgaac ggacaagatc tcgattggccg tagcatcact 300
gttaacgagg ctcaagtcacg aggaagcggt ggcggcgagg gccaccgtgg aggtggtggc 360
gggtgtggag gttactccgg tggaggtggt agctacggag gtggcgggg tasacgcgag 420
gggtggaggag gatacagcgg cgggcgcggt tactctctaa gaggtgtgg tggcggaagc 480
tacgggtggt gaagacgtga gggaggagga ggatacgggt gtggtgaagg aggaggttac 540
ggaggaaagc gtggtggtgg aggatggtaa ttcCtGthR attaggtttg ggattaccaa 600
tgaatgttct ctctctcgtc tgttatgctt ctactttggt ttgtgtgttc tctattttgt 660
tcctggtctg ctttagattt gatgtaacag ttcgtgatta ggtattttgg tatctgg

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1566598

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

Met Ala Ser Gly Asp Val Glu Tyr Arg Cys Phe Val Gly Gly Leu Ala
1 5 10 15
Trp Ala Thr Asp Asp Arg Ala Leu Glu Thr Ala Phe Ala Gln Tyr Gly
20 25 30
Asp Val Ile Asp Ser Lys Ile Ile Asn Asp Arg Glu Thr Gly Arg Ser
35 40 45
Arg Gly Phe Gly Phe Val Thr Phe Lys Asp Glu Lys Ala Met Lys Asp
50 55 60
Ala Ile Glu Gly Met Asn Gly Gln Asp Leu Asp Gly Arg Ser Ile Thr
65 70 75 80
Val Asn Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Gly His Arg
85 90 95
Gly Gly Gly Gly Gly Gly Gly Tyr Ser Gly Gly Gly Gly Ser Tyr
100 105 110
Gly Gly Gly Gly Gly Xaa Arg Glu Gly Gly Gly Tyr Ser Gly Gly
115 120 125
Gly Gly Tyr Ser Ser Arg Gly Gly Gly Gly Ser Tyr Gly Gly Gly
130 135 140
Arg Arg Glu Gly Gly Gly Gly Tyr Gly Gly Gly Gly Gly Tyr
145 150 155 160
Gly Gly Ser Gly Gly Gly Gly Gly Trp
165

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1566599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

Met Lys Asp Ala Ile Glu Gly Met Asn Gly Gln Asp Leu Asp Gly Arg
1 5 10 15
Ser Ile Thr Val Asn Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Gly
20 25 30
Gly His Arg Gly Gly Gly Gly Gly Gly Gly Tyr Ser Gly Gly Gly
35 40 45
Gly Ser Tyr Gly Gly Gly Gly Gly Xaa Arg Glu Gly Gly Gly Tyr

50	55	60
Ser Gly Gly Gly Gly Tyr Ser Ser Arg Gly Gly Gly Gly Ser Tyr		
65	70	75
Gly Gly Gly Arg Arg Glu Gly Gly Gly Gly Tyr Gly Gly Gly Glu Gly		80
	85	90
Gly Gly Tyr Gly Gly Ser Gly Gly Gly Gly Gly Trp		95
	100	105

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Met Ala Val Ala Ser Leu Leu Thr Arg Leu Ser His Glu Glu Ala Val	
1	5
Ala Ala Glu Ala Thr Val Glu Val Val Ala Val Val Glu Val Thr Pro	15
	20
Val Glu Val Val Ala Thr Glu Val Ala Ala Val Xaa Ala Arg Val Glu	25
	30
Glu Asp Thr Ala Ala Ala Ala Val Thr Pro Gln Glu Val Val Val Ala	35
	40
Glu Ala Thr Val Val Glu Asp Val Arg Glu Glu Glu Asp Thr Val Val	45
	50
65	55
Val Lys Glu Glu Val Thr Glu Glu Ala Val Val Glu Asp Gly Asn	60
	65
	70
Ser Cys Xaa Ile Arg Phe Gly Ile Thr Asn Glu Cys Ser Leu Ser Arg	75
	80
	85
Leu Leu Cys Phe Tyr Phe Val Leu Cys Val Leu Tyr Phe Val Leu Val	90
	95
	100
	105
	110
	115
	120
	125
Leu Leu	
130	

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1567

(D) OTHER INFORMATION: / Ceres Seq. ID 1566608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

atttttgat	tctatcactt	ctcttcttca	tcctctttct	tgtcttgccc	gccttcaaac	60
gcaaaaatca	tgggaaacat	cgacgaatac	catctctccc	tggtttttcca	atcatcggaa	120
acttacatca	gctcgagaaa	ttacaacatc	agtctctatg	gaagctctca	aagaagtatg	180
gccagtgat	gcttttgaa	cttggaagaa	tccccacagt	catactttct	tcatcagaaa	240
gcacaaaca	agctctaaga	gactatgacc	tctattgttg	tagccgtccct	tccttagcag	300
gaggaagaga	gctctcttca	aacaatctgg	atatgtcttc	ctctccttat	aatgaatatt	360
ggaaagaact	aaggaagctc	tgacgtcaag	aactctttga	tgctaataaa	attcaatcga	420
ttcaacctat	taaggacagag	gaggtcaaga	aagttatcga	ttcaatcgcg	gaatcatctt	480
ctcttaagaa	tcoggttaac	ttgacgaaga	cgttctctgc	tttaactaca	agtgtagtat	540
gcaaggcagc	atttggtgtg	agttttgagg	gaactgtgct	caacagtgat	agattcaata	600
agttagtcgc	agatactttc	gagatgttgg	gaagctttct	tgccctcagat	ttattccgtc	660
atgtcgatg	gatcatcgat	aagttcaatg	gtttacaagg	gtggagaaga	aaaagctttc	720

gagatcttga	tgcgttctat	gaacaaaattt	ttgatctgca	taaggaagag	aaggaagtag	780
gaagtgaaga	tttagtggat	gtgctcttga	ggttggagaa	agaagaaaatt	gttgttggaa	840
atggcaagct	cacaagaagt	cataatcaaa	caattttgat	gaacattctt	ttaggaggaa	900
tcgatacttc	tgcaataaca	atgacatggg	caatggcaga	acttgctaaa	aaccttagag	960
tgatgaagaa	agttcaagca	gaaatcagaa	gccaaatcaa	agaatcacgt		1020
ttgatgcacac	tgataagctc	gagtacttaa	aaatggtgat	caaagaacaa	tgaggtttac	1080
atcctccaac	acctcttctc	ctcccaagag	ttgtaatcac	tgaattttgag	atcaaatggct	1140
acacgattcc	tgccaaaaaca	cgacttcaatg	tgaatttttg	ggctatttggg	cgtgatccctg	1200
atacatggaa	agatccagaa	atgtttctcc	cggaaaggtt	taatgatagt	aacattgatg	1260
caaaaggaca	gaactttgag	ttgttgcgt	ttgggagtg	taggagaatt	tgtcctggac	1320
tgtaactggg	aacaacaatg	gtggagtttg	gcctagctaa	tatgtttgat	cattttgatt	1380
ggaagtgtacc	agaaggcatg	gtagtcagaa	gatatcgata	tggaagaagc	tcctggacctt	1440
actgtgagca	aaaaaagtga	gcttctactt	gttcacgtga	agtatttaga	ccattgattc	1500
acgtgaatta	gttcttctac	gattgtacta	tgaataagaa	cgaatgata	atgagaattt	1560
tcaatgt						

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 485 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..485

(D) OTHER INFORMATION: / Ceres Seq. ID 1566609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

Ph	Trp	Ile	Leu	Ser	Leu	Leu	Phe	Phe	Ile	Phe	Leu	Leu	Leu	Ala
1			5						10				15	
Ala	Phe	Lys	Arg	Lys	Asn	His	Gly	Lys	His	Arg	Arg	Ile	Pro	Ser
			20					25				30	Ser	Pro
Pro	Gly	Phe	Pro	Ile	Ile	Gly	Asn	Leu	His	Gln	Leu	Gly	Glu	Leu
			35				40				45			Gln
His	Gln	Ser	Leu	Trp	Lys	Leu	Ser	Lys	Lys	Tyr	Gly	Pro	Val	Met
			50			55					60			Leu
Leu	Lys	Leu	Gly	Lys	Val	Pro	Thr	Val	Ile	Leu	Ser	Ser	Ser	Glu
			65		70				75					80
Ala	Lys	Gln	Ala	Leu	Arg	Asp	Tyr	Asp	Leu	Tyr	Cys	Cys	Ser	Arg
			85					90					95	Pro
Ser	Leu	Ala	Gly	Gly	Arg	Glu	Leu	Ser	Tyr	Asn	Asn	Leu	Asp	Met
			100					105					110	Ser
Ser	Ser	Pro	Tyr	Asn	Glu	Tyr	Trp	Lys	Glu	Leu	Arg	Lys	Leu	Cys
			115				120					125		Ser
Gln	Glu	Leu	Phe	Ser	Ala	Asn	Lys	Ile	Gln	Ser	Ile	Gln	Pro	Ile
			130			135					140			Lys
Asp	Glu	Glu	Val	Lys	Lys	Val	Ile	Asp	Ser	Ile	Ala	Glu	Ser	Ser
			145		150					155				Ser
Leu	Lys	Asn	Pro	Val	Asn	Leu	Ser	Lys	Thr	Phe	Leu	Ala	Leu	Thr
			165						170				175	Thr
Ser	Val	Val	Cys	Lys	Ala	Ala	Phe	Gly	Val	Ser	Phe	Glu	Gly	Thr
			180				185						190	Val
Leu	Asn	Ser	Asp	Arg	Phe	Asn	Lys	Leu	Val	Arg	Asp	Thr	Phe	Glu
			195				200				205			Met
Leu	Gly	Ser	Phe	Ser	Ala	Ser	Asp	Phe	Ile	Pro	Tyr	Val	Gly	Trp
			210			215					220			Ile
Ile	Asp	Lys	Phe	Asn	Gly	Leu	Gln	Gly	Trp	Arg	Lys	Lys	Ser	Phe
			225		230				235					Arg
Asp	Leu	Asp	Ala	Phe	Tyr	Glu	Gln	Ile	Phe	Asp	Leu	His	Lys	Glu
			245					250					255	
Lys	Glu	Val	Gly	Ser	Glu	Asp	Leu	Val	Asp	Val	Leu	Leu	Arg	Glu
			260				265						270	

Lys Glu Glu Ile Val Val Gly Asn Gly Lys Leu Thr Arg Asn His Ile
275 280 285
Lys Ala Ile Leu Met Asn Ile Leu Leu Gly Gly Ile Asp Thr Ser Ala
290 295 300
Ile Thr Met Thr Trp Ala Met Ala Glu Leu Ala Lys Asn Pro Arg Val
305 310 315 320
Met Lys Lys Val Gln Ala Glu Ile Arg Ser Gln Ile Lys Asn Lys Glu
325 330 335
Arg Ile Ser Phe Asp Asp Thr Asp Lys Leu Glu Tyr Leu Lys Met Val
340 345 350
Ile Lys Glu Thr Trp Arg Leu His Pro Pro Thr Pro Leu Leu Leu Pro
355 360 365
Arg Val Val Ile Thr Glu Phe Glu Ile Asn Gly Tyr Thr Ile Pro Ala
370 375 380
Lys Thr Arg Leu His Val Asn Val Trp Ala Ile Gly Arg Asp Pro Asp
385 390 395 400
Thr Trp Lys Asp Pro Glu Met Phe Leu Pro Glu Arg Phe Asn Asp Ser
405 410 415
Asn Ile Asp Ala Lys Gly Gln Asn Phe Glu Leu Leu Ser Phe Gly Ser
420 425 430
Gly Arg Arg Ile Cys Pro Gly Leu Tyr Met Gly Thr Thr Met Val Glu
435 440 445
Phe Gly Leu Ala Asn Met Leu Tyr His Phe Asp Trp Lys Leu Pro Glu
450 455 460
Gly Met Val Val Arg Arg Tyr Arg Tyr Gly Arg Ser Ser Trp Thr Tyr
465 470 475 480
Cys Glu Gln Lys Lys
485

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..423

(D) OTHER INFORMATION: / Ceres Seq. ID 1566610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

Met Leu Leu Lys Lys Leu Gly Lys Val Pro Thr Val Ile Leu Ser Ser Ser
1 5 10 15
Glu Thr Ala Lys Gln Ala Leu Arg Asp Tyr Asp Leu Tyr Cys Cys Ser
20 25 30
Arg Pro Ser Leu Ala Gly Gly Arg Glu Leu Ser Tyr Asn Asn Leu Asp
35 40 45
Met Ser Ser Ser Pro Tyr Asn Glu Tyr Trp Lys Glu Leu Arg Lys Leu
50 55 60
Cys Ser Gln Glu Leu Phe Ser Ala Asn Lys Ile Gln Ser Ile Gln Pro
65 70 75 80
Ile Lys Asp Glu Glu Val Lys Lys Val Ile Asp Ser Ile Ala Glu Ser
85 90 95
Ser Ser Leu Lys Asn Pro Val Asn Leu Ser Lys Thr Phe Leu Ala Leu
100 105 110
Thr Thr Ser Val Val Cys Lys Ala Ala Phe Gly Val Ser Phe Glu Gly
115 120 125
Thr Val Leu Asn Ser Asp Arg Phe Asn Lys Leu Val Arg Asp Thr Phe
130 135 140
Glu Met Leu Gly Ser Phe Ser Ala Ser Asp Phe Ile Pro Tyr Val Gly
145 150 155 160
Trp Ile Ile Asp Lys Phe Asn Gly Leu Gln Gly Trp Arg Lys Lys Ser

	165		170		175
Phe Arg Asp	Leu Asp Ala Phe Tyr Glu Gln Ile Phe Asp	Leu His Lys			
	180		185		190
Glu Glu Lys	Glu Val Gly Ser Glu Asp	Leu Val Asp Val Leu Leu Arg			
	195		200		205
Leu Glu Lys	Glu Glu Ile Val Val Gly Asn Gly Lys	Leu Thr Arg Asn			
	210		215		220
His Ile Lys	Ala Ile Leu Met Asn Ile Leu Leu Gly Gly Ile Asp Thr				
	225		230		235
Ser Ala Ile	Thr Met Thr Trp Ala Met Ala Glu	Leu Ala Lys Asn Pro			
	245		250		255
Arg Val Met	Lys Lys Val Gln Ala Glu Ile Arg Ser Gln Ile Lys Asn				
	260		265		270
Lys Glu Arg	Ile Ser Phe Asp Asp Thr Asp Lys	Leu Glu Tyr Leu Lys			
	275		280		285
Met Val Ile	Lys Glu Thr Trp Arg Leu His Pro	Pro Thr Pro Leu Leu			
	290		295		300
Leu Pro Arg	Val Val Ile Thr Glu Phe Glu Ile Asn Gly Tyr Thr Ile				
	305		310		315
Pro Ala Lys	Thr Arg Leu His Val Asn Val Trp Ala Ile Gly Arg Asp				
	325		330		335
Pro Asp Thr	Trp Lys Asp Pro Glu Met Phe Leu Pro Glu Arg Phe Asn				
	340		345		350
Asp Ser Asn	Ile Asp Ala Lys Gly Gln Asn Phe Glu Leu Leu Ser Phe				
	355		360		365
Gly Ser Gly	Arg Arg Ile Cys Pro Gly Leu Tyr Met Gly Thr Thr Met				
	370		375		380
Val Glu Phe	Gly Leu Ala Asn Met Leu Tyr His Phe Asp Trp Lys Leu				
	385		390		395
Pro Glu Gly	Met Val Val Arg Arg Tyr Arg Tyr Gly Arg Ser Ser Trp				
	405		410		415
Thr Tyr Cys	Glu Gln Lys Lys				
	420				

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Met Ser Ser Ser Pro Tyr Asn Glu Tyr Trp Lys Glu Leu Arg Lys Leu	
1	5 10 15
Cys Ser Gln Glu Leu Phe Ser Ala Asn Lys Ile Gln Ser Ile Gln Pro	
	20 25 30
Ile Lys Asp Glu Glu Val Lys Lys Val Ile Asp Ser Ile Ala Glu Ser	
	35 40 45
Ser Ser Leu Lys Asn Pro Val Asn Leu Ser Lys Thr Phe Leu Ala Leu	
	50 55 60
Thr Thr Ser Val Val Cys Lys Ala Ala Phe Gly Val Ser Phe Glu Gly	
	65 70 75 80
Thr Val Leu Asn Ser Asp Arg Phe Asn Lys Leu Val Arg Asp Thr Phe	
	85 90 95
Glu Met Leu Gly Ser Phe Ser Ala Ser Asp Phe Ile Pro Tyr Val Gly	
	100 105 110
Trp Ile Ile Asp Lys Phe Asn Gly Leu Gln Gly Trp Arg Lys Lys Ser	
	115 120 125

Phe Arg Asp Leu Asp Ala Phe Tyr Glu Gln Ile Phe Asp Leu His Lys
130 135 140
Glu Glu Lys Glu Val Gly Ser Glu Asp Leu Val Asp Val Leu Leu Arg
145 150 155 160
Leu Glu Lys Glu Glu Ile Val Val Gly Asn Gly Lys Leu Thr Arg Asn
165 170 175
His Ile Lys Ala Ile Leu Met Asn Ile Leu Leu Gly Gly Ile Asp Thr
180 185 190
Ser Ala Ile Thr Met Thr Trp Ala Met Ala Glu Leu Ala Lys Asn Pro
195 200 205
Arg Val Met Lys Lys Val Gln Ala Glu Ile Arg Ser Gln Ile Lys Asn
210 215 220
Lys Glu Arg Ile Ser Phe Asp Asp Thr Asp Lys Leu Glu Tyr Leu Lys
225 230 235 240
Met Val Ile Lys Glu Thr Trp Arg Leu His Pro Pro Thr Pro Leu Leu
245 250 255
Leu Pro Arg Val Val Ile Thr Glu Phe Glu Ile Asn Gly Tyr Thr Ile
260 265 270
Pro Ala Lys Thr Arg Leu His Val Asn Val Trp Ala Ile Gly Arg Asp
275 280 285
Pro Asp Thr Trp Lys Asp Pro Glu Met Phe Leu Pro Glu Arg Phe Asn
290 295 300
Asp Ser Asn Ile Asp Ala Lys Gly Gln Asn Phe Glu Leu Leu Ser Phe
305 310 315 320
Gly Ser Gly Arg Arg Ile Cys Pro Gly Leu Tyr Met Gly Thr Thr Met
325 330 335
Val Glu Phe Gly Leu Ala Asn Met Leu Tyr His Phe Asp Trp Lys Leu
340 345 350
Pro Glu Gly Met Val Val Arg Arg Tyr Arg Tyr Gly Arg Ser Ser Trp
355 360 365
Thr Tyr Cys Glu Gln Lys Lys
370 375

(2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1049 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1049
(D) OTHER INFORMATION: / Ceres Seq. ID 1566616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

aactgcacaaa	actcttcaact	taattctccg	gcgtatacaaa	gtcgcggcgga	aaaatgtcga	60
tgctgcaaaaag	ctcccaagatg	cttcagttca	taaaactacag	gatgcgagta	acaatccaag	120
acggaagacac	gctaactcgga	aaattcctatg	cggttcgatcg	ccacatgaat	cttggttcttg	180
gcgactgcga	agagttttcga	aaacttctctc	cgggcgaaaag	taataagaag	acgagcggaag	240
aaagagaagaa	gcgtcgctact	ctaggttttgg	ttttacttag	aggagaagaa	gtgatttcga	300
tgactgtcga	aggctccaccg	ccaccgcgaag	aatctcgcgc	caaatctgga	ctgtgtaccg	360
ccgtgtcgtcg	tcctggaatc	ggctgtgctg	ctggacgcgg	agtagctact	ggctcgttag	420
ttcaagctca	gcctggttta	ctctgtcctg	ttcgtggaat	tggttgacct	gctcctggaa	480
tgatgcagcc	tcagatctct	agaccaccac	agattattcg	tcctccggga	caaatgccac	540
cacagcctcc	ttttgttgtt	caaggaggctc	ctcctccacc	ttatggtatg	agaccaccgt	600
atctctggtcc	accacgcctc	caagtatggtg	gacagcaaa	gccaatgatg	attcctccac	660
ctggtggtat	gatgagagga	ctcctccacc	ctcatgggtat	gcaaggaccg	ctcctctctc	720
gccctggaaat	acctcccccc	gggtgtgctc	cgatgtttGc	tcgcgctcat	cttggtcgtc	780
ccactgCtcc	gccaaatcac	cataatcagc	aacattgatt	aggagtcact	tcactcacaa	840
cgaagcgaac	atccacatga	ttgagttacc	ctcgggctag	tcgtagcgtt	ttctctccgtg	900
aagctcagag	aattgatgag	ttcatatttg	tgattttctg	tggaaaaagc	aactgatttt	960
agaaatagtg	aactgttagg	agttacaacc	ttgctccatg	aacttgtaag	tattacttgt	1020

aaaagaggct ctcaatgggtt ttgactggc

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1566617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Met	Ser	Met	Ser	Lys	Ser	Ser	Lys	Met	Leu	Gln	Phe	Ile	Asn	Tyr	Arg	
1				5				10						15		
Met	Arg	Val	Thr	Ile	Gln	Asp	Gly	Arg	Gln	Leu	Ile	Gly	Lys	Phe	Met	
		20					25						30			
Ala	Phe	Asp	Arg	His	Met	Asn	Leu	Val	Leu	Gly	Asp	Cys	Glu	Glu	Phe	
		35				40					45					
Arg	Lys	Leu	Pro	Pro	Ala	Lys	Gly	Asn	Lys	Lys	Thr	Ser	Glu	Glu	Arg	
	50				55					60						
Glu	Glu	Arg	Arg	Thr	Leu	Gly	Leu	Val	Leu	Arg	Gly	Glu	Glu	Val		
65				70					75					80		
Ile	Ser	Met	Thr	Val	Glu	Gly	Pro	Pro	Pro	Pro	Glu	Glu	Ser	Arg	Ala	
			85					90					95			
Lys	Ser	Gly	Ser	Val	Thr	Ala	Val	Ala	Gly	Pro	Gly	Ile	Gly	Arg	Ala	
			100					105					110			
Ala	Gly	Arg	Gly	Val	Pro	Thr	Gly	Pro	Leu	Val	Gln	Ala	Gln	Pro	Gly	
		115					120					125				
Leu	Ser	Gly	Pro	Val	Arg	Gly	Ile	Gly	Gly	Pro	Ala	Pro	Gly	Met	Met	
	130					135				140						
Gln	Pro	Gln	Ile	Ser	Arg	Pro	Pro	Gln	Ile	Ile	Arg	Pro	Pro	Gly	Gln	
145				150						155					160	
Met	Pro	Pro	Gln	Pro	Phe	Ala	Gly	Gln	Gly	Gly	Pro	Pro	Pro	Pro		
			165					170						175		
Tyr	Gly	Met	Arg	Pro	Pro	Tyr	Pro	Gly	Pro	Pro	Pro	Pro	Gln	Tyr	Gly	
		180						185						190		
Gly	Gln	Gln	Arg	Pro	Met	Met	Ile	Pro	Pro	Pro	Gly	Gly	Met	Met	Arg	
		195						200					205			
Gly	Pro	Pro	Pro	Pro	His	Gly	Met	Gln	Gly	Pro	Pro	Pro	Ser	Arg	Pro	
	210					215						220				
Gly	Ile	Pro	Pro	Pro	Gly	Gly	Ala	Pro	Met	Phe	Ala	Pro	Pro	His	Pro	
225					230					235					240	
Gly	Met	Pro	Pro	Ala	Pro	Pro	Asn	His	His	Asn	Gln	Gln	His			
				245						250						

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..252

(D) OTHER INFORMATION: / Ceres Seq. ID 1566618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

Met	Ser	Lys	Ser	Ser	Lys	Met	Leu	Gln	Phe	Ile	Asn	Tyr	Arg	Met	Arg	
1				5				10					15			
Val	Thr	Ile	Gln	Asp	Gly	Arg	Gln	Leu	Ile	Gly	Lys	Phe	Met	Ala	Phe	
			20					25					30			

```

Asp Arg His Met Asn Leu Val Leu Gly Asp Cys Glu Glu Phe Arg Lys
    35          40          45
Leu Pro Pro Ala Lys Gly Asn Lys Lys Thr Ser Glu Glu Arg Glu Glu
    50          55          60
Arg Arg Thr Leu Gly Leu Val Leu Leu Arg Gly Glu Glu Val Ile Ser
    65          70          75          80
Met Thr Val Glu Gly Pro Pro Pro Pro Glu Glu Ser Arg Ala Lys Ser
    85          90          95
Gly Ser Val Thr Ala Val Ala Gly Pro Gly Ile Gly Arg Ala Ala Gly
    100         105         110
Arg Gly Val Pro Thr Gly Pro Leu Val Gln Ala Gln Pro Gly Leu Ser
    115         120         125
Gly Pro Val Arg Gly Ile Gly Gly Pro Ala Pro Gly Met Met Gln Pro
    130         135         140
Gln Ile Ser Arg Pro Pro Gln Ile Ile Arg Pro Pro Gly Gln Met Pro
    145         150         155         160
Pro Gln Pro Pro Phe Ala Gly Gln Gly Gly Pro Pro Pro Tyr Gly
    165         170         175
Met Arg Pro Pro Tyr Pro Gly Pro Pro Pro Gln Tyr Gly Gly Gln
    180         185         190
Gln Arg Pro Met Met Ile Pro Pro Pro Gly Gly Met Met Arg Gly Pro
    195         200         205
Pro Pro Pro His Gly Met Gln Gly Pro Pro Pro Ser Arg Pro Gly Ile
    210         215         220
Pro Pro Pro Gly Gly Ala Pro Met Phe Ala Pro His Pro Gly Met
    225         230         235         240
Pro Pro Ala Pro Pro Asn His His Asn Gln His
    245         250

```

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..246

(D) OTHER INFORMATION: / Ceres Seq. ID 1566619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

```

Met Leu Gln Phe Ile Asn Tyr Arg Met Arg Val Thr Ile Gln Asp Gly
1          5          10          15
Arg Gln Leu Ile Gly Lys Phe Met Ala Phe Asp Arg His Met Asn Leu
    20          25          30
Val Leu Gly Asp Cys Glu Glu Phe Arg Lys Leu Pro Pro Ala Lys Gly
    35          40          45
Asn Lys Lys Thr Ser Glu Glu Arg Glu Glu Arg Arg Thr Leu Gly Leu
    50          55          60
Val Leu Leu Arg Gly Glu Glu Val Ile Ser Met Thr Val Glu Gly Pro
    65          70          75          80
Pro Pro Pro Glu Glu Ser Arg Ala Lys Ser Gly Ser Val Thr Ala Val
    85          90          95
Ala Gly Pro Gly Ile Gly Arg Ala Ala Gly Arg Gly Val Pro Thr Gly
    100         105         110
Pro Leu Val Gln Ala Gln Pro Gly Leu Ser Gly Pro Val Arg Gly Ile
    115         120         125
Gly Gly Pro Ala Pro Gly Met Met Gln Pro Gln Ile Ser Arg Pro Pro
    130         135         140
Gln Ile Ile Arg Pro Pro Gly Gln Met Pro Pro Gln Pro Pro Phe Ala
    145         150         155         160
Gly Gln Gly Gly Pro Pro Pro Tyr Gly Met Arg Pro Pro Tyr Pro

```

(2) INFORMATION FOR SEQ ID NO:327:

(A) LENGTH: 1570 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: sing

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

```
(ix) FEATURE:
```

(A) NAME

(B) LOCATION: 1

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:327:

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:327:
taccgtc tctgttttcgt tcgscgtgat tcctagtctgt c

atccacccg	tctgttttt	tccgcgtgat	tcatagctg	tccgcgttcat	ctgcacacct	120
accgctctct	tctctccatt	tcagcagatt	ttgttagatt	tgttagtggt	tctcaggcaaa	180
ctttattctt	aaggtccagg	cttttgcctc	gtctgtaacca	aacattgttat	catattatcc	240
ctctgtgagat	tgatcatgga	atggatttcac	tctctgaaga	aacattctcag	agaagtatcc	300
atagctttct	tcacaaagaa	tcogttaaaca	atcttgattt	ctccaaagtt	tctgaggaa	360
gcttaccatt	gcctcttgct	cccagcttgc	gttttgcctt	ctatcgattt	atgtcaagtg	420
cacctgggtg	tggttcagag	aagattgggt	tgattgtctga	cattgcagaa	gtcataacctg	480
actcaaacat	gcgaagtgtg	ccagctcagg	ctgctgtctgc	tgctcagtga	gttacactcg	540
cagctgtctg	ctctttcttc	ctctatcgcg	cccttcagca	gtcgattgat	atggtgcata	600
catctacagg	cttttgagtg	ttggatctcca	ttgtttgagc	aacatttttg	atcgcattgat	660
caacaggttc	tctcttgatc	aaacaaatga	aagacacacac	caagttatgc	ctgatgagtc	720
ccaggttgga	gtctcatcgg	gaggaatctg	aaacacacagg	aatggatctc	gtaacgatgg	780
cagaagaaga	aaaaaagatg	aagaaattgt	ttaaagaata	tgtgtcaact	ccattcaccc	840
caatgaaagg	gatgtttatt	cagggacccg	tgttcatctg	ctttttcttc	gctattcgaa	900
atatggcgga	gaaggtacct	tcattcccca	caggagggtc	attatggttt	accgattotaa	960
caactcccca	cagctttatc	attctgcggg	ttataaacagg	attgacattc	ttgataaacg	1020
tttgagttaa	tgcaacaagaa	ggcatctgaag	ggaactgcat	ggctggcaat	gtaaaacatg	1080
tttgcgggtg	ttttgctctc	ctccagctgc	cgatgacaat	gagttttcca	caggccattg	1140
tttgttactg	tgacacatcc	aacctgtctt	ctctcatgta	tgcactgttg	ataaaggctc	1200
ctcaagtgaa	gaagatgtta	ctactacctg	attctgcctcc	accttttcca	gtgccaacaac	1260
cttcatctga	ctctgttttca	gctctcaaga	aaatgaaagc	gcatacacag	gaccatcac	1320
agaaccagat	aggaaccact	tcgcagcaat	accocaggct	ttctctcaac	tcgctgagtc	1380
ctgttagtaa	ggggctcaag	gctttggaga	gccaaagtaa	gggaagggaag	agaataagca	1440
cgaaagaaag	gttgatttaa	ccaggtgcata	ctatttttgt	taaggaggcc	aaacgaaaaa	1500
aaataataaag	cttttgatgc	gaagtgatga	acagaatttt	ctcactgagt	aaactctctt	1560
gttagcttaa	aagctggagg	cagctattgt	aagtttgttt	tgaccaatta	tagaatagaa	
gattgattttt						

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..429

(D) OTHER INFORMATION: / Ceres Seq. ID 1566631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Met Ala Phe Arg Gln Thr Leu Ser Ile Arg Ser Arg Leu Phe Ala Arg
1 5 10 15
Arg Asn Gln Pro Val Tyr His Ile Ile Pro Arg Glu Ser Asp His Glu
20 25 30
Arg Asp Ser Phe Cys Gln Glu Thr Ser Gln Arg Ser Tyr His Ser Phe
35 40 45
Leu His Gln Arg Ser Val Asn Asn Ser Asp Phe Ser Lys Val Ser Gly
50 55 60
Gly Ser Leu His Leu Pro Leu Ala Pro Thr Ser Gly Phe Ala Phe Tyr
65 70 75 80
Arg Tyr Met Ser Ser Ala Pro Gly Val Gly Ser Glu Lys Ile Gly Val
85 90 95
Met Ser Asp Ile Ala Glu Val Ile Thr Asp Ser Thr Leu Gln Asp Val
100 105 110
Pro Ala Gln Ala Ala Ala Val Ser Glu Val Thr Leu Ala Ala Ala
115 120 125
Asp Ser Phe Phe Pro Ile Ala Ala Leu Gln Gln Cys Ile Asp Met Val
130 135 140
His Thr Phe Thr Gly Phe Glu Trp Trp Ala Ser Ile Val Val Ala Thr
145 150 155 160
Ile Leu Ile Arg Ser Ser Thr Val Pro Leu Leu Ile Lys Gln Met Lys
165 170 175
Asp Thr Thr Lys Leu Ala Leu Met Arg Pro Arg Leu Glu Ser Ile Arg
180 185 190
Glu Glu Met Gln Asn Lys Gly Met Asp Ser Val Thr Met Ala Glu Gly
195 200 205
Gln Lys Lys Met Lys Asn Leu Phe Lys Glu Tyr Gly Val Thr Pro Phe
210 215 220
Thr Pro Met Lys Gly Met Phe Ile Gln Gly Pro Leu Phe Ile Cys Phe
225 230 235 240
Phe Leu Ala Ile Arg Asn Met Ala Glu Lys Val Pro Ser Phe Gln Thr
245 250 255
Gly Gly Ala Leu Trp Phe Thr Asp Leu Thr Thr Pro Asp Ser Leu Tyr
260 265 270
Ile Leu Pro Val Ile Thr Gly Leu Thr Phe Leu Ile Thr Val Glu Cys
275 280 285
Asn Ala Gln Glu Gly Met Glu Gly Asn Pro Met Ala Gly Thr Val Lys
290 295 300
Thr Val Cys Arg Val Phe Ala Leu Leu Thr Val Pro Met Thr Met Ser
305 310 315 320
Phe Pro Gln Ala Ile Phe Cys Tyr Trp Ile Thr Ser Asn Leu Phe Ser
325 330 335
Leu Met Tyr Gly Leu Val Ile Lys Arg Pro Gln Val Lys Lys Met Leu
340 345 350
Arg Ile Pro Asp Leu Pro Pro Pro Pro Gly Gln Gln Pro Ser Phe
355 360 365
Asp Leu Phe Ser Ala Leu Lys Lys Met Lys Ala Met Thr Gln Asp His
370 375 380
Thr Gln Asn Gln Ile Glu Pro Pro Ser Pro Val Asn Pro Arg Leu Ser
385 390 395 400
Ser Thr Ser Leu Ser Pro Val Ser Lys Arg Leu Lys Ala Leu Glu Ser
405 410 415
Gln Val Lys Gly Arg Lys Lys Asn Ser Ser Lys Lys Lys
420 425

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 347 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..347

(D) OTHER INFORMATION: / Ceres Seq. ID 1566632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

Met	Ser	Ser	Ala	Pro	Gly	Val	Gly	Ser	Glu	Lys	Ile	Gly	Val	Met	Ser
1			5					10						15	
Asp	Ile	Ala	Glu	Val	Ile	Thr	Asp	Ser	Thr	Leu	Gln	Asp	Val	Pro	Ala
			20					25					30		
Gln	Ala	Ala	Ala	Ala	Val	Ser	Glu	Val	Thr	Leu	Ala	Ala	Ala	Asp	Ser
			35					40				45			
Phe	Phe	Pro	Ile	Ala	Ala	Leu	Gln	Gln	Cys	Ile	Asp	Met	Val	His	Thr
			50					55				60			
Phe	Thr	Gly	Phe	Glu	Trp	Trp	Ala	Ser	Ile	Val	Val	Ala	Thr	Ile	Leu
			65					70				75			80
Ile	Arg	Ser	Ser	Thr	Val	Pro	Leu	Leu	Ile	Lys	Gln	Met	Lys	Asp	Thr
				85					90				95		
Thr	Lys	Leu	Ala	Leu	Met	Arg	Pro	Arg	Leu	Glu	Ser	Ile	Arg	Glu	Glu
			100					105					110		
Met	Gln	Asn	Lys	Gly	Met	Asp	Ser	Val	Thr	Met	Ala	Glu	Gly	Gln	Lys
			115					120					125		
Lys	Met	Lys	Asn	Leu	Phe	Lys	Glu	Tyr	Gly	Val	Thr	Pro	Phe	Thr	Pro
			130					135				140			
Met	Lys	Gly	Met	Phe	Ile	Gln	Gly	Pro	Leu	Phe	Ile	Cys	Phe	Phe	Leu
			145					150				155			160
Ala	Ile	Arg	Asn	Met	Ala	Glu	Lys	Val	Pro	Ser	Phe	Gln	Thr	Gly	Gly
				165					170					175	
Ala	Leu	Trp	Phe	Thr	Asp	Leu	Thr	Thr	Pro	Asp	Ser	Leu	Tyr	Ile	Leu
			180					185					190		
Pro	Val	Ile	Thr	Gly	Leu	Thr	Phe	Leu	Ile	Thr	Val	Glu	Cys	Asn	Ala
			195					200					205		
Gln	Glu	Gly	Met	Glu	Gly	Asn	Pro	Met	Ala	Gly	Thr	Val	Lys	Thr	Val
			210					215					220		
Cys	Arg	Val	Phe	Ala	Leu	Leu	Thr	Val	Pro	Met	Thr	Met	Ser	Phe	Pro
				230						235					240
Gln	Ala	Ile	Phe	Cys	Tyr	Trp	Ile	Thr	Ser	Asn	Leu	Phe	Ser	Leu	Met
				245						250				255	
Tyr	Gly	Leu	Val	Ile	Lys	Arg	Pro	Gln	Val	Lys	Lys	Met	Leu	Arg	Ile
			260					265					270		
Pro	Asp	Leu	Pro	Pro	Pro	Pro	Pro	Gly	Gln	Gln	Pro	Ser	Phe	Asp	Leu
			275					280					285		
Phe	Ser	Ala	Leu	Lys	Lys	Met	Lys	Ala	Met	Thr	Gln	Asp	His	Thr	Gln
				295								300			
Asn	Gln	Ile	Glu	Pro	Pro	Ser	Pro	Val	Asn	Pro	Arg	Leu	Ser	Ser	Thr
				310							315				320
Ser	Leu	Ser	Pro	Val	Ser	Lys	Arg	Leu	Lys	Ala	Leu	Glu	Ser	Gln	Val
				325						330				335	
Lys	Gly	Arg	Lys	Lys	Asn	Ser	Ser	Lys	Lys	Lys					
				340					345						

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..333

(D) OTHER INFORMATION: / Ceres Seq. ID 1566633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Met	Ser	Asp	Ile	Ala	Glu	Val	Ile	Thr	Asp	Ser	Thr	Leu	Gln	Asp	Val
1			5						10				15		
Pro	Ala	Gln	Ala	Ala	Ala	Val	Ser	Glu	Val	Thr	Leu	Ala	Ala	Ala	
		20					25					30			
Asp	Ser	Phe	Phe	Pro	Ile	Ala	Ala	Leu	Gln	Gln	Cys	Ile	Asp	Met	Val
		35					40				45				
His	Thr	Phe	Thr	Gly	Phe	Glu	Trp	Trp	Ala	Ser	Ile	Val	Val	Ala	Thr
	50				55					60					
Ile	Leu	Ile	Arg	Ser	Ser	Thr	Val	Pro	Leu	Leu	Ile	Lys	Gln	Met	Lys
65			70					75					80		
Asp	Thr	Thr	Lys	Leu	Ala	Leu	Met	Arg	Pro	Arg	Leu	Glu	Ser	Ile	Arg
			85					90					95		
Glu	Glu	Met	Gln	Asn	Lys	Gly	Met	Asp	Ser	Val	Thr	Met	Ala	Glu	Gly
		100					105					110			
Gln	Lys	Lys	Met	Lys	Asn	Leu	Phe	Lys	Glu	Tyr	Gly	Val	Thr	Pro	Phe
		115				120					125				
Thr	Pro	Met	Lys	Gly	Met	Phe	Ile	Gln	Gly	Pro	Leu	Phe	Ile	Cys	Phe
	130				135						140				
Phe	Leu	Ala	Ile	Arg	Asn	Met	Ala	Glu	Lys	Val	Pro	Ser	Phe	Gln	Thr
145					150				155						160
Gly	Gly	Ala	Leu	Trp	Phe	Thr	Asp	Leu	Thr	Thr	Pro	Asp	Ser	Leu	Tyr
			165					170					175		
Ile	Leu	Pro	Val	Ile	Thr	Gly	Leu	Thr	Phe	Leu	Ile	Thr	Val	Glu	Cys
		180					185					190			
Asn	Ala	Gln	Glu	Gly	Met	Glu	Gly	Asn	Pro	Met	Ala	Gly	Thr	Val	Lys
		195					200				205				
Thr	Val	Cys	Arg	Val	Phe	Ala	Leu	Leu	Thr	Val	Pro	Met	Thr	Met	Ser
	210				215						220				
Phe	Pro	Gln	Ala	Ile	Phe	Cys	Tyr	Trp	Ile	Thr	Ser	Asn	Leu	Phe	Ser
225					230				235					240	
Leu	Met	Tyr	Gly	Leu	Val	Ile	Lys	Arg	Pro	Gln	Val	Lys	Lys	Met	Leu
			245					250					255		
Arg	Ile	Pro	Asp	Leu	Pro	Pro	Pro	Pro	Gly	Gln	Gln	Pro	Ser	Phe	
		260					265					270			
Asp	Leu	Phe	Ser	Ala	Leu	Lys	Lys	Met	Lys	Ala	Met	Thr	Gln	Asp	His
		275					280				285				
Thr	Gln	Asn	Gln	Ile	Glu	Pro	Pro	Ser	Pro	Val	Asn	Pro	Arg	Leu	Ser
	290				295						300				
Ser	Thr	Ser	Leu	Ser	Pro	Val	Ser	Lys	Arg	Leu	Lys	Ala	Leu	Glu	Ser
305					310				315					320	
Gln	Val	Lys	Gly	Arg	Lys	Lys	Asn	Ser	Ser	Lys	Lys	Lys			
			325					330							

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..681
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

atcgatcact	gaatctctct	ctctctctct	ttctctctct	ttctctctct	ttctctctct	cttctctctt	60
ctctcaagaa	cagatttttt	ttaaaacgagc	ttgatcaata	aattctctct	agatctatgg		120
cggaaagagca	tcgatgtcag	acaccagaaa	gcaaccgtct	ctgtgttaac	aactgtggct		180
ctctcggcag	ctccgccacc	atgaatctct	gttctaattg	ttaacggcgat	ctttgtctca		240
aacaacaaca	acaatctctc	tcctatcaaat	ccaccgttga	atcagcaaca	gaggccgaat		300
cgggtgcacga	cgtgtaggaa	acgggtcggg	ttaaccggat	tcaagtgcgc	gtcgcgttacg		360

atgtttttcgcg	gggttcacatg	gtaccgccgag	atccatggat	gcagctacga	tttcaaatcg	420
gccgcagcgtg	aagagatcgc	gaaagcSaat	ccgttggtga	aagcagcgaa	gcttcagaag	480
atatgatcag	agccggttcga	tgcggttgact	tttctctcgc	taagtcttca	tttctacgcg	540
tatgtgtgtc	ctccgcctccc	cgagaaatac	ggatggtgtc	gatttgattg	atctcagccg	600
ttggatcaaa	aatgggttat	tattgtaaaa	gattgattat	gtatttatca	aagggacacg	660
tgtaacgtgg	ttttaggatg	g				

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Met	Ala	Glu	Glu	His	Arg	Cys	Gln	Thr	Pro	Glu	Ser	Asn	Arg	Leu	Cys
1				5					10					15	
Val	Asn	Asn	Cys	Gly	Phe	Leu	Gly	Ser	Ser	Ala	Thr	Met	Asn	Leu	Cys
			20					25					30		
Ser	Asn	Cys	Tyr	Gly	Asp	Leu	Cys	Leu	Lys	Gln	Gln	Gln	Gln	Ser	Ser
		35				40					45				
Ser	Ile	Lys	Ser	Thr	Val	Glu	Ser	Ala	Thr	Glu	Ala	Glu	Ser	Val	His
		50			55					60					
Asp	Val														
65															

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..38
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Met	Asn	Leu	Cys	Ser	Asn	Cys	Tyr	Gly	Asp	Leu	Cys	Leu	Lys	Gln	Gln
1			5					10					15		
Gln	Gln	Ser	Ser	Ser	Ile	Lys	Ser	Thr	Val	Glu	Ser	Ala	Thr	Glu	Ala
			20					25					30		
Glu	Ser	Val	His	Asp	Val										
		35													

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..41
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

Met	Phe	Cys	Gly	Val	His	Arg	Tyr	Pro	Glu	Ile	His	Gly	Cys	Ser	Tyr
1				5				10					15		
Asp	Phe	Lys	Ser	Ala	Gly	Arg	Glu	Ile	Ala	Lys	Xaa	Asn	Pro	Leu	

20 25 30
Val Lys Ala Ala Lys Leu Gln Lys Ile
35 40

(2) INFORMATION FOR SEQ ID NO:335:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 556 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..556
(D) OTHER INFORMATION: / Ceres Seq. ID 1566650
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:
acytagaaca tctcaatcga aaaacaaggg ttgaaaatga agggacgtca aggagagaga 60
gttagattgt atgttcgtgg aacagtcctc ggctacaaga ggtccaagtc gaaccaatat 120
cccaacactt ctctcatcca gattgaaggt gtgaacactc aagaggagggt caattgggtac 180
aagggtgaagc gtttggctta catctacaag gcaaagacaa agaagaacgg ttctcactac 240
cgttgcattt ggggcaaaagt cactaggcct catggtaaca gcggtgttgt ccgttctaag 300
ttcacttcaa acctaccacc caagtcaatg ggagctagag tcagagtctt catgtaccct 360
agcaacatat gaggaggata gatttcaaga agtatcgtaa ggaatcgcca ttatcatttc 420
tcaggagctg tagtttatct attcactttt gttctaaact ctctgttggt ttgtatttta 480
tccttagacg aagTwaRaac attttcttc ttgagataat attaatggaa cttcagaaaa 540
cctatgatcc cggtct

(2) INFORMATION FOR SEQ ID NO:336:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..111
(D) OTHER INFORMATION: / Ceres Seq. ID 1566651
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:
Met Lys Gly Arg Gln Gly Glu Arg Val Arg Leu Tyr Val Arg Gly Thr
1 5 10 15
Val Leu Gly Tyr Lys Arg Ser Lys Ser Asn Gln Tyr Pro Asn Thr Ser
20 25 30
Leu Ile Gln Ile Glu Gly Val Asn Thr Gln Glu Glu Val Asn Trp Tyr
35 40 45
Lys Gly Lys Arg Leu Ala Tyr Ile Tyr Lys Ala Lys Thr Lys Lys Asn
50 55 60
Gly Ser His Tyr Arg Cys Ile Trp Gly Lys Val Thr Arg Pro His Gly
65 70 75 80
Asn Ser Gly Val Val Arg Ser Lys Phe Thr Ser Asn Leu Pro Pro Lys
85 90 95
Ser Met Gly Ala Arg Val Arg Val Phe Met Tyr Pro Ser Asn Ile
100 105 110

(2) INFORMATION FOR SEQ ID NO:337:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1566652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

Met	Arg	Arg	Ile	Asp	Phe	Lys	Lys	Tyr	Arg	Lys	Glu	Ser	Pro	Leu	Ser
1			5					10						15	
Phe	Leu	Arg	Ser	Cys	Ser	Leu	Ser	Ile	His	Phe	Cys	Ser	Lys	Leu	Ser
			20					25						30	
Val	Gly	Phe	Asp	Phe	Ile	Phe	Arg	Arg	Ser	Xaa	Asn	Ile	Phe	Leu	Leu
			35					40						45	
Glu	Ile	Ile	Leu	Met	Glu	Leu	Gln	Lys	Thr	Tyr	Asp	Pro	Gly		
			50					55						60	

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..675

(D) OTHER INFORMATION: / Ceres Seq. ID 1566661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

atactatcaa	attgaagaag	aggaagatcc	aattggaaaag	ggttatccta	attcccagtc	60
attgatcgga	gaagatgagt	gctgttcgga	ttaaccacct	ttttggctta	ccggagacga	120
tcgagaagct	aattctcccg	atttctcggt	ccggcgaaaag	taataacacg	agtcgtggaa	180
gaggaagtag	caataaatatc	ccaatagaca	ttttggaatc	tcocaaaaaa	tacatatatt	240
atctcgatat	ccccgggaatt	tcaaaatcag	atatccaggt	tacagtggag	gaagagagga	300
ctttagtgat	aaagagtaat	gggaagagga	agagagatga	tgatgagagt	gaagaagggt	360
ctaagtatat	tagactcgag	aggagacttg	ctcagaattt	gggtaaagaag	ttccggttac	420
cagaagatgc	tgatatggct	tctgtaacgg	ctaaatatca	agaaggtatt	ttgacagttg	480
ttatcaagaa	gctaccgcga	cagcgcgcga	aacotaagac	tgttcaaatc	gctgtttctt	540
gagtagtttc	tgtgtttttg	ttttgtgtgt	gtttgttttc	tagtAttgta	attttcttgt	600
ttttggataa	aaagactctg	ttttctttat	gtgttctcta	gtcgaaattt	tgaattgaa	660
gaaataaata	ggtttt					

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1566662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

Met	Ser	Ala	Val	Ala	Ile	Asn	His	Phe	Phe	Gly	Leu	Pro	Glu	Thr	Ile
1			5					10						15	
Glu	Lys	Leu	Ile	Leu	Pro	Ile	Ser	Arg	Ser	Gly	Glu	Ser	Asn	Asn	Glu
			20					25						30	
Ser	Arg	Gly	Arg	Gly	Ser	Ser	Asn	Asn	Ile	Pro	Ile	Asp	Ile	Leu	Glu
			35					40						45	
Ser	Pro	Lys	Lys	Tyr	Ile	Phe	Tyr	Leu	Asp	Ile	Pro	Gly	Ile	Ser	Lys
			50					55						60	
Ser	Asp	Ile	Gln	Val	Thr	Val	Glu	Glu	Glu	Arg	Thr	Leu	Val	Ile	Lys
			65					70						80	
Ser	Asn	Gly	Lys	Arg	Lys	Arg	Asp	Asp	Asp	Glu	Ser	Glu	Glu	Gly	Ser
			85					90						95	
Lys	Tyr	Ile	Arg	Leu	Glu	Arg	Arg	Leu	Ala	Gln	Asn	Leu	Val	Lys	Lys
			100					105						110	
Phe	Arg	Leu	Pro	Glu	Asp	Ala	Asp	Met	Ala	Ser	Val	Thr	Ala	Lys	Tyr

115 120 125
Gln Glu Gly Ile Leu Thr Val Val Ile Lys Lys Leu Pro Pro Gln Pro
130 135 140
Pro Lys Pro Lys Thr Val Gln Ile Ala Val Ser
145 150 155

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..512

(D) OTHER INFORMATION: / Ceres Seq. ID 1566663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

attttgcttt	tcactttctc	cgaacatcca	aaagcttgta	gcttgctcct	caaatcttct	60
tgaaaaatga	aggttgccgc	tgctttctct	ctcgccgttt	tgggcgga	cgtaaatcct	120
tcagccgaga	atatcaaaga	tatcatcgga	gctggttggt	ctgatgtga	tgagagagac	180
attgagcttc	tattgaaaga	agtgagtggt	aaggacattg	ctgagctgat	tgcttctggt	240
agggagaaat	tagcgctctgt	gccatctggt	ggtggtgtgg	ctgtttcagc	tgctccatca	300
agcggtggtg	gtgggtgctgc	tgctgtgcc	ctgcgcgaga	agaaagaagc	caagaaggaa	360
gagaaagaag	agtcctgatga	tgacatggga	ttcagctctc	tcgagtaagg	ttttgtccc	420
cacggaaagg	agtcagagatt	tgattttt	gttctcttag	tggtctggt	ttttgctcct	480
ctttgtaacc	ttggtctagt	tagcgggttt	tt			

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1566664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Met Lys Val Ala Ala Ala Phe Leu Leu Ala Val Leu Gly Gly Asn Ala	
1 5 10 15	
Asn Pro Ser Ala Glu Asn Ile Lys Asp Ile Ile Gly Ala Val Gly Ala	
20 25 30	
Asp Val Asp Gly Glu Ser Ile Glu Leu Leu Lys Glu Val Ser Gly	
35 40 45	
Lys Asp Ile Ala Glu Leu Ile Ala Ser Gly Arg Glu Lys Leu Ala Ser	
50 55 60	
Val Pro Ser Gly Gly Gly Val Ala Val Ser Ala Ala Pro Ser Ser Gly	
65 70 75 80	
Gly Gly Gly Ala Ala Ala Ala Pro Ala Glu Lys Lys Glu Ala Lys	
85 90 95	
Lys Glu Glu Lys Glu Glu Ser Asp Asp Asp Met Gly Phe Ser Leu Phe	
100 105 110	

Glu

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..822

(D) OTHER INFORMATION: / Ceres Seq. ID 1566665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

gtcgcgtctca	attaaaacct	aaaaccctcc	tcagaagaga	ggcagagaga	aaaaaaaaacgc	60
agTcttttcg	gaatctgtga	aaggagaaaa	gatgagacca	ccaatgagag	gcggcgggggg	120
tttccgtgga	aggggaggac	gagacggtgg	tgggtggcgt	aggttcggtg	gaggaggcgg	180
tagattccgt	ggaggaggag	gacgcttttg	tgggtggaggc	ggtcgctttg	gtgggttttag	240
agacgaaggt	cctcctagcg	aagtcgtgga	tgttgcaact	ttcgttcacg	cttcgcgaggg	300
agatgctgtg	accaaactct	cacaggagaa	gattcctcat	tttaacgcctc	cgatctacct	360
agagaacaa	actcagatgt	ggaagtaga	tgaaactctt	ggcccaatta	atgaatcttt	420
gtttttctat	aaatgatgg	aaggtattgt	agccacctcg	tattctccag	gagataagtt	480
cttcacgac	ccttcaaac	ttttgccact	cgctcgattc	cttcctcagc	caaaagggtca	540
gtcaacgggt	ggacgtggag	gtgcaggctg	tggaaagggt	gatagtagag	gtcgtggaag	600
aggtggatca	tttagtagag	gtagaggtgc	tccaaggagt	ggtagatttc	caccacgcgg	660
tggctctcgt	ggaagctttg	gagcccgagg	aagattttag	gtctctctcc	tgctttataa	720
gccttatcca	aactgttacc	ctttgtttta	tgaatgacta	tcgttctccc	gtatttctcaa	780
ttttcaagac	tttggtttta	tctatggagt	aaaaatattt	gc		

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..202

(D) OTHER INFORMATION: / Ceres Seq. ID 1566666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

Met	Arg	Pro	Met	Arg	Gly	Gly	Gly	Gly	Phe	Arg	Gly	Gly	
1			5			10					15		
Arg	Asp	Gly	Gly	Gly	Gly	Phe	Gly	Gly	Gly	Gly	Arg	Phe	
		20				25					30		
Gly	Gly	Gly	Gly	Gly	Arg	Phe	Gly	Gly	Gly	Gly	Arg	Phe	Gly
		35				40					45		
Phe	Arg	Asp	Glu	Gly	Pro	Ser	Glu	Val	Val	Asp	Val	Ala	Thr
		50				55				60			
Val	His	Ala	Cys	Glu	Gly	Asp	Ala	Val	Thr	Lys	Leu	Ser	Gln
		65				70				75			80
Ile	Pro	His	Phe	Asn	Ala	Pro	Ile	Tyr	Leu	Glu	Asn	Lys	Thr
		85				90						95	
Gly	Lys	Val	Asp	Glu	Ile	Phe	Gly	Pro	Ile	Asn	Glu	Ser	Leu
		100				105						110	
Ile	Lys	Met	Met	Glu	Gly	Ile	Val	Ala	Thr	Ser	Tyr	Ser	Pro
		115				120						125	
Lys	Phe	Phe	Ile	Asp	Pro	Tyr	Lys	Leu	Leu	Pro	Leu	Ala	Arg
		130				135					140		
Pro	Gln	Pro	Lys	Gly	Gln	Ser	Thr	Gly	Gly	Arg	Gly	Gly	Ala
		145				150				155			160
Gly	Arg	Gly	Asp	Ser	Arg	Gly	Arg	Gly	Gly	Ser	Phe	Ser	Arg
		165				170						175	
Gly	Arg	Gly	Ala	Pro	Arg	Gly	Gly	Arg	Phe	Pro	Pro	Arg	Gly
		180				185						190	
Arg	Gly	Ser	Phe	Arg	Gly	Arg	Gly	Arg	Phe				
		195				200							

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..198
(D) OTHER INFORMATION: / Ceres Seq. ID 1566667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

Met Arg Gly Gly Gly Gly Phe Arg Gly Arg Gly Arg Asp Gly Gly
1 5 10 15
Gly Gly Gly Arg Phe Gly Gly Gly Gly Gly Arg Phe Gly Gly Gly Gly
20 25 30
Gly Arg Phe Phe Gly Gly Gly Gly Gly Arg Phe Gly Gly Phe Arg Asp Glu
35 40 45
Gly Pro Pro Ser Glu Val Val Asp Val Ala Thr Phe Val His Ala Cys
50 55 60
Glu Gly Asp Ala Val Thr Lys Leu Ser Gln Glu Lys Ile Pro His Phe
65 70 75 80
Asn Ala Pro Ile Tyr Leu Glu Asn Lys Thr Gln Ile Gly Lys Val Asp
85 90 95
Glu Ile Phe Gly Pro Ile Asn Glu Ser Leu Phe Ser Ile Lys Met Met
100 105 110
Glu Gly Ile Val Ala Thr Ser Tyr Ser Pro Gly Asp Lys Phe Phe Ile
115 120 125
Asp Pro Tyr Lys Leu Leu Pro Leu Ala Arg Phe Leu Pro Gln Pro Lys
130 135 140
Gly Gln Ser Thr Gly Gly Arg Gly Gly Ala Gly Arg Gly Arg Gly Asp
145 150 155 160
Ser Arg Gly Arg Gly Arg Gly Gly Ser Phe Ser Arg Gly Arg Gly Ala
165 170 175
Pro Arg Gly Gly Arg Phe Pro Pro Arg Gly Gly Ser Arg Gly Ser Phe
180 185 190
Arg Gly Arg Gly Arg Phe
195

(2) INFORMATION FOR SEQ ID NO:345:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1622 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1622
(D) OTHER INFORMATION: / Ceres Seq. ID 1566671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

ttaaaggat aaataacgat ggcttcgcga tgacgagttc gcacgccaag ctatagctgg 60
gataaaccog gtcaacatag aacgagtcac gtcttatcca ccggtcagca atcttgacc 120
tgaatctcac ggaccaggtc ttoactccgc tctcacggaa gaccacatca tcggtcaact 180
tgatggctta acggtacaac aagcggtaga gatgaaccgt ttgtttatgg tggactacca 240
tgacatatac ttaccggttc tagatagaat caacgcgctt gatggacgca aggcttacgc 300
gactcgaaac atattgtct tgaccggaact cggtaacact aagcctatcg ccacgagct 360
aagctccctc tctcaatcaa gctcaaacca aaagtccaag cgcgttggtc cactccag 420
agacgaacac tccaactgga tgtggcagct agccaaggcc cagcttgggt ccaatgacgc 480
tgggtgtcac cagcttgtga atcattgtgt acgtactcat cgcgttttgg aacgcgttat 540
attagctgct catagacaaat taagcgcaat gcatccgata ttcaaatatt tagaccc 600
catgaggtac actttggaga tcaatgccgt ggcacgacag actttgatta gtccggacgg 660
tgtgatcgaa tcgtgtctca ctgctgtgtca atacggtcta gagattagtt ccgctgcgta 720
taagaacaag tggcggtttg atatggaag tctccctgct gatctcatcc gaagggggat 780
ggctgttcca gacccaacac aaccacatgg gcttaaat 840
ccaacgacgg tctcttatta tgggtccgca tccaaacttg ggtccgaacc tacgtggaac 900

gttattacgc	aaactcgaac	ctaataccaaa	cgcatactga	gctccaagcc	tggtactctg	960
agtcacatca	cgtaRgtcac	gctgatacacc	gcgcgcgcga	gtgggtggccg	aaagctttcca	1020
agtcggaaga	tctcgtctccc	gtcactcccca	ccatcatctg	gctcgccctcc	gcacacacag	1080
cgcgcactcaa	cttcgggacaa	tatccttaacg	gtggctacgt	cccgaaccgga	ccaccgctaa	1140
tgctcgtggt	gattcccgac	gagtcagatc	cgcagttcac	gagttttatc	gaagatcctc	1200
aaaagtattt	tttctcgtcg	atgcccgagtt	tattgcaaac	gacgaagttt	atggcgggtgg	1260
ttgatcacatt	gtcgacacat	tgcgcggatg	aggagtatat	cggagagaga	caacaaccgt	1320
cgatatggac	tgagagatgct	gagatcgtag	atgcgtttta	tggattctctc	gcggaaatcg	1380
gacggataga	gaagagagatt	gacaagagga	atcgtgatcc	tagctgtagg	aatcgtctgtg	1440
gcgcgggagt	gttaccgtag	gagttgatgg	ctccgaggttc	tgaaccgggtg	gttacgtgtga	1500
gaggagtccc	taatagtgta	tctatttaga	attattcaat	ttttcaaggt	atagagaatt	1560
ttataagtat	ataaattagat	tttgacgcag	tatggtttat	ttgcgatat	tgtaaaattc	1620

tt
(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Ser	Lys	Asp	Lys	Tyr	Ala	Trp	Leu	Arg	Asp	Asp	Glu	Phe	Ala	Arg	Gln
1			5					10						15	
Ala	Ile	Ala	Gly	Ile	Asn	Pro	Val	Asn	Ile	Glu	Arg	Val	Thr	Ser	Tyr
			20					25					30		
Pro	Pro	Val	Ser	Asn	Leu	Asp	Pro	Glu	Ile	Tyr	Gly	Pro	Gly	Leu	His
			35				40					45			
Ser	Ala	Leu	Thr	Glu	Asp	His	Ile	Ile	Gly	Gln	Leu	Asp	Gly	Leu	Thr
			50				55					60			
Val	Gln	Gln	Ala	Leu	Glu	Met	Asn	Arg	Leu	Phe	Met	Val	Asp	Tyr	His
						70				75				80	
Asp	Ile	Tyr	Leu	Pro	Phe	Leu	Asp	Arg	Ile	Asn	Ala	Leu	Asp	Gly	Arg
						85				90				95	
Lys	Ala	Tyr	Ala	Thr	Arg	Thr	Ile	Leu	Phe	Leu	Thr	Arg	Leu	Gly	Thr
			100				105						110		
Leu	Lys	Pro	Ile	Ala	Ile	Glu	Leu	Ser	Leu	Pro	Ser	Gln	Ser	Ser	Ser
			115				120					125			
Asn	Gln	Lys	Ser	Lys	Arg	Val	Val	Thr	Pro	Pro	Val	Asp	Ala	Thr	Ser
						135						140			
Asn	Trp	Met	Trp	Gln	Leu	Ala	Lys	Ala	His	Val	Gly	Ser	Asn	Asp	Ala
						150				155				160	
Gly	Val	His	Gln	Leu	Val	Asn	His	Trp	Leu	Arg	Thr	His	Ala	Cys	Leu
						165				170				175	
Glu	Pro	Phe	Ile	Leu	Ala	Ala	His	Arg	Gln	Leu	Ser	Ala	Met	His	Pro
						180				185				190	
Ile	Phe	Lys	Leu	Leu	Asp	Pro	His	Met	Arg	Tyr	Thr	Leu	Glu	Ile	Asn
						200						205			
Ala	Val	Ala	Arg	Gln	Thr	Leu	Ile	Ser	Ala	Asp	Gly	Val	Ile	Glu	Ser
						215						220			
Cys	Phe	Thr	Ala	Gly	Gln	Tyr	Gly	Leu	Glu	Ile	Ser	Ser	Ala	Ala	Tyr
						230				235				240	
Lys	Asn	Lys	Trp	Arg	Phe	Asp	Met	Glu	Gly	Leu	Pro	Ala	Asp	Leu	Ile
						245				250				255	
Arg	Arg	Gly	Met	Ala	Val	Pro	Asp	Pro	Thr	Gln	Pro	His	Gly	Leu	Lys
						260				265				270	
Leu	Leu	Val	Glu	Asp	Tyr	Pro	Cys	Gln	Arg	Arg	Ser	Leu	Ile	Met	Val
						275				280				285	

Arg Asn Pro Asn Leu Gly Pro Asn Leu Arg Gly Thr Leu Leu Arg Lys
290 295 300
Leu Glu Pro Asn Pro Asn Arg Tyr
305 310

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..242
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Met Asn Arg Leu Phe Met Val Asp Tyr His Asp Ile Tyr Leu Pro Phe
1 5 10 15
Leu Asp Arg Ile Asn Ala Leu Asp Gly Arg Lys Ala Tyr Ala Thr Arg
20 25 30
Thr Ile Leu Phe Leu Thr Arg Leu Gly Thr Leu Lys Pro Ile Ala Ile
35 40 45
Glu Leu Ser Leu Pro Ser Gln Ser Ser Asn Gln Lys Ser Lys Arg
50 55 60
Val Val Thr Pro Pro Val Asp Ala Thr Ser Asn Trp Met Trp Gln Leu
65 70 75 80
Ala Lys Ala His Val Gly Ser Asn Asp Ala Gly Val His Gln Leu Val
85 90 95
Asn His Trp Leu Arg Thr His Ala Cys Leu Glu Pro Phe Ile Leu Ala
100 105 110
Ala His Arg Gln Leu Ser Ala Met His Pro Ile Phe Lys Leu Leu Asp
115 120 125
Pro His Met Arg Tyr Thr Leu Glu Ile Asn Ala Val Ala Arg Gln Thr
130 135 140
Leu Ile Ser Ala Asp Gly Val Ile Glu Ser Cys Phe Thr Ala Gly Gln
145 150 155 160
Tyr Gly Leu Glu Ile Ser Ser Ala Ala Tyr Lys Asn Lys Trp Arg Phe
165 170 175
Asp Met Glu Gly Leu Pro Ala Asp Leu Ile Arg Arg Gly Met Ala Val
180 185 190
Pro Asp Pro Thr Gln Pro His Gly Leu Lys Leu Leu Val Glu Asp Tyr
195 200 205
Pro Cys Gln Arg Arg Ser Leu Ile Met Val Arg Asn Pro Asn Leu Gly
210 215 220
Pro Asn Leu Arg Gly Thr Leu Leu Arg Lys Leu Glu Pro Asn Pro Asn
225 230 235 240
Arg Tyr

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..240
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

Met Gly Leu Asn Tyr Leu Leu Lys Thr Thr His Ala Asn Asp Gly Leu

1	5	10	15
Leu Leu Trp Ser Ala Ile Gln Thr Trp Val Arg Thr Tyr Val Glu Arg			
	20	25	30
Tyr Tyr Ala Asn Ser Asn Leu Ile Gln Thr Asp Thr Glu Leu Gln Ala			
	35	40	45
Trp Tyr Ser Glu Ser Ile Asn Val Xaa His Ala Asp His Arg Asp Ala			
	50	55	60
Glu Trp Trp Pro Lys Leu Ser Thr Val Glu Asp Leu Val Ser Val Ile			
	65	70	75
Thr Thr Ile Ile Trp Leu Ala Ser Ala Gln His Ala Ala Leu Asn Phe			
	85	90	95
Gly Gln Tyr Pro Tyr Gly Gly Tyr Val Pro Asn Arg Pro Pro Leu Met			
	100	105	110
Arg Arg Leu Ile Pro Asp Glu Ser Asp Pro Glu Phe Thr Ser Phe Ile			
	115	120	125
Glu Asp Pro Gln Lys Tyr Phe Phe Ser Ser Met Pro Ser Leu Leu Gln			
	130	135	140
Thr Thr Lys Phe Met Ala Val Val Asp Thr Leu Ser Thr His Ser Pro			
	145	150	155
Asp Glu Glu Tyr Ile Gly Glu Arg Gln Gln Pro Ser Ile Trp Thr Gly			
	165	170	175
Asp Ala Glu Ile Val Asp Ala Phe Tyr Gly Phe Ser Ala Glu Ile Gly			
	180	185	190
Arg Ile Glu Lys Glu Ile Asp Lys Arg Asn Arg Asp Pro Ser Cys Arg			
	195	200	205
Asn Arg Cys Gly Ala Gly Val Leu Pro Tyr Glu Leu Met Ala Pro Ser			
	210	215	220
Ser Glu Pro Gly Val Thr Cys Arg Gly Val Pro Asn Ser Val Ser Ile			
	225	230	235
			240

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..847
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

atgactgctt	cactttctct	ttctcttttt	ttcaagtagt	ttgggagaga	gaagagaaga	60
agaagacacc	ctttaagcaa	aacagaggat	tttcattctc	tgttctggtt	gaattattac	120
taactatca	tcttgtgtgt	ctcttcgtcg	acaatgtcgg	gaaacaaga	agaagaggat	180
ctcgtatcc	atggaatcaa	aactaagatc	cggtctgctc	cagattttcc	caagaaagga	240
ataatgtttc	aagacataac	aacagtgttg	ttggatccga	aagccctcaa	agacacaatt	300
gatctgtttg	tgagagagga	caagagacaag	aacatctcag	tggttcgagc	aatagaggct	360
cggtgttttc	tattcggtcc	accgatcgcg	ctaGccattg	gagcaaaaatt	tgttcctctg	420
cgcaaaccca	agaaactacc	tggtgaaaca	atatttgagg	aatacagagt	ggaatatgga	480
aatgacgcgc	tagagatgca	cataggagcc	gtcgaggctg	gcgatcgatc	tttggtogtt	540
gatgatctta	tcgcgactgg	tggtactctc	tcgcgctgcc	ttactctgct	cgagagggtt	600
ggagcagaag	ttgtggaaatg	tgcatgtgtg	atcgagttac	ccgaattaaa	gggaagcgag	660
agacttaagg	ggaagccact	atgtatgctt	gtggagtacc	gatgatgatt	ttagctttac	720
ttatttggat	aaaattattc	gggttaattaa	tttatgctcc	gaaaattcgg	attatgcaga	780
ctctttatta	ttggattcta	caataatttg	atttaaattc	tagcggatta	gctggaagaa	840
ataatcc						

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..183
(D) OTHER INFORMATION: / Ceres Seq. ID 1566684
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Met	Ser	Gly	Asn	Lys	Glu	Glu	Glu	Asp	Pro	Arg	Ile	His	Gly	Ile	Lys
1			5					10					15		
Thr	Lys	Ile	Arg	Val	Val	Pro	Asp	Phe	Pro	Lys	Lys	Gly	Ile	Met	Phe
			20					25					30		
Gln	Asp	Ile	Thr	Thr	Val	Leu	Leu	Asp	Pro	Lys	Ala	Phe	Lys	Asp	Thr
			35					40					45		
Ile	Asp	Leu	Phe	Val	Glu	Arg	Tyr	Arg	Asp	Lys	Asn	Ile	Ser	Val	Val
			50					55				60			
Ala	Gly	Ile	Glu	Ala	Arg	Gly	Phe	Leu	Phe	Gly	Pro	Pro	Ile	Ala	Leu
65								70							80
Ala	Ile	Gly	Ala	Lys	Phe	Val	Pro	Leu	Arg	Lys	Pro	Lys	Lys	Leu	Pro
								85							
Gly	Glu	Thr	Ile	Phe	Glu	Glu	Tyr	Glu	Leu	Glu	Tyr	Gly	Asn	Asp	Arg
								100					110		
Leu	Glu	Met	His	Ile	Gly	Ala	Val	Glu	Ala	Gly	Asp	Arg	Ser	Leu	Val
								115					125		
Val	Asp	Asp	Leu	Ile	Ala	Thr	Gly	Gly	Thr	Leu	Cys	Ala	Ala	Ile	Asn
								130					140		
Leu	Leu	Glu	Arg	Val	Gly	Ala	Glu	Val	Val	Glu	Cys	Ala	Cys	Val	Ile
								145					155		160
Glu	Leu	Pro	Glu	Leu	Lys	Gly	Arg	Gln	Arg	Leu	Lys	Gly	Lys	Pro	Leu
								165					175		
Cys	Met	Leu	Val	Glu	Tyr	Arg									
															180

(2) INFORMATION FOR SEQ ID NO:351:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..153
(D) OTHER INFORMATION: / Ceres Seq. ID 1566685
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

Met	Phe	Gln	Asp	Ile	Thr	Thr	Val	Leu	Leu	Asp	Pro	Lys	Ala	Phe	Lys
1				5						10				15	
Asp	Thr	Ile	Asp	Leu	Phe	Val	Glu	Arg	Tyr	Arg	Asp	Lys	Asn	Ile	Ser
				20						25				30	
Val	Val	Ala	Gly	Ile	Glu	Ala	Arg	Gly	Phe	Leu	Phe	Gly	Pro	Pro	Ile
				35						40				45	
Ala	Leu	Ala	Ile	Gly	Ala	Lys	Phe	Val	Pro	Leu	Arg	Lys	Pro	Lys	Lys
								55					60		
Leu	Pro	Gly	Glu	Thr	Ile	Phe	Glu	Glu	Tyr	Glu	Leu	Glu	Tyr	Gly	Asn
								70					75		80
Asp	Arg	Leu	Glu	Met	His	Ile	Gly	Ala	Val	Glu	Ala	Gly	Asp	Arg	Ser
								85					90		95
Leu	Val	Val	Asp	Asp	Leu	Ile	Ala	Thr	Gly	Gly	Thr	Leu	Cys	Ala	Ala
								100					110		
Ile	Asn	Leu	Leu	Glu	Arg	Val	Gly	Ala	Glu	Val	Val	Glu	Cys	Ala	Cys
								115					120		125

Val Ile Glu Leu Pro Glu Leu Lys Gly Arg Gln Arg Leu Lys Gly Lys
130 135 140
Pro Leu Cys Met Leu Val Glu Tyr Arg
145 150

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..604
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

gcgactctcc	tctctgtttc	gttttttttt	cccttcattc	ttcttatctc	ctcactactt	60
tcgaacaagg	aggaacccta	atctcaagat	gaatagggaa	aagttgatga	agatggctaa	120
caccgtccgc	actggcgga	aggggtacagt	cagaagaaag	aagaaggctg	tgcaacaagac	180
caatacaact	gatgacaaga	ggctccagag	cacacttaag	agaattggag	ttaactccat	240
tcccgtattt	gaagaagtta	acatctttta	ggatgatgtt	gttattcagt	tcatacaacc	300
taaggttcaa	gcttcaattg	ctgcaaacac	atgggtgtgt	agcgggttct	ctcagaccaa	360
aaaattgcaa	gatatccctc	ctcagatcat	cagccaactt	ggaccagaca	acatggacaa	420
cctgaagaag	ctagcagagc	agttccagaa	acaggtctct	ggtgaaggta	atgccgcctc	480
agcaaccatt	caagaagagg	atgatgacga	tgctccagag	cttggtggag	agacattcga	540
aactgctgct	gaagagaaag	caccagctgc	tgctgcttct	tcttagagag	aaaagagcga	600

gacc

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..194
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

Arg	Leu	Ser	Ser	Leu	Phe	Arg	Phe	Phe	Phe	Leu	Ser	Phe	Phe	Leu	Ser
1			5					10					15		
Pro	His	Thr	Leu	Arg	Thr	Arg	Arg	Asn	Pro	Asn	Leu	Lys	Met	Asn	Arg
			20					25					30		
Glu	Lys	Leu	Met	Lys	Met	Ala	Asn	Thr	Val	Arg	Thr	Gly	Gly	Lys	Gly
			35				40					45			
Thr	Val	Arg	Arg	Lys	Lys	Lys	Ala	Val	His	Lys	Thr	Asn	Thr	Thr	Asp
			50			55					60				
Asp	Lys	Arg	Leu	Gln	Ser	Thr	Leu	Lys	Arg	Ile	Gly	Val	Asn	Ser	Ile
			65			70				75				80	
Pro	Ala	Ile	Glu	Glu	Val	Asn	Ile	Phe	Lys	Asp	Asp	Val	Val	Ile	Gln
				85				90					95		
Phe	Ile	Asn	Pro	Lys	Val	Gln	Ala	Ser	Ile	Ala	Ala	Asn	Thr	Trp	Val
			100				105						110		
Val	Ser	Gly	Ser	Pro	Gln	Thr	Lys	Lys	Leu	Gln	Asp	Ile	Leu	Pro	Gln
			115				120					125			
Ile	Ile	Ser	Gln	Leu	Gly	Pro	Asp	Asn	Met	Asp	Asn	Leu	Lys	Lys	Leu
			130			135					140				
Ala	Glu	Gln	Phe	Gln	Lys	Gln	Ala	Ser	Gly	Glu	Gly	Asn	Ala	Ala	Ser
			145			150				155				160	
Ala	Thr	Ile	Gln	Glu	Glu	Asp	Asp	Asp	Asp	Val	Pro	Glu	Leu	Gly	Gly
			165					170						175	

Glu Thr Phe Glu Thr Ala Ala Glu Glu Lys Ala Pro Ala Ala Ala Ala
180 185 190
Ser Ser

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

Met Asn Arg Glu Lys Leu Met Lys Met Ala Asn Thr Val Arg Thr Gly
1 5 10 15
Gly Lys Gly Thr Val Arg Arg Lys Lys Lys Ala Val His Lys Thr Asn
20 25 30
Thr Thr Asp Asp Lys Arg Leu Gln Ser Thr Leu Lys Arg Ile Gly Val
35 40 45
Asn Ser Ile Pro Ala Ile Glu Glu Val Asn Ile Phe Lys Asp Asp Val
50 55 60
Val Ile Gln Phe Ile Asn Pro Lys Val Gln Ala Ser Ile Ala Ala Asn
65 70 75 80
Thr Trp Val Val Ser Gly Ser Pro Gln Thr Lys Lys Leu Gln Asp Ile
85 90 95
Leu Pro Gln Ile Ile Ser Gln Leu Gly Pro Asp Asn Met Asp Asn Leu
100 105 110
Lys Lys Leu Ala Glu Gln Phe Gln Lys Gln Ala Ser Gly Glu Gly Asn
115 120 125
Ala Ala Ser Ala Thr Ile Gln Glu Glu Asp Asp Asp Val Pro Glu
130 135 140
Leu Val Gly Glu Thr Phe Glu Thr Ala Ala Glu Glu Lys Ala Pro Ala
145 150 155 160
Ala Ala Ala Ser Ser
165

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

Met Lys Met Ala Asn Thr Val Arg Thr Gly Lys Gly Thr Val Arg
1 5 10 15
Arg Lys Lys Lys Ala Val His Lys Thr Asn Thr Thr Asp Asp Lys Arg
20 25 30
Leu Gln Ser Thr Leu Lys Arg Ile Gly Val Asn Ser Ile Pro Ala Ile
35 40 45
Glu Glu Val Asn Ile Phe Lys Asp Asp Val Val Ile Gln Phe Ile Asn
50 55 60
Pro Lys Val Gln Ala Ser Ile Ala Ala Asn Thr Trp Val Val Ser Gly
65 70 75 80
Ser Pro Gln Thr Lys Lys Leu Gln Asp Ile Leu Pro Gln Ile Ile Ser

	85		90		95									
Gln	Leu	Gly	Pro	Asn	Met	Asp	Asn	Leu	Lys	Lys	Leu	Ala	Glu	Gln
	100						105						110	
Phe	Gln	Lys	Gln	Ala	Ser	Gly	Glu	Gly	Asn	Ala	Ala	Ser	Ala	Thr
	115						120						125	
Gln	Glu	Glu	Asp	Asp	Asp	Asp	Val	Pro	Glu	Leu	Val	Gly	Glu	Thr
	130						135						140	
Glu	Thr	Ala	Ala	Glu	Glu	Lys	Ala	Pro	Ala	Ala	Ala	Ala	Ser	Ser
	145						150						155	

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..930
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

accacaaaatg	cccttttgccc	ctctctctct	atatccaaacc	catgtctcct	ctttatctct	60
ctaacttttc	cccttagagag	attcctcttt	ctctcaaac	aggggtttcc	ctctgaaaaac	120
aacaaaaata	tcaccaataat	tgcaaaatct	acttgaagat	ttttcattct	ccctttcttat	180
aattaatgcc	caagagagaa	acaaagaaga	tcaaaccttc	tcaagaagtt	atcaaggaag	240
gaaccttttc	tgttacgatc	catttaaagg	ggatatatat	tcggaactac	acaaactcac	300
cgtgtgcagc	atgcaaatcc	ctccggcgta	aatgcacgtc	agactgcgta	ttcgaccctc	360
attttccgcc	ggaggaacct	acaaagtgtt	cgaacgtcca	ccggatattc	ggggcaagca	420
atgtgagcaa	gatcctccac	gaaGTggcNt	ccccatcagc	gggaagatgc	gggtcaactcg	480
ctggcttaag	aggcggaaag	acgacttaaa	gatccagtgt	atggctgcgt	tggagcgatc	540
tcgggtgcC	aaagacaggt	cttgagggtg	caaaagggaac	tcgaggagac	aaatgctgat	600
ctcatggagt	acgctgggtg	tctcgggtgt	gaaacgacgt	cggcttatgg	tggtcgaggg	660
gggtgactgg	tcaacgagag	ttgattagtc	atcatcactc	tttgagaaaa	ttagcggcgg	720
agaagtataa	agagagagag	gatgggtgat	gtgatggtaa	gtgttattag	tcgtatgtat	780
atatgtgtaa	atatggggac	aggcatgcat	gtatatattat	gtttattttc	atgtatatat	840
ttatgcgtat	gtgtaattta	acttggtaatt	ttttttcatg	ggagaggcca	aggaatattt	900
ttgatgatgt	tgaataacta	gatcttgctc				

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

Met	Pro	Lys	Arg	Glu	Thr	Lys	Lys	Ile	Lys	Pro	Ser	Gln	Glu	Val	Ile
1		5						10					15		
Lys	Glu	Gly	Pro	Phe	Leu	Val	Thr	Ile	His	Leu	Lys	Gly	Ile	Tyr	Met
		20						25					30		
Ser	Asn	Tyr	Thr	Asn	Ser	Pro	Cys	Ala	Ala	Cys	Lys	Phe	Leu	Arg	Arg
		35						40					45		
Lys	Cys	Thr	Ser	Asp	Cys	Val	Phe	Ala	Pro	Tyr	Phe	Pro	Pro	Glu	Glu
		50						55					60		
Pro	Thr	Lys	Phe	Ala	Asn	Val	His	Arg	Ile	Phe	Gly	Ala	Ser	Asn	Val
		65						70					75		80
Ser	Lys	Ile	Leu	His	Glu	Val	Xaa	Ser	Pro	Ser	Ala	Gly	Arg	Cys	Gly
		85						90					95		

Gln Leu Ala Gly Leu Arg Gly Gly Ser Thr Thr
100 105

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1566701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

Met Ser Asn Tyr Thr Asn Ser Pro Cys Ala Ala Cys Lys Phe Leu Arg
1 5 10 15
Arg Lys Cys Thr Ser Asp Cys Val Phe Ala Pro Tyr Phe Pro Pro Glu
20 25 30
Glu Pro Thr Lys Phe Ala Asn Val His Arg Ile Phe Gly Ala Ser Asn
35 40 45
Val Ser Lys Ile Leu His Glu Val Xaa Ser Pro Ser Ala Gly Arg Cys
50 55 60
Gly Gln Leu Ala Gly Leu Arg Gly Gly Ser Thr Thr
65 70 75

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1566702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

Met His Val Arg Leu Arg Ile Arg Thr Leu Phe Ser Ala Gly Gly Thr
1 5 10 15
Tyr Lys Val Cys Glu Arg Pro Pro Asp Ile Arg Gly Lys Gln Cys Glu
20 25 30
Gln Asp Pro Pro Arg Ser Gly Xaa Pro Ile Ser Gly Lys Met Arg Ser
35 40 45
Thr Arg Trp Leu Thr Arg Arg Lys His Asp Leu Lys Ile Gln Cys Met
50 55 60
Ala Ala Leu Glu Arg Ser Arg Cys Ser Lys Asp Arg Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 960 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..960

(D) OTHER INFORMATION: / Ceres Seq. ID 1566707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

accattaaac	caggtctttaa	gtacaaaact	tcaaacaaaa	ggctcaaaagc	taatttcttt	60
tttttgctaa	gaaaaactaa	tttcttctc	ttcgacctc	caagtctcaa	gcatactag	120
ataaacaat	ctatttccg	tcattggcagc	aatgaccgcg	gcagcagttc	cagcaactgg	180

atctttccag	aaacaagacg	aggagtggcg	tgccgttctg	tctcctgagc	agtttaggg	240
tctcagacta	aaaggcacag	agtaagaagt	cctctagggt	ttttattttt	atttttctgt	300
ttactttgag	agcaagaagt	ttacctgaac	atgttgtaa	tggttaattt	gggtatttag	360
taaacggagg	aaaggagagt	ttacaagaa	gttcgaggaa	gggacttata	gttgtgctgg	420
ttgtggaact	gctctttata	aatcgaccac	taagtctgac	tccggttgcc	gttgccctgc	480
gttcttcgac	gccatccccc	gtgctattaa	acaaactgta	attogttcac	tctttctctc	540
tagcaaataa	catattttga	gcatccatat	tctgaaact	cattgactat	aacattgact	600
attttagcca	aaccggcaaa	cccatttaag	gattgtaatt	acaataacta	atttgatgtt	660
tttaaatgta	tatagccaga	agcaggtgga	agaagaatgg	agataacatg	tcagatgtgt	720
gatggacatt	taggccaagt	tttcaaaagg	gaagggttact	ctactccaac	cgatcaacgt	780
caCtgcggtt	acagtgcttc	tctcaaattc	tctctgctgt	gttctcccca	ataatcatat	840
cattgatcgg	accaatttat	ctcatgaaat	caagaatcta	ttctatgata	tcgtgtgagct	900
tgctaggttt	ctttcccata	ctcatgtaat	attatgattc	ctatgtgtgt	gtttttctct	960

(2) INFORMATION FOR SEQ ID NO:361:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..40
(D) OTHER INFORMATION: / Ceres Seq. ID 1566708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

Met	Ala	Ala	Met	Thr	Ala	Ala	Ala	Val	Pro	Ala	Thr	Gly	Ser	Phe	Gln
1			5					10					15		
Lys	Gln	Asp	Glu	Glu	Trp	Arg	Ala	Val	Leu	Ser	Pro	Glu	Gln	Phe	Arg
			20					25					30		
Val	Leu	Arg	Leu	Lys	Gly	Thr	Glu								
			35				40								

(2) INFORMATION FOR SEQ ID NO:362:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..45
(D) OTHER INFORMATION: / Ceres Seq. ID 1566709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

Met	Glu	Ile	Thr	Cys	Ala	Val	Cys	Asp	Gly	His	Leu	Gly	His	Val	Phe
1				5				10					15		
Lys	Gly	Glu	Gly	Tyr	Ser	Thr	Pro	Thr	Asp	Gln	Arg	His	Cys	Val	Asn
				20				25					30		
Ser	Val	Ser	Leu	Lys	Phe	Ser	Ser	Ala	Gly	Ser	Ser	Gln			
			35				40					45			

(2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..66
(D) OTHER INFORMATION: / Ceres Seq. ID 1566710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

Met Phe Ser Lys Ala Lys Val Thr Leu Leu Gln Pro Ile Asn Val Thr
1 5 10 15
Ala Leu Thr Val Ser Leu Ser Asn Ser Leu Leu Leu Val Pro Pro Asn
20 25 30
Asn His Ile Ile Asp Arg Thr Thr Leu Ser His Glu Ile Lys Asn Leu
35 40 45
Phe Tyr Asp Leu Cys Glu Leu Ala Arg Phe Leu Ser His Thr His Val
50 55 60
Ile Leu
65

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1279
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

gttttgggtgt ttcttgcgtcg acgtgcgttat ctccaatctct attactcccc ttcttcaatg 60
atcataaaac ctacttcgat tctactcctt atcaactgaa tcaccgaaaa acctcacctt 120
ttttcttttt ccgatcatgg ggaatctgat cagtttgatc ttctgtgtcg ggagaaggca 180
gaggagcaat attctctcgg cgaatggaaac ggctctcttt gaactccac cgaacagatt 240
tgtattcgcc gcgcgcgcac catatctgaa ccttaaccct aactacgttg accagtatcc 300
aggttaactgc ctctctcgcg cagtaactga gcgcgcgatg ctacgtgaca atttcaacca 360
tttgcatacac tatctctccc acagttacca actactctat cctttgttcc acggcggtag 420
ataccctata ctgcgcgcctc ctacgtacgt ccaccagaaa gccgtcacga ttcgtaacga 480
tgttaactctg aagaagaaga ctttaacgct cataccgcac ccggagaatc cgaatcgact 540
tcttgtctcc ttcaactattg atgcattccat gcccggaagg atcacagttg ttttttttgc 600
tacagaagat gcagaatgta atcttagagc tacaaaaggaa gatactttgc ctccaatcac 660
ttttgatitc ggagaaggac ttggtcagaa gtccatacaa tcactcggaa cgggtataga 720
cttgacggcg tttaaagatt ccgagctatt caaggagggtg gatacagatg tcttcccggt 780
ggcggttaag gcggaggcaa ctccagcgga agaaggaaa tctGgttcca ccaatgtgca 840
gattactcaa gtgggtgata ccaaggagaa agggagagatt aaaatagaag tgggtgaagca 900
gataactatg gtgaataaga ggaggtatga gctgcttgag atttatggga ttgagaacac 960
gggtgatggt tccgatgagg gaaaggaaatg tgtgtgatgc ttgtctgaac caccgcatac 1020
aactgttctt cctctgcagc acatgtgtat gtgtagcggg tgcgcaaaag cgttaaagtt 1080
tcagacaaat ctgtgccagc ttgtcagaca aactgttgag atgcttttgc agattaacaa 1140
gaacggatga aatggagatg gagaatgaac aaattttagt aagcaatcga cttgtgtaat 1200
atatgccatg cttaattaag acgtaaaacg ttatggttca atatattata agtggaaact 1260
gagttcttaa atagcaatg

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..337
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

Met Gly Asn Leu Ile Ser Leu Ile Phe Cys Cys Gly Arg Arg Gln Arg
1 5 10 15
Ser Asn Ile Pro Pro Ala Met Glu Thr Ala Pro Leu Glu Leu Pro Pro
20 25 30

Asn Arg Phe Val Phe Ala Ala Ala Pro Pro Tyr Leu Asn Pro Asn Pro
35 40 45
Asn Tyr Val Asp Gln Tyr Pro Gly Asn Cys Leu Pro Pro Val Thr
50 55 60
Glu Pro Pro Met Leu Pro Tyr Asn Phe Asn His Leu His His Tyr Pro
65 70 75 80
Pro Asn Ser Tyr Gln Leu Pro His Pro Leu Phe His Gly Gly Arg Tyr
85 90 95
Pro Ile Leu Pro Pro Pro Thr Tyr Val His Gln Lys Ala Val Thr Ile
100 105 110
Arg Asn Asp Val Asn Leu Lys Lys Lys Thr Leu Thr Leu Ile Pro Asp
115 120 125
Pro Glu Asn Pro Asn Arg Leu Leu Val Ser Phe Thr Phe Asp Ala Ser
130 135 140
Met Pro Gly Arg Ile Thr Val Val Phe Phe Ala Thr Glu Asp Ala Glu
145 150 155 160
Cys Asn Leu Arg Ala Thr Lys Glu Asp Thr Leu Pro Pro Ile Thr Phe
165 170 175
Asp Phe Gly Glu Gly Leu Gly Gln Lys Phe Ile Gln Ser Ser Gly Thr
180 185 190
Gly Ile Asp Leu Thr Ala Phe Lys Asp Ser Glu Leu Phe Lys Glu Val
195 200 205
Asp Thr Asp Val Phe Pro Leu Ala Val Lys Ala Glu Ala Thr Pro Ala
210 215 220
Glu Glu Gly Lys Ser Gly Ser Thr Asn Val Gln Ile Thr Gln Val Val
225 230 235 240
Tyr Thr Lys Glu Lys Gly Glu Ile Lys Ile Glu Val Val Lys Gln Ile
245 250 255
Leu Trp Val Asn Lys Arg Arg Tyr Glu Leu Leu Glu Ile Tyr Gly Ile
260 265 270
Glu Asn Thr Val Asp Gly Ser Asp Glu Gly Lys Glu Cys Val Val Cys
275 280 285
Leu Ser Glu Pro Arg Asp Thr Thr Val Leu Pro Cys Arg His Met Cys
290 295 300
Met Cys Ser Gly Cys Ala Lys Ala Leu Arg Phe Gln Thr Asn Leu Cys
305 310 315 320
Pro Val Cys Arg Gln Pro Val Glu Met Leu Leu Glu Ile Asn Lys Asn
325 330 335
Gly

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..315

(D) OTHER INFORMATION: / Ceres Seq. ID 1566713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

Met Glu Thr Ala Pro Leu Glu Leu Pro Pro Asn Arg Phe Val Phe Ala
1 5 10 15
Ala Ala Pro Pro Tyr Leu Asn Pro Asn Pro Asn Tyr Val Asp Gln Tyr
20 25 30
Pro Gly Asn Cys Leu Pro Pro Pro Val Thr Glu Pro Pro Met Leu Pro
35 40 45
Tyr Asn Phe Asn His Leu His His Tyr Pro Pro Asn Ser Tyr Gln Leu
50 55 60
Pro His Pro Leu Phe His Gly Gly Arg Tyr Pro Ile Leu Pro Pro Pro

65	Thr	Tyr	Val	His	Gln	Lys	Ala	Val	Thr	Ile	Arg	Asn	Asp	Val	Asn	Leu
				85						90				95		
Lys	Lys	Lys	Thr	Leu	Thr	Leu	Ile	Pro	Asp	Pro	Glu	Asn	Pro	Asn	Arg	
			100					105					110			
Leu	Leu	Val	Ser	Phe	Thr	Phe	Asp	Ala	Ser	Met	Pro	Gly	Arg	Ile	Thr	
		115					120					125				
Val	Val	Phe	Phe	Ala	Thr	Glu	Asp	Ala	Glu	Cys	Asn	Leu	Arg	Ala	Thr	
	130					135					140					
Lys	Glu	Asp	Thr	Leu	Pro	Pro	Ile	Thr	Phe	Asp	Phe	Gly	Glu	Gly	Leu	
145				150					155						160	
Gly	Gln	Lys	Phe	Ile	Gln	Ser	Ser	Gly	Thr	Gly	Ile	Asp	Leu	Thr	Ala	
			165					170					175			
Phe	Lys	Asp	Ser	Glu	Leu	Phe	Lys	Glu	Val	Asp	Thr	Asp	Val	Phe	Pro	
	180						185						190			
Leu	Ala	Val	Lys	Ala	Glu	Ala	Thr	Pro	Ala	Glu	Glu	Gly	Lys	Ser	Gly	
	195						200					205				
Ser	Thr	Asn	Val	Gln	Ile	Thr	Gln	Val	Val	Tyr	Thr	Lys	Glu	Lys	Gly	
	210					215					220					
Glu	Ile	Lys	Ile	Glu	Val	Val	Lys	Gln	Ile	Leu	Trp	Val	Asn	Lys	Arg	
225				230						235					240	
Arg	Tyr	Glu	Leu	Leu	Glu	Ile	Tyr	Gly	Ile	Glu	Asn	Thr	Val	Asp	Gly	
			245					250						255		
Ser	Asp	Glu	Gly	Lys	Glu	Cys	Val	Val	Cys	Leu	Ser	Glu	Pro	Arg	Asp	
	260							265					270			
Thr	Thr	Val	Leu	Pro	Cys	Arg	His	Met	Cys	Met	Cys	Ser	Gly	Cys	Ala	
	275						280					285				
Lys	Ala	Leu	Arg	Phe	Gln	Thr	Asn	Leu	Cys	Pro	Val	Cys	Arg	Gln	Pro	
	290					295					300					
Val	Glu	Met	Leu	Leu	Glu	Ile	Asn	Lys	Asn	Gly						
305					310					315						

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..270
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

Met	Leu	Pro	Tyr	Asn	Phe	Asn	His	Leu	His	His	Tyr	Pro	Pro	Asn	Ser
1				5				10					15		
Tyr	Gln	Leu	Pro	His	Pro	Leu	Phe	His	Gly	Gly	Arg	Tyr	Pro	Ile	Leu
			20					25					30		
Pro	Pro	Pro	Thr	Tyr	Val	His	Gln	Lys	Ala	Val	Thr	Ile	Arg	Asn	Asp
		35				40					45				
Val	Asn	Leu	Lys	Lys	Lys	Thr	Leu	Thr	Leu	Ile	Pro	Asp	Pro	Glu	Asn
	50				55					60					
Pro	Asn	Arg	Leu	Leu	Val	Ser	Phe	Thr	Phe	Asp	Ala	Ser	Met	Pro	Gly
65				70					75					80	
Arg	Ile	Thr	Val	Val	Phe	Phe	Ala	Thr	Glu	Asp	Ala	Glu	Cys	Asn	Leu
			85					90					95		
Arg	Ala	Thr	Lys	Glu	Asp	Thr	Leu	Pro	Pro	Ile	Thr	Phe	Asp	Phe	Gly
	100						105					110			
Glu	Gly	Leu	Gly	Gln	Lys	Phe	Ile	Gln	Ser	Ser	Gly	Thr	Gly	Ile	Asp
	115					120						125			
Leu	Thr	Ala	Phe	Lys	Asp	Ser	Glu	Leu	Phe	Lys	Glu	Val	Asp	Thr	Asp
	130					135						140			

Val Phe Pro Leu Ala Val Lys Ala Glu Ala Thr Pro Ala Glu Glu Gly	
145	150 155 160
Lys Ser Gly Ser Thr Asn Val Gln Ile Thr Gln Val Val Tyr Thr Lys	
	165 170 175
Glu Lys Gly Glu Ile Lys Ile Glu Val Val Lys Gln Ile Leu Trp Val	
	180 185 190
Asn Lys Arg Arg Tyr Glu Leu Leu Glu Ile Tyr Gly Ile Glu Asn Thr	
	195 200 205
Val Asp Gly Ser Asp Glu Gly Lys Glu Cys Val Val Cys Leu Ser Glu	
	210 215 220
Pro Arg Asp Thr Thr Val Leu Pro Cys Arg His Met Cys Met Cys Ser	
225	230 235 240
Gly Cys Ala Lys Ala Leu Arg Phe Gln Thr Asn Leu Cys Pro Val Cys	
	245 250 255
Arg Gln Pro Val Glu Met Leu Leu Glu Ile Asn Lys Asn Gly	
	260 265 270

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1537
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

aatcaacacaca	cacaaacaca	cacacacaca	gcctttttcc	ttcgttgatc	gattgttaag	60
ctcgatccaa	tggcggataa	caccgataat	cggagatcct	tatggggagt	tccggagaag	120
cttcagcttc	acatagcgat	gctgacgttg	caattcggtt	acgcgcgatt	ccacgtgggtg	180
tctcagctgc	ctcttaacat	gggaatcagc	aaactcgtct	tccctgttta	tcgtaacatc	240
atgccttgc	ttcttctct	tccttctcgt	tacttctctg	aaaagaagga	gagaccagcg	300
attactctca	actttctcat	ccagttcttc	tttttggcac	tcataggaat	aacagcgaac	360
caaggatttt	acttgttggg	actggacaac	acttcaccaa	catttgcttc	ctccatgcaa	420
aaactctgtt	cgcccatcac	ctttctcatg	gctgctcttc	tcaggattga	gaaagtaaga	480
ataaacagaa	gagacgggat	ctccaaaatc	ttaggaaacg	ctctttgtgt	cgccggagct	540
tcctgcatca	ccctctataa	aggtccaacc	atctacactc	cggctagcca	ccctccagct	600
catctactca	ccacaaactc	cgccgtctta	gcgcgcctag	gaaacgcgcg	gcctaaaaac	660
tggacccctg	gttgcatcta	ccctaactgg	cactgtctct	cgttggtcagg	ctggcttgtt	720
ttccaagctc	cggtttctaa	gtcttatcca	gcgaggtctc	cggtttacct	ttacacttgt	780
ttctctggaa	tcattoagtt	cttgatcatt	gctgctttct	gtgaaagaga	ttctcaggct	840
tgggtttttc	acgtcgggtg	ggagcttttc	accatcctct	acgcgcggaat	cgtagcgtct	900
ggaatcgcgt	ttgcggttca	gatttgggtg	attgacagag	gggggtccagt	cttcgttgct	960
gtttaccagc	ctgttcagac	tcttctgtgt	gcgatcatgg	ctctatttgc	gttaggcgaa	1020
gaattttatt	tgggggggat	tattggagcg	gtcttgatca	tagcgggact	ttActtcgtta	1080
ttgtacggta	agagcgaaga	gaggaataat	gcagcgcgtg	agaaggcaga	gattccagctc	1140
tcgcggagcg	atggtattga	acgtgcacct	gtttctcgca	actccatcaa	gtcgtccatc	1200
acaacaccac	tactccatca	gtcaacggag	aatgtttgac	tactttggac	aaatcaactct	1260
ccagcttaata	attacaagt	ccattaccaca	attaaaaggg	aacaatgggtg	tgccgtttgtg	1320
ttttatgact	tttgtgtctg	ctttttttct	tagtgttttc	tcttcttttt	tttttctaaa	1380
aaattattaa	ttaccttaaga	aaggtttttg	aagaaaaggaa	aaaaaatgg	tggatgagac	1440
atcattgttc	atgaggatga	tgatgatgat	gatagtgatg	aagaagacta	tgtgggagct	1500
ttgattggag	acttttctat	atataatc	tggctgg			

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..389

(D) OTHER INFORMATION: / Ceres Seq. ID 1566716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

Met Ala Asp Asn Thr Asp Asn Arg Arg Ser Leu Trp Gly Val Pro Glu
1 5 10 15
Lys Leu Gln Leu His Ile Ala Met Leu Thr Leu Gln Phe Gly Tyr Ala
20 25 30
Gly Phe His Val Val Ser Arg Ala Ala Leu Asn Met Gly Ile Ser Lys
35 40 45
Leu Val Phe Pro Val Tyr Arg Asn Ile Ile Ala Leu Leu Leu Leu
50 55 60
Pro Phe Ala Tyr Phe Leu Glu Lys Lys Glu Arg Pro Ala Ile Thr Leu
65 70 75 80
Asn Phe Leu Ile Gln Phe Phe Phe Leu Ala Leu Ile Gly Ile Thr Ala
85 90 95
Asn Gln Gly Phe Tyr Leu Leu Gly Leu Asp Asn Thr Ser Pro Thr Phe
100 105 110
Ala Ser Ser Met Gln Asn Ser Val Pro Ala Ile Thr Phe Leu Met Ala
115 120 125
Ala Leu Leu Arg Ile Glu Lys Val Arg Ile Asn Arg Arg Asp Gly Ile
130 135 140
Ser Lys Ile Leu Gly Thr Ala Leu Cys Val Ala Gly Ala Ser Val Ile
145 150 155 160
Thr Leu Tyr Lys Gly Pro Thr Ile Tyr Thr Pro Ala Ser His Leu His
165 170 175
Ala His Leu Leu Thr Thr Asn Ser Ala Val Leu Ala Pro Leu Gly Asn
180 185 190
Ala Ala Pro Lys Asn Trp Thr Leu Gly Cys Ile Tyr Leu Ile Gly His
195 200 205
Cys Leu Ser Trp Ser Gly Trp Leu Val Phe Gln Ala Pro Val Leu Lys
210 215 220
Ser Tyr Pro Ala Arg Leu Ser Val Thr Ser Tyr Thr Cys Phe Phe Gly
225 230 235 240
Ile Ile Gln Phe Leu Ile Ile Ala Ala Phe Cys Glu Arg Asp Ser Gln
245 250 255
Ala Trp Val Phe His Ser Gly Trp Glu Leu Phe Thr Ile Leu Tyr Ala
260 265 270
Gly Ile Val Ala Ser Gly Ile Ala Phe Ala Val Gln Ile Trp Cys Ile
275 280 285
Asp Arg Gly Gly Pro Val Phe Val Ala Val Tyr Gln Pro Val Gln Thr
290 295 300
Leu Val Val Ala Ile Met Ala Ser Ile Ala Leu Gly Glu Glu Phe Tyr
305 310 315 320
Leu Gly Gly Ile Ile Gly Ala Val Leu Ile Ile Ala Gly Leu Tyr Phe
325 330 335
Val Leu Tyr Gly Lys Ser Glu Glu Arg Lys Phe Ala Ala Leu Glu Lys
340 345 350
Ala Glu Ile Gln Ser Ser Ala Glu His Gly Ile Glu Arg Ala Pro Val
355 360 365
Ser Arg Asn Ser Ile Lys Ser Ser Ile Thr Thr Pro Leu Leu His Gln
370 375 380
Ser Thr Asp Asn Val
385

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..366

(D) OTHER INFORMATION: / Ceres Seq. ID 1566717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

Met	Leu	Thr	Leu	Gln	Phe	Gly	Tyr	Ala	Gly	Phe	His	Val	Val	Ser	Arg
1			5						10					15	
Ala	Ala	Leu	Asn	Met	Gly	Ile	Ser	Lys	Leu	Val	Phe	Pro	Val	Tyr	Arg
			20					25					30		
Asn	Ile	Ile	Ala	Leu	Leu	Leu	Leu	Pro	Phe	Ala	Tyr	Phe	Leu	Glu	
		35					40				45				
Lys	Lys	Glu	Arg	Pro	Ala	Ile	Thr	Leu	Asn	Phe	Leu	Ile	Gln	Phe	Phe
		50				55				60					
Phe	Leu	Ala	Leu	Ile	Gly	Ile	Thr	Ala	Asn	Gln	Gly	Phe	Tyr	Leu	Leu
		65			70				75					80	
Gly	Leu	Asp	Asn	Thr	Ser	Pro	Thr	Phe	Ala	Ser	Ser	Met	Gln	Asn	Ser
			85						90				95		
Val	Pro	Ala	Ile	Thr	Phe	Leu	Met	Ala	Ala	Leu	Leu	Arg	Ile	Glu	Lys
			100					105					110		
Val	Arg	Ile	Asn	Arg	Arg	Asp	Gly	Ile	Ser	Lys	Ile	Leu	Gly	Thr	Ala
		115					120					125			
Leu	Cys	Val	Ala	Gly	Ala	Ser	Val	Ile	Thr	Leu	Tyr	Lys	Gly	Pro	Thr
		130				135					140				
Ile	Tyr	Thr	Pro	Ala	Ser	His	Leu	His	Ala	His	Leu	Leu	Thr	Thr	Asn
		145			150				155					160	
Ser	Ala	Val	Leu	Ala	Pro	Leu	Gly	Asn	Ala	Ala	Pro	Lys	Asn	Trp	Thr
			165					170					175		
Leu	Gly	Cys	Ile	Tyr	Leu	Ile	Gly	His	Cys	Leu	Ser	Trp	Ser	Gly	Trp
		180					185						190		
Leu	Val	Phe	Gln	Ala	Pro	Val	Leu	Lys	Ser	Tyr	Pro	Ala	Arg	Leu	Ser
		195					200					205			
Val	Thr	Ser	Tyr	Thr	Cys	Phe	Phe	Gly	Ile	Ile	Gln	Phe	Leu	Ile	Ile
		210				215					220				
Ala	Ala	Phe	Cys	Glu	Arg	Asp	Ser	Gln	Ala	Trp	Val	Phe	His	Ser	Gly
		225			230				235					240	
Trp	Glu	Leu	Phe	Thr	Ile	Leu	Tyr	Ala	Gly	Ile	Val	Ala	Ser	Gly	Ile
			245						250				255		
Ala	Phe	Ala	Val	Gln	Ile	Trp	Cys	Ile	Asp	Arg	Gly	Gly	Pro	Val	Phe
		260					265					270			
Val	Ala	Val	Tyr	Gln	Pro	Val	Gln	Thr	Leu	Val	Val	Ala	Ile	Met	Ala
		275					280					285			
Ser	Ile	Ala	Leu	Gly	Glu	Glu	Phe	Tyr	Leu	Gly	Gly	Ile	Ile	Gly	Ala
		290				295					300				
Val	Leu	Ile	Ile	Ala	Gly	Leu	Tyr	Phe	Val	Leu	Tyr	Gly	Lys	Ser	Glu
		305			310				315					320	
Glu	Arg	Lys	Phe	Ala	Ala	Leu	Glu	Lys	Ala	Glu	Ile	Gln	Ser	Ser	Ala
			325					330					335		
Glu	His	Gly	Ile	Glu	Arg	Ala	Pro	Val	Ser	Arg	Asn	Ser	Ile	Lys	Ser
		340					345						350		
Ser	Ile	Thr	Thr	Pro	Leu	Leu	His	Gln	Ser	Thr	Asp	Asn	Val		
		355				360						365			

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..346

(D) OTHER INFORMATION: / Ceres Seq. ID 1566718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

Met Gly Ile Ser Lys Leu Val Phe Pro Val Tyr Arg Asn Ile Ile Ala
1 5 10 15
Leu Leu Leu Leu Leu Pro Phe Ala Tyr Phe Leu Glu Lys Lys Glu Arg
20 25 30
Pro Ala Ile Thr Leu Asn Phe Leu Ile Gln Phe Phe Phe Leu Ala Leu
35 40 45
Ile Gly Ile Thr Ala Asn Gln Gly Phe Tyr Leu Leu Gly Leu Asp Asn
50 55 60
Thr Ser Pro Thr Phe Ala Ser Ser Met Gln Asn Ser Val Pro Ala Ile
65 70 75 80
Thr Phe Leu Met Ala Leu Leu Arg Ile Glu Lys Val Arg Ile Asn
85 90 95
Arg Arg Asp Gly Ile Ser Lys Ile Leu Gly Thr Ala Leu Cys Val Ala
100 105 110
Gly Ala Ser Val Ile Thr Leu Tyr Lys Gly Pro Thr Ile Tyr Thr Pro
115 120 125
Ala Ser His Leu His Ala His Leu Leu Thr Thr Asn Ser Ala Val Leu
130 135 140
Ala Pro Leu Gly Asn Ala Ala Pro Lys Asn Trp Thr Leu Gly Cys Ile
145 150 155 160
Tyr Leu Ile Gly His Cys Leu Ser Trp Ser Gly Trp Leu Val Phe Gln
165 170 175
Ala Pro Val Leu Lys Ser Tyr Pro Ala Arg Leu Ser Val Thr Ser Tyr
180 185 190
Thr Cys Phe Phe Gly Ile Ile Gln Phe Leu Ile Ile Ala Ala Phe Cys
195 200 205
Glu Arg Asp Ser Gln Ala Trp Val Phe His Ser Gly Trp Glu Leu Phe
210 215 220
Thr Ile Leu Tyr Ala Gly Ile Val Ala Ser Gly Ile Ala Phe Ala Val
225 230 235 240
Gln Ile Trp Cys Ile Asp Arg Gly Gly Pro Val Phe Val Ala Val Tyr
245 250 255
Gln Pro Val Gln Thr Leu Val Val Ala Ile Met Ala Ser Ile Ala Leu
260 265 270
Gly Glu Glu Phe Tyr Leu Gly Gly Ile Ile Gly Ala Val Leu Ile Ile
275 280 285
Ala Gly Leu Tyr Phe Val Leu Tyr Gly Lys Ser Glu Glu Arg Lys Phe
290 295 300
Ala Ala Leu Glu Lys Ala Glu Ile Gln Ser Ser Ala Glu His Gly Ile
305 310 315 320
Glu Arg Ala Pro Val Ser Arg Asn Ser Ile Lys Ser Ser Ile Thr Thr
325 330 335
Pro Leu Leu His Gln Ser Thr Asp Asn Val
340 345

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1009 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1009

(D) OTHER INFORMATION: / Ceres Seq. ID 1566719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

catctttctaa gaaagaaaca aagaaagact tcacatttta ccattatttg ctctgagctc 60
agtaggagag ttcaagaaac aatggcaaac atgcaattat caatctttat cgctgtcgtt 120


```

gcgcttatcg tctgctctgc atctgctaaa accgcaagcc ctccagctcc agtgctgcc 180
ccgacaccag ctccagacc agccccggaa aatgtgaatc tcaccgagct ttttaagtta 240
gctggctcgt tccacacatt cctgcactac cttctctcga ctggagtcac tgagactttc 300
caaaaccaag ctaacaacac tgaggaaggg atcacaatct ttgtccctaa agatgatgct 360
ttcaagctc agaagaatcc tctttgttca aatctcacaa aggatcagct taagcagctt 420
gttctcttcc atgctcttcc tcattactat tcgctttcgg aattcaagaa cttgagccaa 480
tctggctccag tgagcacctt tgctgggtgt caatactcct tgaatttcac tgatgtttct 540
ggcacgggta ggattgattc tttatggacc aggactaaag tcagcagcag tgttttctcc 600
actgacctcg ttgcgggttta ccaattgaac cgcgtgcttc tacccgaagc aatctttggt 660
actgatgtcc ctccaatgcc tgcctccagct cctgctccta tcgttagtgc tCcttcggat 720
ctctcttcag ttgctgattc tgaaggagct tcttcaccaa agtcctcaca caagaactcc 780
ggacaaaagc tgcctacttc accaatctcc atggttattt ccggtttggt gcatctgttc 840
ttgtgatcac atggttttgc agattgagtt atgtttttaa gttacaatgt gaagattgt 900
attactcatc ttgaattgtc tttttgattt ttgaaccoca ttttttatta tacattttta 960
tcattattat tgtttgtcat tacgattttg tgaattgaaa ttgttcttc

```

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..281

(D) OTHER INFORMATION: / Ceres Seq. ID 1566720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

```

His Leu Leu Arg Lys Lys Gln Arg Lys Thr Ser His Phe Thr Ile Ile
1 5 10 15
Cys Ser Glu Leu Ser Arg Arg Val Gln Glu Thr Met Ala Lys Met Gln
20 25 30
Leu Ser Ile Phe Ile Ala Val Val Ala Leu Ile Val Cys Ser Ala Ser
35 40 45
Ala Lys Thr Ala Ser Pro Pro Ala Pro Val Leu Pro Pro Thr Pro Ala
50 55 60
Pro Ala Pro Ala Pro Glu Asn Val Asn Leu Thr Glu Leu Leu Ser Val
65 70 75 80
Ala Gly Pro Phe His Thr Phe Leu Asp Tyr Leu Leu Ser Thr Gly Val
85 90 95
Ile Glu Thr Phe Gln Asn Gln Ala Asn Asn Thr Glu Glu Gly Ile Thr
100 105 110
Ile Phe Val Pro Lys Asp Asp Ala Phe Lys Ala Gln Lys Asn Pro Pro
115 120 125
Leu Ser Asn Leu Thr Lys Asp Gln Leu Lys Gln Leu Val Leu Phe His
130 135 140
Ala Leu Pro His Tyr Tyr Ser Leu Ser Glu Phe Lys Asn Leu Ser Gln
145 150 155 160
Ser Gly Pro Val Ser Thr Phe Ala Gly Gly Gln Tyr Ser Leu Lys Phe
165 170 175
Thr Asp Val Ser Gly Thr Val Arg Ile Asp Ser Leu Trp Thr Arg Thr
180 185 190
Lys Val Ser Ser Ser Val Phe Ser Thr Asp Pro Val Ala Val Tyr Gln
195 200 205
Leu Asn Arg Val Leu Leu Pro Glu Ala Ile Phe Gly Thr Asp Val Pro
210 215 220
Pro Met Pro Ala Pro Ala Pro Ala Pro Ile Val Ser Ala Pro Ser Asp
225 230 235 240
Ser Pro Ser Val Ala Asp Ser Glu Gly Ala Ser Ser Pro Lys Ser Ser
245 250 255
His Lys Asn Ser Gly Gln Lys Leu Leu Leu Ala Pro Ile Ser Met Val
260 265 270

```

Ile Ser Gly Leu Val Ala Leu Phe Leu
275 280

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..254
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

```
Met Ala Lys Met Gln Leu Ser Ile Phe Ile Ala Val Val Ala Leu Ile
1      5      10      15
Val Cys Ser Ala Ser Ala Lys Thr Ala Ser Pro Pro Ala Pro Val Leu
20      25      30
Pro Pro Thr Pro Ala Pro Ala Pro Ala Pro Glu Asn Val Asn Leu Thr
35      40      45
Glu Leu Leu Ser Val Ala Gly Pro Phe His Thr Phe Leu Asp Tyr Leu
50      55      60
Leu Ser Thr Gly Val Ile Glu Thr Phe Gln Asn Gln Ala Asn Asn Thr
65      70      75      80
Glu Glu Gly Ile Thr Ile Phe Val Pro Lys Asp Asp Ala Phe Lys Ala
85      90      95
Gln Lys Asn Pro Pro Leu Ser Asn Leu Thr Lys Asp Gln Leu Lys Gln
100     105     110
Leu Val Leu Phe His Ala Leu Pro His Tyr Tyr Ser Leu Ser Glu Phe
115     120     125
Lys Asn Leu Ser Gln Ser Gly Pro Val Ser Thr Phe Ala Gly Gly Gln
130     135     140
Tyr Ser Leu Lys Phe Thr Asp Val Ser Gly Thr Val Arg Ile Asp Ser
145     150     155     160
Leu Trp Thr Arg Thr Lys Val Ser Ser Ser Val Phe Ser Thr Asp Pro
165     170     175
Val Ala Val Tyr Gln Leu Asn Arg Val Leu Leu Pro Glu Ala Ile Phe
180     185     190
Gly Thr Asp Val Pro Pro Met Pro Ala Pro Ala Pro Ala Pro Ile Val
195     200     205
Ser Ala Pro Ser Asp Ser Pro Ser Val Ala Asp Ser Glu Gly Ala Ser
210     215     220
Ser Pro Lys Ser Ser His Lys Asn Ser Gly Gln Lys Leu Leu Leu Ala
225     230     235     240
Pro Ile Ser Met Val Ile Ser Gly Leu Val Ala Leu Phe Leu
245     250
```

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..251
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

```
Met Gln Leu Ser Ile Phe Ile Ala Val Val Ala Leu Ile Val Cys Ser
1      5      10      15
Ala Ser Ala Lys Thr Ala Ser Pro Pro Ala Pro Val Leu Pro Pro Thr
```

20	25	30
Pro Ala Pro Ala Pro Ala Pro Glu Asn Val Asn Leu Thr Glu Leu Leu		
35	40	45
Ser Val Ala Gly Pro Phe His Thr Phe Leu Asp Tyr Leu Leu Ser Thr		
50	55	60
Gly Val Ile Glu Thr Phe Gln Asn Gln Ala Asn Asn Thr Glu Glu Gly		
65	70	75
Ile Thr Ile Phe Val Pro Lys Asp Asp Ala Phe Lys Ala Gln Lys Asn		
85	90	95
Pro Pro Leu Ser Asn Leu Thr Lys Asp Gln Leu Lys Gln Leu Val Leu		
100	105	110
Phe His Ala Leu Pro His Tyr Tyr Ser Leu Ser Glu Phe Lys Asn Leu		
115	120	125
Ser Gln Ser Gly Pro Val Ser Thr Phe Ala Gly Gly Gln Tyr Ser Leu		
130	135	140
Lys Phe Thr Asp Val Ser Gly Thr Val Arg Ile Asp Ser Leu Trp Thr		
145	150	155
Arg Thr Lys Val Ser Ser Ser Val Phe Ser Thr Asp Pro Val Ala Val		
165	170	175
Tyr Gln Leu Asn Arg Val Leu Leu Pro Glu Ala Ile Phe Gly Thr Asp		
180	185	190
Val Pro Pro Met Pro Ala Pro Ala Pro Ala Pro Ile Val Ser Ala Pro		
195	200	205
Ser Asp Ser Pro Ser Val Ala Asp Ser Glu Gly Ala Ser Ser Pro Lys		
210	215	220
Ser Ser His Lys Asn Ser Gly Gln Lys Leu Leu Leu Ala Pro Ile Ser		
225	230	235
Met Val Ile Ser Gly Leu Val Ala Leu Phe Leu		
245	250	

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 877 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..877
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566727

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

agattaggat	taaattagggg	cataaccctt	atcggagatt	tgaagccatg	ggaagaagaa	60
aaatcgagat	caagcgaatc	gagaacaaaa	gcagtcgaca	agtcactttc	tccaaacgac	120
gcaatggtct	catcgacaaa	gctcgcacaac	tttcgattct	ctgtgaatcc	tcctgcctgt	180
ttgtcgtcgt	atctgcctcc	ggaaaactct	atgactcttc	ctccggtgac	gagatagaag	240
cgctgttcaa	gccggagaaa	ctcctaatgt	ttgaactcga	tcttgaagaa	aaaattcaga	300
attatcttcc	acacaaggag	ttactagaaa	cagtcocaa	caagcttgaa	gaaccaaatg	360
tcgataaagt	aagtgttagat	tctctaattt	ctctggagga	acaacttgag	actgtctctg	420
ccgtaagttag	agctaggaga	gcagaaactga	tgatggagta	tatcgagctc	cttaaaagaaa	480
aggagaaatt	gctgagagaa	gagaaccagg	ttctggctag	ccagatggga	aagaatacgt	540
tgctggcaac	agatgatgag	agaggaaatgt	ttccgggga	tagctccggc	aacaaaatac	600
cgagactct	cccgctgctc	aattagcoac	catcatcaac	ggctgagitt	tcaccttaaa	660
ctcaaagcct	gattcataat	taagagaata	aatttgtata	ttataaaaa	ctgtgtaatc	720
tcaaaccttt	tatcttctct	taagtgggaa	tttaaggta	aaaaaaaaa	gagaaagtat	780
ggatcagttg	tgtaacctct	tcggagacaa	gatcagagtt	tgtgtgtttg	tgctgtgaatg	840
taaggattgg	atttttaaa	ttgtgctttc	tttcttcc			

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..207
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566728
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:
Ile Arg Ile Lys Leu Gly His Asn Pro Tyr Arg Arg Phe Glu Ala Met
1 5 10 15
Gly Arg Arg Lys Ile Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser Arg
 20 25 30
Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile Asp Lys Ala Arg
 35 40 45
Gln Leu Ser Ile Leu Cys Glu Ser Ser Val Ala Val Val Val Ser
 50 55 60
Ala Ser Gly Lys Leu Tyr Asp Ser Ser Ser Gly Asp Glu Ile Glu Ala
65 70 75 80
Leu Phe Lys Pro Glu Lys Pro Gln Cys Phe Glu Leu Asp Leu Glu Glu
 85 90 95
Lys Ile Gln Asn Tyr Leu Pro His Lys Glu Leu Leu Glu Thr Val Gln
 100 105 110
Ser Lys Leu Glu Glu Pro Asn Val Asp Asn Val Ser Val Asp Ser Leu
 115 120 125
Ile Ser Leu Glu Glu Gln Leu Glu Thr Ala Leu Ser Val Ser Arg Ala
130 135 140
Arg Lys Ala Glu Leu Met Met Glu Tyr Ile Glu Ser Leu Lys Glu Lys
145 150 155 160
Glu Lys Leu Leu Arg Glu Glu Asn Gln Val Leu Ala Ser Gln Met Gly
 165 170 175
Lys Asn Thr Leu Leu Ala Thr Asp Asp Glu Arg Gly Met Phe Pro Gly
 180 185 190
Ser Ser Ser Gly Asn Lys Ile Pro Glu Thr Leu Pro Leu Leu Asn
 195 200 205

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..192
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566729
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:
Met Gly Arg Arg Lys Ile Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
1 5 10 15
Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile Asp Lys Ala
 20 25 30
Arg Gln Leu Ser Ile Leu Cys Glu Ser Ser Ser Gly Asp Glu Ile Glu
 35 40 45
Ser Ala Ser Gly Lys Leu Tyr Asp Ser Ser Ser Gly Asp Glu Ile Glu
50 55 60
Ala Leu Phe Lys Pro Glu Lys Pro Gln Cys Phe Glu Leu Asp Leu Glu
65 70 75 80
Glu Lys Ile Gln Asn Tyr Leu Pro His Lys Glu Leu Leu Glu Thr Val
 85 90 95
Gln Ser Lys Leu Glu Glu Pro Asn Val Asp Asn Val Ser Val Asp Ser
 100 105 110
Leu Ile Ser Leu Glu Glu Gln Leu Glu Thr Ala Leu Ser Val Ser Arg
115 120 125

Ala	Arg	Lys	Ala	Glu	Leu	Met	Met	Glu	Tyr	Ile	Glu	Ser	Leu	Lys	Glu
130						135					140				
Lys	Glu	Lys	Leu	Leu	Arg	Glu	Glu	Asn	Gln	Val	Leu	Ala	Ser	Gln	Met
145					150					155					160
Gly	Lys	Asn	Thr	Leu	Leu	Ala	Thr	Asp	Asp	Glu	Arg	Gly	Met	Phe	Pro
			165					170						175	
Gly	Ser	Ser	Ser	Gly	Asn	Lys	Ile	Pro	Glu	Thr	Leu	Pro	Leu	Leu	Asn
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2022 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2022

(D) OTHER INFORMATION: / Ceres Seq. ID 1566737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

acagtaacaa	tctctctctc	gcaccttctt	aaagctgtct	ctatttcttc	gcttccctct	60
tctcttcaat	cacaaaaaat	tttgttctaa	tcccgcaact	gctaaaaaca	aacctctttg	120
tcaaaaaat	ctctcttcgg	tgggtgacaga	aatctattgc	aggaaatggc	agaagcagca	180
tacacagtag	catcacagac	tgaaaacact	ggagaggaga	aatcatcatc	atctccttca	240
ttacccgaaa	tcgcctctgg	tatcgacatt	gggtactctc	aatgcagtat	agctgtttgg	300
aacggttctc	aagttcacat	cttgaggaaac	acaagaaacc	agaagctcat	caaatctatt	360
gtcactttca	aagatgaagt	tctctgtcgt	gggtgttaga	accagctcgc	acatgagcag	420
gaaatgcata	ccggagccgc	tactttcaac	atgaagcggc	tcgttgtgtg	tgtagacact	480
gatctctgtg	ttcacgctag	caagaacctt	ccttctcttg	tcaaaactct	tgatatttga	540
gttagaccgt	ttattgcagc	tttgtgtgaac	aatgcttggg	gatcaacaac	accagaggaa	600
gttttagcta	tatttctcgt	ggagttacgt	ctgatggctg	aagctcagtt	gaaacgtcct	660
gtgagaaagt	tagtgcttac	ggttccgggt	tcgttctcta	ggttcacgt	cacacggttc	720
gaaagagcgt	gcgctatggc	tggacttcat	gttctctgtt	tgatgccgga	accaactgct	780
attgcgttgc	tttatgcgca	acagcagcag	atgactacgc	atgataaact	gggaagcggg	840
agcgagaggg	ttgcggttat	attcaatatg	ggagctgggt	actgcgcatg	tcggtttact	900
gctactcgtg	gtggtgtttc	acagataaaa	gctttagctg	gtagcccatc	tgggggtgaa	960
gacattttgc	agagcacaat	tcgccatata	gctccaccta	atgaagaagc	ttcgggggtg	1020
ctctctgtgt	cggcaccaga	cgcgattcac	aggctaaccg	atcaagaaaa	tgtccaaatt	1080
gaaatgcatt	tgggaaatgg	taacaagata	tccaaggctc	ttgatagctt	agagttttag	1140
gaagtgaacc	agaaggtatt	taggagaatg	gagagacttg	ttgtgcagtg	cctgcgagat	1200
gcgagagctc	atgggtgtgt	tatcgatgat	ttgataatgg	tggaggggtg	ttcgtacatc	1260
ccgaaagtta	gaactattat	caagaacgta	tgcagaaggg	atgagatata	caaaagcggtg	1320
aatctctttg	aagctgcggt	tagaggagct	gctttggaag	gtcgggtgac	ttcagggggt	1380
catgatccct	ttgggagcgt	agatctgtta	accatacaag	ccacacactc	tcgagttgga	1440
gcgaagagta	acggaacaaa	attcataccc	gtgattcctc	gtaacacgat	gggtccagcg	1500
cggaaagacc	tctttttcac	aacgggttca	gacaaccaga	aggaaagctc	gatcattata	1560
tacgaaggag	aaggagagac	tgttgaagag	aatcatcttc	ttggttattt	caagctcgtt	1620
gggattccgc	cagcaccgaa	aggtgttcca	gagatcaatg	tttgatgag	catcgatgcg	1680
ctgaatgctt	tacgggtttt	cgcagctgtg	ttgatgccgg	gatcttcgac	tcggctgtgt	1740
cotgtgattg	aggtgaggtg	gcctacgggt	gatgatggac	atggttgtgt	tgctcaagct	1800
ttgaatgtga	aatatggagc	tactcttgat	ttgattactt	ttcagagaaa	gatgtaaagt	1860
taaaaataaa	tgggtgttgt	gatagatttt	agattagatg	taagatagca	ggatgctctg	1920
tatagaaaaa	agtttgttaa	gtttgtgtgt	gttttgggtg	ttgtcgttga	agtggttaac	1980
aatgttttat	tggttaatga	agtaataatg	ctttgcagat	tg		

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 563 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..563
(D) OTHER INFORMATION: / Ceres Seq. ID 1566738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

Met	Ala	Glu	Ala	Ala	Tyr	Thr	Val	Ala	Ser	Asp	Ser	Glu	Asn	Thr	Gly	
1				5					10				15			
Glu	Glu	Lys	Ser	Ser	Ser	Ser	Pro	Ser	Leu	Pro	Glu	Ile	Ala	Leu	Gly	
		20						25				30				
Ile	Asp	Ile	Gly	Thr	Ser	Gln	Cys	Ser	Ile	Ala	Val	Trp	Asn	Gly	Ser	
		35					40					45				
Gln	Val	His	Ile	Leu	Arg	Asn	Thr	Arg	Asn	Gln	Lys	Leu	Ile	Lys	Ser	
		50				55					60					
Phe	Val	Thr	Phe	Lys	Asp	Glu	Val	Pro	Ala	Gly	Gly	Val	Ser	Asn	Gln	
65				70					75					80		
Leu	Ala	His	Glu	Gln	Glu	Met	Leu	Thr	Gly	Ala	Ala	Ile	Phe	Asn	Met	
			85						90				95			
Lys	Arg	Leu	Val	Gly	Arg	Val	Asp	Thr	Asp	Pro	Val	Val	His	Ala	Ser	
		100						105					110			
Lys	Asn	Leu	Pro	Phe	Leu	Val	Gln	Thr	Leu	Asp	Ile	Gly	Val	Arg	Pro	
		115					120					125				
Phe	Ile	Ala	Ala	Leu	Val	Asn	Asn	Ala	Trp	Arg	Ser	Thr	Thr	Pro	Glu	
	130				135							140				
Glu	Val	Leu	Ala	Ile	Phe	Leu	Val	Glu	Leu	Arg	Leu	Met	Ala	Glu	Ala	
145				150					155					160		
Gln	Leu	Lys	Arg	Pro	Val	Arg	Asn	Val	Val	Leu	Thr	Val	Pro	Val	Ser	
		165							170					175		
Phe	Ser	Arg	Phe	Gln	Leu	Thr	Arg	Phe	Glu	Arg	Ala	Cys	Ala	Met	Ala	
	180							185					190			
Gly	Leu	His	Val	Leu	Arg	Leu	Met	Pro	Glu	Pro	Thr	Ala	Ile	Ala	Leu	
	195						200					205				
Leu	Tyr	Ala	Gln	Gln	Gln	Gln	Met	Thr	Thr	His	Asp	Asn	Met	Gly	Ser	
	210					215					220					
Gly	Ser	Glu	Arg	Leu	Ala	Val	Ile	Phe	Asn	Met	Gly	Ala	Gly	Tyr	Cys	
225				230					235					240		
Asp	Val	Ala	Val	Thr	Ala	Thr	Ala	Gly	Gly	Val	Ser	Gln	Ile	Lys	Ala	
		245							250					255		
Leu	Ala	Gly	Ser	Pro	Ile	Gly	Gly	Glu	Asp	Ile	Leu	Gln	Ser	Thr	Ile	
		260					265						270			
Arg	His	Ile	Ala	Pro	Pro	Asn	Glu	Glu	Ala	Ser	Gly	Leu	Leu	Arg	Val	
	275						280						285			
Ala	Ala	Gln	Asp	Ala	Ile	His	Arg	Leu	Thr	Asp	Gln	Glu	Asn	Val	Gln	
	290					295					300					
Ile	Glu	Val	Asp	Leu	Gly	Asn	Gly	Asn	Lys	Ile	Ser	Lys	Val	Leu	Asp	
305				310					315					320		
Arg	Leu	Glu	Phe	Glu	Glu	Val	Asn	Gln	Lys	Val	Phe	Glu	Glu	Cys	Glu	
		325							330					335		
Arg	Leu	Val	Val	Gln	Cys	Leu	Arg	Asp	Ala	Arg	Val	Asn	Gly	Gly	Asp	
		340						345					350			
Ile	Asp	Asp	Leu	Ile	Met	Val	Gly	Gly	Cys	Ser	Tyr	Ile	Pro	Lys	Val	
	355						360					365				
Arg	Thr	Ile	Ile	Lys	Asn	Val	Cys	Lys	Lys	Asp	Glu	Ile	Tyr	Lys	Gly	
	370					375					380					
Val	Asn	Pro	Leu	Glu	Ala	Ala	Val	Arg	Gly	Ala	Ala	Leu	Glu	Gly	Ala	
385				390					395					400		
Val	Thr	Ser	Gly	Ile	His	Asp	Pro	Phe	Gly	Ser	Leu	Asp	Leu	Leu	Thr	
		405							410					415		
Ile	Gln	Ala	Thr	Pro	Leu	Ala	Val	Gly	Ala	Arg	Ala	Asn	Gly	Asn	Lys	
		420					425						430			

Phe	Ile	Pro	Val	Ile	Pro	Arg	Asn	Thr	Met	Val	Pro	Ala	Arg	Lys	Asp	
	435						440					445				
Leu	Phe	Phe	Thr	Thr	Val	Gln	Asp	Asn	Gln	Lys	Glu	Ala	Leu	Ile	Ile	
	450					455					460					
Ile	Tyr	Glu	Gly	Glu	Gly	Glu	Thr	Val	Glu	Glu	Asn	His	Leu	Leu	Gly	
	465				470				475						480	
Tyr	Phe	Lys	Leu	Val	Gly	Ile	Pro	Pro	Ala	Pro	Lys	Gly	Val	Pro	Glu	
			485						490					495		
Ile	Asn	Val	Cys	Met	Asp	Ile	Asp	Ala	Ser	Asn	Ala	Leu	Arg	Val	Phe	
		500					505						510			
Ala	Ala	Val	Leu	Met	Pro	Gly	Ser	Ser	Thr	Pro	Val	Val	Pro	Val	Ile	
		515				520						525				
Glu	Val	Arg	Met	Pro	Thr	Val	Asp	Asp	Gly	His	Gly	Trp	Cys	Ala	Gln	
	530					535					540					
Ala	Leu	Asn	Val	Lys	Tyr	Gly	Ala	Thr	Leu	Asp	Leu	Ile	Thr	Phe	Gln	
			550						555						560	
Arg	Lys	Met														

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..477

(D) OTHER INFORMATION: / Ceres Seq. ID 1566739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

Met	Leu	Thr	Gly	Ala	Ala	Ile	Phe	Asn	Met	Lys	Arg	Leu	Val	Gly	Arg	
1			5						10				15			
Val	Asp	Thr	Asp	Pro	Val	Val	His	Ala	Ser	Lys	Asn	Leu	Pro	Phe	Leu	
			20					25					30			
Val	Gln	Thr	Leu	Asp	Ile	Gly	Val	Arg	Pro	Phe	Ile	Ala	Ala	Leu	Val	
		35				40						45				
Asn	Asn	Ala	Trp	Arg	Ser	Thr	Thr	Pro	Glu	Glu	Val	Leu	Ala	Ile	Phe	
		50			55						60					
Leu	Val	Glu	Leu	Arg	Leu	Met	Ala	Glu	Ala	Gln	Leu	Lys	Arg	Pro	Val	
		65		70				75					80			
Arg	Asn	Val	Val	Leu	Thr	Val	Pro	Val	Ser	Phe	Ser	Arg	Phe	Gln	Leu	
		85						90					95			
Thr	Arg	Phe	Glu	Arg	Ala	Cys	Ala	Met	Ala	Gly	Leu	His	Val	Leu	Arg	
		100				105						110				
Leu	Met	Pro	Glu	Pro	Thr	Ala	Ile	Ala	Leu	Leu	Tyr	Ala	Gln	Gln	Gln	
		115				120						125				
Gln	Met	Thr	Thr	His	Asp	Asn	Met	Gly	Ser	Gly	Ser	Glu	Arg	Leu	Ala	
		130				135						140				
Val	Ile	Phe	Asn	Met	Gly	Ala	Gly	Tyr	Cys	Asp	Val	Ala	Val	Thr	Ala	
		145			150				155					160		
Thr	Ala	Gly	Gly	Val	Ser	Gln	Ile	Lys	Ala	Leu	Ala	Gly	Ser	Pro	Ile	
			165					170					175			
Gly	Gly	Glu	Asp	Ile	Leu	Gln	Ser	Thr	Ile	Arg	His	Ile	Ala	Pro	Pro	
		180						185					190			
Asn	Glu	Glu	Ala	Ser	Gly	Leu	Leu	Arg	Val	Ala	Ala	Gln	Asp	Ala	Ile	
		195				200						205				
His	Arg	Leu	Thr	Asp	Gln	Glu	Asn	Val	Gln	Ile	Glu	Val	Asp	Leu	Gly	
		210				215						220				
Asn	Gly	Asn	Lys	Ile	Ser	Lys	Val	Leu	Asp	Arg	Leu	Glu	Phe	Glu	Glu	
		225				230				235				240		
Val	Asn	Gln	Lys	Val	Phe	Glu	Glu	Cys	Glu	Arg	Leu	Val	Val	Gln	Cys	

245 250 255
Leu Arg Asp Ala Arg Val Asn Gly Gly Asp Ile Asp Asp Leu Ile Met
260 265 270
Val Gly Gly Cys Ser Tyr Ile Pro Lys Val Arg Thr Ile Ile Lys Asn
275 280 285
Val Cys Lys Lys Asp Glu Ile Tyr Lys Gly Val Asn Pro Leu Glu Ala
290 295 300
Ala Val Arg Gly Ala Ala Leu Glu Gly Ala Val Thr Ser Gly Ile His
305 310 315
Asp Pro Phe Gly Ser Leu Asp Leu Leu Thr Thr Ile Gln Ala Thr Pro Leu
325 330 335
Ala Val Gly Ala Arg Ala Asn Gly Asn Lys Phe Ile Pro Val Ile Pro
340 345 350
Arg Asn Thr Met Val Pro Ala Arg Lys Asp Leu Phe Phe Thr Thr Val
355 360 365
Gln Asp Asn Gln Lys Glu Ala Leu Ile Ile Ile Tyr Glu Gly Glu Gly
370 375 380
Glu Thr Val Glu Glu Asn His Leu Leu Gly Tyr Phe Lys Leu Val Gly
385 390 395
Ile Pro Pro Ala Pro Lys Gly Val Pro Glu Ile Asn Val Cys Met Asp
400 405 410
Ile Asp Ala Ser Asn Ala Leu Arg Val Phe Ala Ala Val Leu Met Pro
420 425 430
Gly Ser Ser Thr Pro Val Val Pro Val Ile Glu Val Arg Met Pro Thr
435 440 445
Val Asp Asp Gly His Gly Trp Cys Ala Gln Ala Leu Asn Val Lys Tyr
450 455 460
Gly Ala Thr Leu Asp Leu Ile Thr Phe Gln Arg Lys Met
465 470 475

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 468 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..468

(D) OTHER INFORMATION: / Ceres Seq. ID 1566740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

Met Lys Arg Leu Val Gly Arg Val Asp Thr Asp Pro Val Val His Ala
1 5 10 15
Ser Lys Asn Leu Pro Phe Leu Val Gln Thr Leu Asp Ile Gly Val Arg
20 25 30
Pro Phe Ile Ala Ala Leu Val Asn Asn Ala Trp Arg Ser Thr Thr Pro
35 40 45
Glu Glu Val Leu Ala Ile Phe Leu Val Glu Leu Arg Leu Met Ala Glu
50 55 60
Ala Gln Leu Lys Arg Pro Val Arg Asn Val Val Leu Thr Val Pro Val
65 70 75
Ser Phe Ser Arg Phe Gln Leu Thr Arg Phe Glu Arg Ala Cys Ala Met
85 90 95
Ala Gly Leu His Val Leu Arg Leu Met Pro Glu Pro Thr Ala Ile Ala
100 105 110
Leu Leu Tyr Ala Gln Gln Gln Gln Met Thr Thr His Asp Asn Met Gly
115 120 125
Ser Gly Ser Glu Arg Leu Ala Val Ile Phe Asn Met Gly Ala Gly Tyr
130 135 140
Cys Asp Val Ala Val Thr Ala Thr Ala Gly Gly Val Ser Gln Ile Lys
145 150 155 160

Ala Leu Ala Gly Ser Pro Ile Gly Gly Glu Asp Ile Leu Gln Ser Thr
165 170 175
Ile Arg His Ile Ala Pro Pro Asn Glu Glu Ala Ser Gly Leu Leu Arg
180 185 190
Val Ala Ala Gln Asp Ala Ile His Arg Leu Thr Asp Gln Glu Asn Val
195 200 205
Gln Ile Glu Val Asp Leu Gly Asn Gly Asn Lys Ile Ser Lys Val Leu
210 215 220
Asp Arg Leu Glu Phe Glu Glu Val Asn Gln Lys Val Phe Glu Glu Cys
225 230 235 240
Glu Arg Leu Val Val Gln Cys Leu Arg Asp Ala Arg Val Asn Gly Gly
245 250 255
Asp Ile Asp Asp Leu Ile Met Val Gly Gly Cys Ser Tyr Ile Pro Lys
260 265 270
Val Arg Thr Ile Ile Lys Asn Val Cys Lys Lys Asp Glu Ile Tyr Lys
275 280 285
Gly Val Asn Pro Leu Glu Ala Ala Val Arg Gly Ala Ala Leu Glu Gly
290 295 300
Ala Val Thr Ser Gly Ile His Asp Pro Phe Gly Ser Leu Asp Leu Leu
305 310 315 320
Thr Ile Gln Ala Thr Pro Leu Ala Val Gly Ala Arg Ala Asn Gly Asn
325 330 335
Lys Phe Ile Pro Val Ile Pro Arg Asn Thr Met Val Pro Ala Arg Lys
340 345 350
Asp Leu Phe Phe Thr Thr Val Gln Asp Asn Gln Lys Glu Ala Leu Ile
355 360 365
Ile Ile Tyr Glu Gly Glu Gly Glu Thr Val Glu Glu Asn His Leu Leu
370 375 380
Gly Tyr Phe Lys Leu Val Gly Ile Pro Pro Ala Pro Lys Gly Val Pro
385 390 395 400
Glu Ile Asn Val Cys Met Asp Ile Asp Ala Ser Asn Ala Leu Arg Val
405 410 415
Phe Ala Ala Val Leu Met Pro Gly Ser Ser Thr Pro Val Val Pro Val
420 425 430
Ile Glu Val Arg Met Pro Thr Val Asp Asp Gly His Gly Trp Cys Ala
435 440 445
Gln Ala Leu Asn Val Lys Tyr Gly Ala Thr Leu Asp Leu Ile Thr Phe
450 455 460
Gln Arg Lys Met
465

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1957
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

atagtgtctg	tctaattaat	atattgttcc	aaagaaaaat	atgtatctac	gtcttgccctc	60
taaacctctt	ttttcacatc	acaagcatct	taaaattttc	taaatcacctc	ttttgcgcgt	120
gagacatgtc	tttttcgagg	gtttggtttc	gatctctttg	gtcatcttgg	agttgagcta	180
tgctgtttgc	ccaatctcat	cgatcaatg	ggtctgtctg	tattctcaac	gttttcattc	240
tgaggccaac	aagcagggtta	tagtgatcaa	cgacatgttc	cctggaccga	tccttaattgc	300
aacagcaaac	gatatcattg	tcgttaaacat	tttcaacaat	ttgcccgaac	ccttccctcat	360
gacttggaat	ggattgcaat	tcgcggaagaa	ctcgtgggcaa	gatggagttc	gagggcacaaa	420
ctgtcccata	ctaccgggga	caaattggac	gtaccgtttt	caggtgaagg	atcaaatggg	480
aagttaacttt	tattttccga	cccttctact	tcagaaaagct	gccggaggat	acggtgctat	540

tagaatctat	ccccagaac	ttgtccagt	cccattocct	aagcccgaag	aagaatacga	600
catctctgatt	ggagatgggt	tttatctcga	ccatacagtt	atgagagctt	cacttgacgc	660
tggtcacagt	ttgcacaaatc	ctgatggat	tctttttaac	ggcggtggcc	ctgaagagac	720
cttcttttga	tttgaaaccg	gcaaaacata	taggctaaga	atatcaaacg	tgggtctcaa	780
aacatgctta	aactctcagRa	rTSCaagnc	acgatatgnt	tctagtttag	acagagggta	840
cgatatgttca	aaaacgtggt	tactcgagcc	tggacatcca	cgtagggcaa	tcaatactcta	900
ttcttctcac	tgccaaaaac	gacccgggtg	gaatttacgc	gttactactac	atattcgcca	960
cagctcgagt	cactgatctc	tacottggcg	gtatagcttt	aattcgatat	cccggtctcc	1020
cacttgaccc	agtcggacaa	gggtccactcg	ccactgcttt	gcaagatttt	gggtctctac	1080
ttgaacaagc	cotttccatt	agaatggacc	tgaacgttgg	agcagcaaga	tgcgaaccctc	1140
aaggttctga	ccaactatgga	cgaataaacg	taaccagaa	gataatatta	cataacgacg	1200
ttatgttatac	gtcgggcacaa	ctacggtata	cgattaaacg	gctttcgcttt	gtctaaccccg	1260
agaactccgtt	aaagctcgtt	gatcattttc	agctaaatga	cacgataatc	cctggcagtg	1320
tcccggtttta	tccatccaac	aaaacaccga	ctcttggaa	ttcagtggtc	gatattcatt	1380
acaaagattt	catccacatc	gtgttccaga	accctctatt	tggattggag	agttatcaca	1440
togatgttga	caattttctc	gttctcggat	atggatttgg	agcttggctc	gaaagcaaaa	1500
aagctggata	taacttagta	gatgccgttt	cacgggtcaac	agttcaggtt	tatccattat	1560
cgtggacagc	aatattgata	gctatggata	atcaaggaat	gtggaaacgtg	agatcacaga	1620
aagcagagca	atgggtatctt	gggtcaagac	tttatatgag	agttaaaggt	gaaggagaa	1680
aaagatccttc	gactattccg	gttagagatg	aaaatccgat	accggggaat	gtcatccggt	1740
gtggcaaaagt	tcgataataa	ttaattgtct	gaaataataa	aaacctagaa	aagtctattt	1800
taattagcaaa	aactaaagaa	cggtttaaag	gaatgatcac	agagtattag	gatctgtggt	1860
gatcttaagg	tttgtggtt	gattgcgatt	cgatcaactt	gtgtaattgc	agaagacgga	1920
tggttaattta	aagagatgat	cttaggggtt	gtggtct			

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..236
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

Met	Arg	His	Val	Phe	Val	Glu	Val	Leu	Val	Leu	Ile	Ser	Leu	Val	Ile
1			5						10					15	
Leu	Glu	Leu	Ser	Tyr	Ala	Phe	Ala	Pro	Ile	Ser	Ser	Tyr	Gln	Trp	Val
			20					25					30		
Val	Ser	Tyr	Ser	Gln	Arg	Phe	Ile	Leu	Gly	Gly	Asn	Lys	Gln	Val	Ile
			35				40				45				
Val	Ile	Asn	Asp	Met	Phe	Pro	Gly	Pro	Ile	Leu	Asn	Ala	Thr	Ala	Asn
			50			55					60				
Asp	Ile	Ile	Val	Val	Asn	Ile	Phe	Asn	Asn	Leu	Pro	Glu	Pro	Phe	Leu
			65			70				75				80	
Met	Thr	Trp	Asn	Gly	Leu	Gln	Leu	Arg	Lys	Asn	Ser	Trp	Gln	Asp	Gly
			85					90					95		
Val	Arg	Gly	Thr	Asn	Cys	Pro	Ile	Leu	Pro	Gly	Thr	Asn	Trp	Thr	Tyr
			100					105					110		
Arg	Phe	Gln	Val	Lys	Asp	Gln	Ile	Gly	Ser	Tyr	Phe	Tyr	Phe	Pro	Thr
			115				120					125			
Leu	Leu	Leu	Gln	Lys	Ala	Ala	Gly	Gly	Tyr	Gly	Ala	Ile	Arg	Ile	Tyr
			130				135				140				
Pro	Pro	Glu	Leu	Val	Pro	Val	Pro	Phe	Pro	Lys	Pro	Asp	Glu	Glu	Tyr
			145			150				155					160
Asp	Ile	Leu	Ile	Gly	Asp	Trp	Phe	Tyr	Leu	Asp	His	Thr	Val	Met	Arg
			165					170					175		
Ala	Ser	Leu	Asp	Ala	Gly	His	Ser	Leu	Pro	Asn	Pro	Asp	Gly	Ile	Leu
			180					185					190		
Phe	Asn	Gly	Arg	Gly	Pro	Glu	Glu	Thr	Phe	Phe	Ala	Phe	Glu	Pro	Gly

(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..217
(D) OTHER INFORMATION: / Ceres Seq. ID 1566748
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

Met	Asp	Leu	Asn	Val	Gly	Ala	Ala	Arg	Ser	Asn	Pro	Gln	Gly	Ser	Tyr
1		5						10					15		
His	Tyr	Gly	Arg	Ile	Asn	Val	Thr	Arg	Thr	Ile	Ile	Leu	His	Asn	Asp
		20						25				30			
Val	Met	Leu	Ser	Ser	Gly	Lys	Leu	Arg	Tyr	Thr	Ile	Asn	Gly	Val	Ser
		35					40					45			
Phe	Val	Tyr	Pro	Glu	Thr	Pro	Leu	Lys	Leu	Val	Asp	His	Phe	Gln	Leu
		50				55				60					
Asn	Asp	Thr	Ile	Ile	Pro	Gly	Met	Phe	Pro	Val	Tyr	Pro	Ser	Asn	Lys
		65			70			75				80			
Thr	Pro	Thr	Leu	Gly	Thr	Ser	Val	Val	Asp	Ile	His	Tyr	Lys	Asp	Phe
			85					90				95			
Ile	His	Ile	Val	Phe	Gln	Asn	Pro	Leu	Phe	Gly	Leu	Glu	Ser	Tyr	His
			100				105					110			
Ile	Asp	Gly	Tyr	Asn	Phe	Phe	Val	Val	Gly	Tyr	Gly	Phe	Gly	Ala	Trp
		115				120						125			
Ser	Glu	Ser	Lys	Lys	Ala	Gly	Tyr	Asn	Leu	Val	Asp	Ala	Val	Ser	Arg
		130				135				140					
Ser	Thr	Val	Gln	Val	Tyr	Pro	Tyr	Ser	Trp	Thr	Ala	Ile	Leu	Ile	Ala
		145			150					155				160	
Met	Asp	Asn	Gln	Gly	Met	Trp	Asn	Val	Arg	Ser	Gln	Lys	Ala	Glu	Gln
			165					170				175			
Trp	Tyr	Leu	Gly	Gln	Glu	Leu	Tyr	Met	Arg	Val	Lys	Gly	Glu	Gly	Glu
		180					185					190			
Glu	Asp	Pro	Ser	Thr	Ile	Pro	Val	Arg	Asp	Glu	Asn	Pro	Ile	Pro	Gly
		195				200						205			
Asn	Val	Ile	Arg	Cys	Gly	Lys	Val	Arg							
		210				215									

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1206 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1206

(D) OTHER INFORMATION: / Ceres Seq. ID 1566749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

tatgaaattg	tagataaatg	gatcaaatcg	ttaaactgga	tgaatttcaa	gagctggcca	60
aacaggccct	ccctaagatg	tactatgatt	tctacaatgg	aggagcagag	gatacaacaca	120
ctctcaatga	aaatgtccaa	gctttccgta	gaatcatggt	taggcctagg	gttctgtgtg	180
atgtgagcaa	catagatatg	tctacaagta	tattgggtta	cccaatctca	gctcccatca	240
tgattgctcc	aacagcaatg	cataagttgg	ctcatcctaa	aggagaaatc	gccacagcga	300
aagctgcagc	tcggtgtaac	actatcatga	tagtaccatt	catgtctact	tgacattattg	360
aggaggttgc	ttccagttgt	aacgtgtgtt	ggttttctca	aatatatgtg	tacaagagac	420
gtgatgtaac	agctcagatt	gtgaaaagag	ctgaaaaaac	tggattccaag	gctatagttc	480
taactgttga	tgttcccaga	cttggtagaa	gggaagcaga	tataaagaac	aaaatgatat	540
ccccacagct	gaagaatttt	gaaggccttag	tttcaaccga	agtcgcagct	aatgaaggtt	600
cagggtttga	agcctttgcc	tctagtgcat	ttgatgtctc	gttaagctgg	aaggatattg	660
aatggtttaag	atctattaca	aagttgcca	ttctgggtcaa	agggttactc	acacgtgaag	720
acgctcttaa	ggctgttgaa	gccggtgtag	atggaaatag	ggatccaac	cacggggctc	780

```
gccagctcga ctattccccc gctacgataa ctgttttaga agaggttggt catgtgttga      840
aaggtaggat tccggttttg ctgtatggag gagtaagacg aggaacagat gttttcaaaG      900
cgSctggcgc tcggagcaca agctgttctt ataggaggcg ctatagtcta tgggcttgca      960
gctaagggtg aaagatggagt gaaaaaagtg attgatatgc tgaaaaatga gtttgagatt      1020
actatggccc tttctggctg tccaaccatt gatgacgtaa ccagaaaacca tgttaggaca      1080
gagaatgaga gaattaaatc tatgctctga tctctaaaacc aacagatcta gtctcagaga      1140
cttaatcaga cagttggaca acagtatgaa atactgtcaa tgcacataaa taaaagctc      1200
tatttc
```

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..315

(D) OTHER INFORMATION: / Ceres Seq. ID 1566750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

```
Met Asp Gln Ile Val Asn Val Asp Glu Phe Gln Glu Leu Ala Lys Gln
1      5      10      15
Ala Leu Pro Lys Met Tyr Tyr Asp Phe Tyr Asn Gly Gly Ala Glu Asp
20      25      30
Gln His Thr Leu Asn Glu Asn Val Gln Ala Phe Arg Arg Ile Met Phe
35      40      45
Arg Pro Arg Val Leu Val Asp Val Ser Asn Ile Asp Met Ser Thr Ser
50      55      60
Ile Leu Gly Tyr Pro Ile Ser Ala Pro Ile Met Ile Ala Pro Thr Ala
65      70      75      80
Met His Lys Leu Ala His Pro Lys Gly Glu Ile Ala Thr Ala Lys Ala
85      90      95
Ala Ala Ala Cys Asn Thr Ile Met Ile Val Pro Phe Met Ser Thr Cys
100     105     110
Thr Ile Glu Glu Val Ala Ser Ser Cys Asn Ala Val Arg Phe Leu Gln
115     120     125
Ile Tyr Val Tyr Lys Arg Arg Asp Val Thr Ala Gln Ile Val Lys Arg
130     135     140
Ala Glu Lys Ala Gly Phe Lys Ala Ile Val Leu Thr Val Asp Val Pro
145     150     155     160
Arg Leu Gly Arg Arg Glu Ala Asp Ile Lys Asn Lys Met Ile Ser Pro
165     170     175
Gln Leu Lys Asn Phe Glu Gly Leu Val Ser Thr Glu Val Arg Pro Asn
180     185     190
Glu Gly Ser Gly Val Glu Ala Phe Ala Ser Ser Ala Phe Asp Ala Ser
195     200     205
Leu Ser Trp Lys Asp Ile Glu Trp Leu Arg Ser Ile Thr Lys Leu Pro
210     215     220
Ile Leu Val Lys Gly Leu Leu Thr Arg Glu Asp Ala Leu Lys Ala Val
225     230     235
Glu Ala Gly Val Asp Gly Ile Val Val Ser Asn His Gly Ala Arg Gln
240     245     250     255
Leu Asp Tyr Ser Pro Ala Thr Ile Thr Val Leu Glu Glu Val Val His
260     265     270
Val Val Lys Gly Arg Ile Pro Val Leu Leu Asp Gly Gly Val Arg Arg
275     280     285
Gly Thr Asp Val Phe Lys Ala Xaa Gly Ala Arg Ser Thr Ser Cys Ser
290     295     300
Tyr Arg Glu Ala Tyr Ser Leu Trp Ala Cys Ser
305     310     315
```

(2) INFORMATION FOR SEQ ID NO:389:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 295 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..295
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566751
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

Met Tyr Tyr Asp Phe Tyr Asn Gly Gly Ala Glu Asp Gln His Thr Leu
1 5 10 15
Asn Glu Asn Val Gln Ala Phe Arg Arg Ile Met Phe Arg Pro Arg Val
20 25 30
Leu Val Asp Val Ser Asn Ile Asp Met Ser Thr Ser Ile Leu Gly Tyr
35 40 45
Pro Ile Ser Ala Pro Ile Met Ile Ala Pro Thr Ala Met His Lys Leu
50 55 60
Ala His Pro Lys Gly Glu Ile Ala Thr Ala Lys Ala Ala Ala Cys
65 70 75 80
Asn Thr Ile Met Ile Val Pro Phe Met Ser Thr Cys Thr Ile Glu Glu
85 90 95
Val Ala Ser Ser Cys Asn Ala Val Arg Phe Leu Gln Ile Tyr Val Tyr
100 105 110
Lys Arg Arg Asp Val Thr Ala Gln Ile Val Lys Arg Ala Glu Lys Ala
115 120 125
Gly Phe Lys Ala Ile Val Leu Thr Val Asp Val Pro Arg Leu Gly Arg
130 135 140
Arg Glu Ala Asp Ile Lys Asn Lys Met Ile Ser Pro Gln Leu Lys Asn
145 150 155 160
Phe Glu Gly Leu Val Ser Thr Glu Val Arg Pro Asn Glu Gly Ser Gly
165 170 175
Val Glu Ala Phe Ala Ser Ser Ala Phe Asp Ala Ser Leu Ser Trp Lys
180 185 190
Asp Ile Glu Trp Leu Arg Ser Ile Thr Lys Leu Pro Ile Leu Val Lys
195 200 205
Gly Leu Leu Thr Arg Glu Asp Ala Leu Lys Ala Val Glu Ala Gly Val
210 215 220
Asp Gly Ile Val Val Ser Asn His Gly Ala Arg Gln Leu Asp Tyr Ser
225 230 235 240
Pro Ala Thr Ile Thr Val Leu Glu Glu Val Val His Val Lys Gly
245 250 255
Arg Ile Pro Val Leu Leu Asp Gly Gly Val Arg Arg Gly Thr Asp Val
260 265 270
Phe Lys Ala Xaa Gly Ala Arg Ser Thr Ser Cys Ser Tyr Arg Glu Ala
275 280 285
Tyr Ser Leu Trp Ala Cys Ser
290 295

- (2) INFORMATION FOR SEQ ID NO:390:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 269 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..269
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566752
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

Met Phe Arg Pro Arg Val Leu Val Asp Val Ser Asn Ile Asp Met Ser
1 5 10 15
Thr Ser Ile Leu Gly Tyr Pro Ile Ser Ala Pro Ile Met Ile Ala Pro
20 25 30
Thr Ala Met His Lys Leu Ala His Pro Lys Gly Glu Ile Ala Thr Ala
35 40 45
Lys Ala Ala Ala Ala Cys Asn Thr Ile Met Ile Val Pro Phe Met Ser
50 55 60
Thr Cys Thr Ile Glu Glu Val Ala Ser Ser Cys Asn Ala Val Arg Phe
65 70 75 80
Leu Gln Ile Tyr Val Tyr Lys Arg Arg Asp Val Thr Ala Gln Ile Val
85 90 95
Lys Arg Ala Glu Lys Ala Gly Phe Lys Ala Ile Val Leu Thr Val Asp
100 105 110
Val Pro Arg Leu Gly Arg Arg Glu Ala Asp Ile Lys Asn Lys Met Ile
115 120 125
Ser Pro Gln Leu Lys Asn Phe Glu Gly Leu Val Ser Thr Glu Val Arg
130 135 140
Pro Asn Glu Gly Ser Gly Val Glu Ala Phe Ala Ser Ser Ala Phe Asp
145 150 155 160
Ala Ser Leu Ser Trp Lys Asp Ile Glu Trp Leu Arg Ser Ile Thr Lys
165 170 175
Leu Pro Ile Leu Val Lys Gly Leu Leu Thr Arg Glu Asp Ala Leu Lys
180 185 190
Ala Val Glu Ala Gly Val Asp Gly Ile Val Val Ser Asn His Gly Ala
195 200 205
Arg Gln Leu Asp Tyr Ser Pro Ala Thr Ile Thr Val Leu Glu Glu Val
210 215 220
Val His Val Val Lys Gly Arg Ile Pro Val Leu Leu Asp Gly Gly Val
225 230 235 240
Arg Arg Gly Thr Asp Val Phe Lys Ala Xaa Gly Ala Arg Ser Thr Ser
245 250 255
Cys Ser Tyr Arg Glu Ala Tyr Ser Leu Trp Ala Cys Ser
260 265

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1178

(D) OTHER INFORMATION: / Ceres Seq. ID 1566763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

taatttgggg	tcagggggtg	gagtagccctc	gactttatgat	gacattttctc	aatacaagagg	60
aggctacaga	gatgcctaca	gtttgcacaa	gagtgcaaca	acagggagacc	gatacgtttg	120
gtccagacag	ccctttgagc	agtttgttgt	agcggagagag	aattggtgtgt	ttggtgagga	180
gtccaggaat	agatcgaatc	cgatcaatat	agacaacaac	gctttttcta	atgttgatgc	240
agaggctaag	cttcttcagt	cgttcaggca	ctgtatttcta	aagctttatta	aacttgaagg	300
atccgagtgg	ttgtttggac	aaagcagatg	agttgatgaa	gaactgtattg	acggggtatg	360
tgccagagag	aagtttatct	atgaagctga	agctcgagaa	ataaaccagg	tggttcacat	420
ggggagacaa	ctaattttcat	cggttcctaa	ctgtggagat	ggttgcgttt	ggagagctga	480
tttgatttgt	agcgtttggag	tttggtgcat	tcaacgtgtc	cttgacttgt	ctctcatgga	540
gagtcggcct	gaagctttgg	gaaagtacac	ttacgtttctc	aacgcgcctac	agggagtgat	600
tgatccggcg	ttctcaaagg	tgccggacacc	aatgacaccg	tgctttttgcc	ttcagattcc	660
agcgagccac	cagagagcga	gtccgacttc	agctaacagg	atgttacctc	cggttcgcaa	720
accggtctaaa	ggcaaatgca	caaccgcagt	cacactttct	gatctaatac	aaagcgttga	780
aattggcaatc	tcttgtagaa	aaggccgaac	cggtacagct	gcaggtgtatg	tggtcttccc	840
aaaggggaaa	gagaatttgg	cttcggtttt	gaagcgggtat	aaacgtcgggt	tatcgaataa	900

accagtaggt atgaatcagg atggaccgg ttcaagaaaa aacgtgactg cgtacggatc 960
attgggttga agaagaagaa cattgtgaga aatctcatga tcaaagtac gtcgagagg 1020
aagccgaaga atcaaaactc tcgttttga ttgtctctct gcttcgttaa ttgtgtatta 1080
agaaaagaag aaaaaaatg gatttttgtt gcttcagaat ttttcgctct ttttttctta 1140
ttttggtgtt aatgttatgt ttatatcat atatcttc

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..322

(D) OTHER INFORMATION: / Ceres Seq. ID 1566764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

Asn	Leu	Gly	Ser	Gly	Val	Gly	Val	Pro	Ser	Thr	Tyr	Asp	Asp	Ile	Ser
1			5					10					15		
Gln	Ser	Arg	Gly	Gly	Tyr	Arg	Asp	Ala	Tyr	Ser	Leu	Pro	Gln	Ser	Ala
			20				25						30		
Thr	Thr	Gly	Thr	Gly	Ser	Leu	Trp	Ser	Arg	Gln	Pro	Phe	Glu	Gln	Phe
			35				40					45			
Val	Val	Ala	Glu	Arg	Asn	Gly	Ala	Val	Gly	Glu	Glu	Leu	Arg	Asn	Arg
			50			55					60				
Ser	Asn	Pro	Ile	Asn	Ile	Asp	Asn	Asn	Ala	Ser	Ser	Asn	Val	Asp	Ala
			65			70				75				80	
Glu	Ala	Lys	Leu	Leu	Gln	Ser	Phe	Arg	His	Cys	Ile	Leu	Lys	Leu	Ile
			85						90				95		
Lys	Leu	Glu	Gly	Ser	Glu	Trp	Leu	Phe	Gly	Gln	Ser	Asp	Gly	Val	Asp
			100					105					110		
Glu	Glu	Leu	Ile	Asp	Arg	Val	Ala	Ala	Arg	Glu	Lys	Phe	Ile	Tyr	Glu
			115				120					125			
Ala	Glu	Ala	Arg	Glu	Ile	Asn	Gln	Val	Gly	His	Met	Gly	Glu	Gln	Leu
			130			135					140				
Ile	Ser	Ser	Val	Pro	Asn	Cys	Gly	Asp	Gly	Cys	Val	Trp	Arg	Ala	Asp
			145			150				155				160	
Leu	Ile	Val	Ser	Phe	Gly	Val	Trp	Cys	Ile	His	Xaa	Val	Leu	Asp	Leu
			165						170					175	
Ser	Leu	Met	Glu	Ser	Arg	Pro	Glu	Leu	Trp	Gly	Lys	Tyr	Thr	Tyr	Val
			180					185					190		
Leu	Asn	Arg	Leu	Gln	Gly	Val	Ile	Asp	Pro	Ala	Phe	Ser	Lys	Leu	Arg
			195					200				205			
Thr	Pro	Met	Thr	Pro	Cys	Phe	Cys	Leu	Gln	Ile	Pro	Ala	Ser	His	Gln
			210			215					220				
Arg	Ala	Ser	Pro	Thr	Ser	Ala	Asn	Gly	Met	Leu	Pro	Pro	Ala	Ala	Lys
			225			230				235				240	
Pro	Ala	Lys	Gly	Lys	Cys	Thr	Thr	Ala	Val	Thr	Leu	Leu	Asp	Leu	Ile
			245						250				255		
Lys	Asp	Val	Glu	Met	Ala	Ile	Ser	Cys	Arg	Lys	Gly	Arg	Thr	Gly	Thr
			260					265					270		
Ala	Ala	Gly	Asp	Val	Ala	Phe	Pro	Lys	Gly	Lys	Glu	Asn	Leu	Ala	Ser
			275					280				285			
Val	Leu	Lys	Arg	Tyr	Lys	Arg	Arg	Leu	Ser	Asn	Lys	Pro	Val	Gly	Met
			290			295					300				
Asn	Gln	Asp	Gly	Pro	Gly	Ser	Arg	Lys	Asn	Val	Thr	Ala	Tyr	Gly	Ser
			305			310				315				320	
Leu	Gly														

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..183
(D) OTHER INFORMATION: / Ceres Seq. ID 1566765
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:
Met Gly Glu Gln Leu Ile Ser Ser Val Pro Asn Cys Gly Asp Gly Cys
1 5 10 15
Val Trp Arg Ala Asp Leu Ile Val Ser Phe Gly Val Trp Cys Ile His
20 25 30
Xaa Val Leu Asp Leu Ser Leu Met Glu Ser Arg Pro Glu Leu Trp Gly
35 40 45
Lys Tyr Thr Tyr Val Leu Asn Arg Leu Gln Gly Val Ile Asp Pro Ala
50 55 60
Phe Ser Lys Leu Arg Thr Pro Met Thr Pro Cys Phe Cys Leu Gln Ile
65 70 75 80
Pro Ala Ser His Gln Arg Ala Ser Pro Thr Ser Ala Asn Gly Met Leu
85 90 95
Pro Pro Ala Ala Lys Pro Ala Lys Gly Lys Cys Thr Thr Ala Val Thr
100 105 110
Leu Leu Asp Leu Ile Lys Asp Val Glu Met Ala Ile Ser Cys Arg Lys
115 120 125
Gly Arg Thr Gly Thr Ala Ala Gly Asp Val Ala Phe Pro Lys Gly Lys
130 135 140
Glu Asn Leu Ala Ser Val Leu Lys Arg Tyr Lys Arg Arg Leu Ser Asn
145 150 155 160
Lys Pro Val Gly Met Asn Gln Asp Gly Pro Gly Ser Arg Lys Asn Val
165 170 175
Thr Ala Tyr Gly Ser Leu Gly
180

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1514 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1514
(D) OTHER INFORMATION: / Ceres Seq. ID 1566766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

atttctctac caccgttgat gttagggttt cggctgtatt ctcaccgctg ctgacgggaga 60
cgccccgaat ccgcaattta atctctcgagg ttcgatttta gtgaagaaca agattcaata 120
gtgatatgca gatctcatgt ctcccaattt cgattctctc gatcactcct cgaacctcaa 180
ttccactctt accatcacct tcctcaaatc ctgcgccgat ttccaacctc acttcaactc 240
agagcccaaa tcactgtttc ttcaaaagat tacataaatc tcagactgtt ttcagcaatc 300
cagttttggc tgccatgaaa agagaagaag atgttgaagt cgatgattcg ttttatatga 360
gaaagtgtgt ggagctagca aaaagagcaa ttgggtgtac aagtcctaatt cctatggtga 420
gttggtgtcat ttgcaaaagt ggtgacattg ttggccaagg gtttcatccc aaagctggtc 480
agcctcatcg tgaggtgttt gctcttagag atgctggaga gttagctgag aatgctactg 540
cttatgttag ttgtgaaaca tgtaatcatt accggaagaac accgccgtgt acagaagcat 600
tgattaaggc taaggtgaga agagttgtta ttgggatggt tgatccgaat ccaattgttt 660
ttctctcggt tattagtctg ttgaaagatg ctggaatcga tgttactgtg agtgttgaag 720
aagagttagt caagaagatg aatgagggat tcattccatcg aatgttaaca gggaaagcctt 780
ttctcgccct caggtattct atgtctgtca atggtgtttt gctagacaag attgggcaag 840
gggcttcgga tagtggtgga tactactcga agctatttga ggaatatgat gcgataatac 900

ttttctctc	gttatcgat	gaactctcga	gcattttctc	acaagaagct	attaatgttt	960
cgatccaacc	tattcagatc	atagtagcta	gcaatgcaca	acagtctcat	atccttgctt	1020
cttccacac	tgtggaagaa	tcgggtccaa	aagttgtagt	tttcaccgca	aaggaatcgg	1080
ttgcagaatc	cgggaatcagt	agtagcgggg	tcgaaaccgt	agtattggaa	aagmtaaaat	1140
tggtattcat	tttgattat	tgttacaacc	gtggactatg	cagtgctctg	ttagatttga	1200
gggggaacgt	caaagacott	gaagttcttc	tgagagatgg	atttgagcag	aaactattgc	1260
agaaagtaat	tattgaggtc	ttgcgggaat	ggagcacaaa	agatgagaga	cagatcgctt	1320
cgatgaagt	gttgaatcaa	aagcatgtga	aagatttgca	gtctaagcaa	ttaggtggaa	1380
gcgttttgc	agagggctat	ttttgatgtt	ttcatgtatg	aatgaataca	agtcagtata	1440
tttaccttt	ttaaagcata	gtattattaa	ggttttacag	atcctattat	taatagattg	1500
ataacagatt	tttg					

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1566767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

Met	Gln	Ile	Ser	Cys	Leu	Pro	Ile	Ser	Ile	Pro	Ser	Ile	Thr	Pro	Arg
1				5					10					15	
Thr	Ser	Ile	Pro	Leu	Leu	Pro	Ser	Leu	Ser	Ser	Asn	Pro	Arg	Arg	Ile
			20					25					30		
Phe	Asn	Leu	Thr	Ser	Leu	Gln	Ser	Pro	Asn	His	Cys	Phe	Phe	Lys	Arg
		35					40					45			
Leu	His	Lys	Ser	Gln	Thr	Gly	Phe	Ser	Asn	Pro	Val	Leu	Ala	Ala	Met
		50				55					60				
Lys	Arg	Glu	Glu	Asp	Val	Glu	Val	Asp	Asp	Ser	Phe	Tyr	Met	Arg	Lys
65				70					75					80	
Cys	Val	Glu	Leu	Ala	Lys	Arg	Ala	Ile	Gly	Cys	Thr	Ser	Pro	Asn	Pro
			85						90					95	
Met	Val	Gly	Cys	Val	Ile	Val	Lys	Asp	Gly	Asp	Ile	Val	Gly	Gln	Gly
		100						105					110		
Phe	His	Pro	Lys	Ala	Gly	Gln	Pro	His	Ala	Glu	Val	Phe	Ala	Leu	Arg
		115					120					125			
Asp	Ala	Gly	Glu	Leu	Ala	Glu	Asn	Ala	Thr	Ala	Tyr	Val	Ser	Leu	Glu
		130				135					140				
Pro	Cys	Asn	His	Tyr	Gly	Arg	Thr	Pro	Pro	Cys	Thr	Glu	Ala	Leu	Ile
145				150						155				160	
Lys	Ala	Lys	Val	Arg	Arg	Val	Val	Ile	Gly	Met	Val	Asp	Pro	Asn	Pro
				165					170					175	
Ile	Val	Phe	Ser	Ser	Gly	Ile	Ser	Arg	Leu	Lys	Asp	Ala	Gly	Ile	Asp
			180					185					190		
Val	Thr	Val	Ser	Val	Glu	Glu	Glu	Leu	Cys	Lys	Lys	Met	Asn	Glu	Gly
			195					200				205			
Phe	Ile	His	Arg	Met	Leu	Thr	Gly	Lys	Pro	Phe	Leu	Ala	Leu	Arg	Tyr
				215							220				
Ser	Met	Ser	Val	Asn	Gly	Cys	Leu	Leu	Asp	Lys	Ile	Gly	Gln	Gly	Ala
225				230						235				240	
Ser	Asp	Ser	Gly	Gly	Tyr	Tyr	Ser	Lys	Leu	Leu	Gln	Glu	Tyr	Asp	Ala
			245						250					255	
Ile	Ile	Leu	Ser	Ser	Ser	Leu	Ser	Asp	Glu	Leu	Ser	Ser	Ile	Ser	Ser
			260					265					270		
Gln	Glu	Ala	Ile	Asn	Val	Ser	Ile	Gln	Pro	Ile	Gln	Ile	Ile	Val	Ala
			275					280					285		
Ser	Asn	Ala	Gln	Gln	Ser	His	Ile	Leu	Ala	Ser	Ser	His	Thr	Val	Glu
290						295						300			

Glu Ser Gly Pro Lys Val Val Val Phe Thr Ala Lys Glu Ser Val Ala
305 310 315 320
Glu Ser Gly Ile Ser Ser Ser Gly Val Glu Thr Val Val Leu Glu Lys
325 330 335
Xaa Asn Leu Asp Ser Ile Leu Asp Tyr Cys Tyr Asn Arg Gly Leu Cys
340 345 350
Ser Val Leu Leu Asp Leu Arg Gly Asn Val Lys Asp Leu Glu Val Leu
355 360 365
Leu Arg Asp Gly Phe Glu Gln Lys Leu Leu Gln Lys Val Ile Ile Glu
370 375 380
Val Leu Pro Glu Trp Ser Thr Lys Asp Glu Arg Gln Ile Ala Ser Met
385 390 395 400
Lys Trp Leu Glu Ser Lys His Val Lys Asp Leu Gln Ser Lys Gln Leu
405 410 415
Gly Gly Ser Val Leu Leu Glu Gly Tyr Phe
420 425

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..363
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

Met Lys Arg Glu Glu Asp Val Glu Val Asp Asp Ser Phe Tyr Met Arg
1 5 10 15
Lys Cys Val Glu Leu Ala Lys Arg Ala Ile Gly Cys Thr Ser Pro Asn
20 25 30
Pro Met Val Gly Cys Val Ile Val Lys Asp Gly Asp Ile Val Gly Gln
35 40 45
Gly Phe His Pro Lys Ala Gly Gln Pro His Ala Glu Val Phe Ala Leu
50 55 60
Arg Asp Ala Gly Glu Leu Ala Glu Asn Ala Thr Ala Tyr Val Ser Leu
65 70 75 80
Glu Pro Cys Asn His Tyr Gly Arg Thr Pro Pro Cys Thr Glu Ala Leu
85 90 95
Ile Lys Ala Lys Val Arg Arg Val Val Ile Gly Met Val Asp Pro Asn
100 105 110
Pro Ile Val Phe Ser Ser Gly Ile Ser Arg Leu Lys Asp Ala Gly Ile
115 120 125
Asp Val Thr Val Ser Val Glu Glu Leu Cys Lys Lys Met Asn Glu
130 135 140
Gly Phe Ile His Arg Met Leu Thr Gly Lys Pro Phe Leu Ala Leu Arg
145 150 155 160
Tyr Ser Met Ser Val Asn Gly Cys Leu Leu Asp Lys Ile Gly Gln Gly
165 170 175
Ala Ser Asp Ser Gly Gly Tyr Tyr Ser Lys Leu Leu Gln Glu Tyr Asp
180 185 190
Ala Ile Ile Leu Ser Ser Ser Leu Ser Asp Glu Leu Ser Ser Ile Ser
195 200 205
Ser Gln Glu Ala Ile Asn Val Ser Ile Gln Pro Ile Gln Ile Ile Val
210 215 220
Ala Ser Asn Ala Gln Gln Ser His Ile Leu Ala Ser Ser His Thr Val
225 230 235 240
Glu Glu Ser Gly Pro Lys Val Val Val Phe Thr Ala Lys Glu Ser Val
245 250 255
Ala Glu Ser Gly Ile Ser Ser Ser Gly Val Glu Thr Val Val Leu Glu

	260		265		270
Lys Xaa Asn Leu Asp Ser Ile Leu Asp Tyr Cys Tyr Asn Arg Gly Leu					
	275		280		285
Cys Ser Val Leu Leu Asp Leu Arg Gly Asn Val Lys Asp Leu Glu Val					
	290		295		300
Leu Leu Arg Asp Gly Phe Glu Gln Lys Leu Leu Gln Lys Val Ile Ile					
305		310		315	320
Glu Val Leu Pro Glu Trp Ser Thr Lys Asp Glu Arg Gln Ile Ala Ser					
	325		330		335
Met Lys Trp Leu Glu Ser Lys His Val Lys Asp Leu Gln Ser Lys Gln					
	340		345		350
Leu Gly Gly Ser Val Leu Leu Glu Gly Tyr Phe					
	355		360		

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 349 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..349

(D) OTHER INFORMATION: / Ceres Seq. ID 1566769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

Met Arg Lys Cys Val Glu Leu Ala Lys Arg Ala Ile Gly Cys Thr Ser	
1	5
Pro Asn Pro Met Val Gly Cys Val Ile Val Lys Asp Gly Asp Ile Val	
	20
Gly Gln Gly Phe His Pro Lys Ala Gly Gln Pro His Ala Glu Val Phe	
	35
Ala Leu Arg Asp Ala Gly Glu Leu Ala Glu Asn Ala Thr Ala Tyr Val	
50	55
Ser Leu Glu Pro Cys Asn His Tyr Gly Arg Thr Pro Pro Cys Thr Glu	
65	70
Ala Leu Ile Lys Ala Lys Val Arg Arg Val Ile Gly Met Val Asp	
	85
Pro Asn Pro Ile Val Phe Ser Ser Gly Ile Ser Arg Leu Lys Asp Ala	
	100
Gly Ile Asp Val Thr Val Ser Val Glu Glu Glu Leu Cys Lys Lys Met	
	115
Asn Glu Gly Phe Ile His Arg Met Leu Thr Gly Lys Pro Phe Leu Ala	
130	135
Leu Arg Tyr Ser Met Ser Val Asn Gly Cys Leu Leu Asp Lys Ile Gly	
145	150
Gln Gly Ala Ser Asp Ser Gly Gly Tyr Tyr Ser Lys Leu Leu Gln Glu	
	165
Tyr Asp Ala Ile Ile Leu Ser Ser Ser Leu Ser Asp Glu Leu Ser Ser	
	180
Ile Ser Ser Gln Glu Ala Ile Asn Val Ser Ile Gln Pro Ile Gln Ile	
	195
Ile Val Ala Ser Asn Ala Gln Gln Ser His Ile Leu Ala Ser Ser His	
	210
Thr Val Glu Glu Ser Gly Pro Lys Val Val Val Phe Thr Ala Lys Glu	
225	230
Ser Val Ala Glu Ser Gly Ile Ser Ser Ser Gly Val Glu Thr Val Val	
	245
Leu Glu Lys Xaa Asn Leu Asp Ser Ile Leu Asp Tyr Cys Tyr Asn Arg	
	260
Gly Leu Cys Ser Val Leu Leu Asp Leu Arg Gly Asn Val Lys Asp Leu	
	275
	280
	285

Glu Val Leu Leu Arg Asp Gly Phe Glu Gln Lys Leu Leu Gln Lys Val
290 295 300
Ile Ile Glu Val Leu Pro Glu Trp Ser Thr Lys Asp Glu Arg Gln Ile
305 310 315 320
Ala Ser Met Lys Trp Leu Glu Ser Lys His Val Lys Asp Leu Gln Ser
325 330 335
Lys Gln Leu Gly Gly Ser Val Leu Glu Gly Tyr Phe
340 345

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1571 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1571

(D) OTHER INFORMATION: / Ceres Seq. ID 1566785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

atcatctctc	tcacttcac	aaaactcaaa	aaaatgtctc	ccattccaaa	accactcttc	60
ttctttctct	tcctcaacta	KtgCtatctc	ttctcaactc	actctctctt	cacctccac	120
tcacatctct	ccctatctcc	accaccacaa	actctcaccg	cttcaccacc	tcctctctct	180
cccggaaaaa	cccatctccg	tcgtctccac	catcaaacct	ccgatcaaga	ttcaaaatac	240
caatggctct	aatcatctca	ctccccatag	gaacaccacc	acaagctcaa	caaatgggtc	300
ttgacactgg	aagccaaact	tcttggatcc	aatgtcatcg	taaaaagctt	ccctccaaac	360
caaaaacatc	atttgatcca	tctctttctt	ctcttttctc	aactttgcct	tgctcaacac	420
ctctttgtaa	accagagaatt	cccgatttta	cccttctctc	ttcttgtgac	ttcaacagggt	480
tatgtcacta	ctcttacttc	tacgtctgatg	gaacctctgc	tgagggtgat	ctcgtcaaac	540
aaaaaatcac	tttctcaaat	accgaaatta	ccctctcttt	gatactaggt	tcgctcacag	600
agctctctga	tgataggggc	attttgggaa	tgaacogtgg	tcgtctctct	tttgtttctc	660
aagctaagat	ttcgaagttc	tcttattgca	tcctcccaaa	atcaaacccg	cccggtttta	720
ctccaacccg	ttcgtttttc	cttggtgata	accggaatc	acacggtttc	aaatacgttt	780
ctttgttgac	ttttctcgaa	agtcacacgaa	tgccgaatct	tgatctctct	gcttaccactg	840
ttctatgat	tgggattaga	tttggtttga	agaagcttaa	catttccggt	tcggttttca	900
gaccogatgc	agggcggtcg	ggtcaaacaa	tggttgatcc	gggatccgag	tttactcatt	960
tagtagacgc	agcttacgat	aaagtaagag	cagagataat	gacacgtgta	ggacgaagat	1020
taaaagaagg	ttacgtctac	ggtggaacag	ctgacatgtg	tttcgatgga	aacgtggcga	1080
tgatccacag	gttgatagga	gatcttctgt	ttgtgttcc	tagaggagtt	gagatatttg	1140
ttccgaagaa	gagggttttg	gttaacgtag	gaggtgggat	tcattgcgct	ggaatccgag	1200
ggtcgagat	ctgtggagct	gctagtaata	taatcgggaa	cgttccatcag	caaaatcttt	1260
gggttgagtt	cgatgtgacc	aatagaagag	tggtgtttgc	taaagctgat	ttgacgagag	1320
tagtgtgagg	aaaagggttc	tgctacggtt	acaaacaaag	gtcttatggt	ggactcgttt	1380
aaagatcgtc	gttcgatgat	gttaatcggg	cggtagacat	taaaatagca	gttttgtatg	1440
aaggaacttt	tattaggggc	ttcgaacaat	gtcctacaaa	taattaaaag	gtttcaactg	1500
agatttttat	gttgatcaggt	ttgtatatta	tatggttcat	attaacttgt	tacataaaaa	1560
tatcttttat	t					

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..441

(D) OTHER INFORMATION: / Ceres Seq. ID 1566786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

His Leu Ser His Phe His Lys Thr Gln Lys Asn Val Ser His Ser Lys
1 5 10 15

Thr Thr Leu Leu Leu Leu Leu Pro Gln Leu Xaa Leu Ser Leu Ser Thr
20 25 30
Ser Leu Ser Leu His Leu Pro Leu Thr Ser Leu Pro Ile Ser Thr Thr
35 40 45
Thr Asn Ser His Arg Phe Thr Thr Ser Leu Leu Ser Arg Lys Asn Pro
50 55 60
Ser Pro Ser Ser Pro Pro Tyr Asn Phe Arg Ser Arg Phe Lys Tyr Ser
65 70 75 80
Met Ala Leu Ile Ile Ser Leu Pro Ile Gly Thr Pro Pro Gln Ala Gln
85 90 95
Gln Met Val Leu Asp Thr Gly Ser Gln Leu Ser Trp Ile Gln Cys His
100 105 110
Arg Lys Lys Leu Pro Pro Lys Pro Lys Thr Ser Phe Asp Pro Ser Leu
115 120 125
Ser Ser Ser Phe Ser Thr Leu Pro Cys Ser His Pro Leu Cys Lys Pro
130 135 140
Arg Ile Pro Asp Phe Thr Leu Pro Thr Ser Cys Asp Ser Asn Arg Leu
145 150 155 160
Cys His Tyr Ser Tyr Phe Tyr Ala Asp Gly Thr Phe Ala Glu Gly Asn
165 170 175
Leu Val Lys Glu Lys Ile Thr Phe Ser Asn Thr Glu Ile Thr Pro Pro
180 185 190
Leu Ile Leu Gly Cys Ala Thr Glu Ser Ser Asp Asp Arg Gly Ile Leu
195 200 205
Gly Met Asn Arg Gly Arg Leu Ser Phe Val Ser Gln Ala Lys Ile Ser
210 215 220
Lys Phe Ser Tyr Cys Ile Pro Pro Lys Ser Asn Arg Pro Gly Phe Thr
225 230 235 240
Pro Thr Gly Ser Phe Tyr Leu Gly Asp Asn Pro Asn Ser His Gly Phe
245 250 255
Lys Tyr Val Ser Leu Leu Thr Phe Pro Glu Ser Gln Arg Met Pro Asn
260 265 270
Leu Asp Pro Leu Ala Tyr Thr Val Pro Met Ile Gly Ile Arg Phe Gly
275 280 285
Leu Lys Lys Leu Asn Ile Ser Gly Ser Val Phe Arg Pro Asp Ala Gly
290 295 300
Gly Ser Gly Gln Thr Met Val Asp Ser Gly Ser Glu Phe Thr His Leu
305 310 315 320
Val Asp Ala Ala Tyr Asp Lys Val Arg Ala Glu Ile Met Thr Arg Val
325 330 335
Gly Arg Arg Leu Lys Lys Gly Tyr Val Tyr Gly Gly Thr Ala Asp Met
340 345 350
Cys Phe Asp Gly Asn Val Ala Met Ile Pro Arg Leu Ile Gly Asp Leu
355 360 365
Val Phe Val Phe Thr Arg Gly Val Glu Ile Phe Val Pro Lys Glu Arg
370 375 380
Val Leu Val Asn Val Gly Gly Ile His Cys Val Gly Ile Gly Arg
385 390 395 400
Ser Ser Met Leu Gly Ala Ala Ser Asn Ile Ile Gly Asn Val His Gln
405 410 415
Gln Asn Leu Trp Val Glu Phe Asp Val Thr Asn Arg Arg Val Gly Phe
420 425 430
Ala Lys Ala Asp Cys Ser Arg Val Val
435 440

(2) INFORMATION FOR SEQ ID NO:400:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1566787

(B) LOCATION: 1..344

Figure 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

(2) INFORMATION FOR SEQ ID NO:402:

(A) LENGTH: 1816 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1816

(D) OTHER INFORMATION: / Ceres Seq. ID 1566797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

atgttctatag ttactacaag agtcactgag aaataaatta tacaaaatat gtctaattgaa 60
aattctgtaa tgcattgag atcgcatctc tggcatctc tgtcttcaag atgtatcaat 120
tgcgttgtaa ggtttattcc ttttcggttg cttgcaagcg aagttaacca acaaaggcgg 180


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accagtacaa tggcctgtgt ttgggataac tcccgagttc ttcccttcctg ttccagatgat 240
gtttggatgg gtcaccccgat gtttgacgaa aagccgagga acgtttccctt aaccaacgat 300
ctgtgtttagt ggaattctac gacccatgac tagtgttccct gcaaacatcg aatacatgct 360
caaaacaaat ttcaagaact ttccataaagg agagtgtttac aaagagagat tccgtgacct 420
actcgaagat ggtatttttca atgcggatga tgaatcttgg aaagaacaga gacggatcat 480
cataacagaa atgcattcca ctccgtctctg ggaatcattct ttccagacga cgagagattt 540
gatagagagg aagctttttaa aagtgatgga gagttttcc aagtcacaa aagcttttga 600
tcttcaagag attctttttt ggttaacatt tgataatata tgcattcgcg gttcttgaga 660
tgatccgggg acttttggatg atgatcttcc tcaagttcca ttccgcaaa cggtttgaga 720
agcaacagag tctactctgt ttccgttccat gatcccgct ttgtgttga aaccaatgaa 780
gttttttcgat atagggtatg agaaagggct tagggaagcg gttgagacg ttcaaacatt 840
tatcgacaag atggtttgtg aacgaatcgc gatgcttaag gaccaaggaa cattagcgaa 900
tagcaaatcc gatgtctctt cgaggctaat acagatcgaa agtcacaaaa gaggcgatga 960
aaatgatoga ttcaaccgca agtttttccg acagttctgc tcaagcttca tcttagccgg 1020
acgagacacg agttcccgctg cgttactctg gttcttctg ttgataacaa aacccccgga 1080
agtcaaaacc aagatccttc acgaaatcag agaaatcttg agccaaagag agaagaacaa 1140
ctacaagctt gatgaaccg gagaacacga gagttctctg cacttcacag tcaagaact 1200
aaacgatatg gtttatctac aagcagcatt gtcagaatct cttagactct atccaccaat 1260
tccaatggaa atgaacaacg cgaccgagga agatgtgttt ccggatggaa ctttcttgag 1320
aaaaggctca aggttttact tctcagtcta tgcaatggga aggatggaa cgatttgggg 1380
aaaagactgt gaaatgttca aaccgaaaag atggatacaa ggaggcgcat acgtgagtga 1440
tgatcagttt aaatcgtctg tgttcaatgc aggtccaaga cttgttttag gaaaacatt 1500
tgcttactgt ccagtgaaaa tgggtggctgc ttcgatcttg ctgaattact aaatcaaggt 1560
tgatcaagat catgtttgtt ttcccgagat aacaacgact ttgtatatga aacatggtct 1620
taagtgacg attacacoga gatctctaga agagaagaag caagattcat aaatatagaa 1680
gaaacaaaca gctaaactgt gaagtgttga ctgaaatata cataaataat ctttgttagt 1740
aaaatgtaca gtgtgtgtat tatgtgtaat tcagatcaaa tgttatatac aaagaaaaaa 1800
Attgcaatca taaggc

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(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..477

(D) OTHER INFORMATION: / Ceres Seq. ID 1566798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

```

Met Phe Gly Trp Val Thr Arg Cys Leu Thr Lys Ser Arg Gly Thr Phe
1 5 10 15
Pro Tyr Gln Arg Ile Trp Phe Ser Gly Ser Tyr Gly Ala Met Thr Ser
20 25 30
Val Pro Ala Asn Ile Glu Tyr Met Leu Lys Thr Asn Phe Lys Asn Phe
35 40 45
Pro Lys Gly Glu Phe Tyr Lys Glu Arg Phe Arg Asp Leu Leu Glu Asp
50 55 60
Gly Ile Phe Asn Ala Asp Asp Glu Ser Trp Lys Glu Gln Arg Arg Ile
65 70 75 80
Ile Ile Thr Glu Met His Ser Thr Arg Phe Val Asp His Ser Phe Gln
85 90 95
Thr Thr Arg Asp Leu Ile Glu Arg Lys Leu Leu Lys Val Met Glu Ser
100 105 110
Phe Ser Lys Ser Gln Glu Ala Phe Asp Leu Gln Glu Ile Leu Leu Arg
115 120 125
Leu Thr Phe Asp Asn Ile Cys Ile Ala Gly Leu Gly Asp Asp Pro Gly
130 135 140
Thr Leu Asp Asp Asp Leu Pro His Val Pro Phe Ala Lys Ala Phe Glu
145 150 155 160
Glu Ala Thr Glu Ser Thr Leu Phe Arg Phe Met Ile Pro Pro Phe Val

```

Met	Thr	Ser	Val	Pro	Ala	Asn	Ile	Glu	Tyr	Met	Leu	Lys	Thr	Asn	Phe
1				5					10					15	
Lys	Asn	Phe	Pro	Lys	Gly	Glu	Phe	Tyr	Lys	Glu	Arg	Phe	Arg	Asp	Leu
			20					25					30		
Leu	Glu	Asp	Gly	Ile	Phe	Asn	Ala	Asp	Asp	Glu	Ser	Trp	Lys	Glu	Gln
		35					40					45			
Arg	Arg	Ile	Ile	Ile	Thr	Glu	Met	His	Ser	Thr	Arg	Phe	Val	Asp	His
	50					55					60				
Ser	Phe	Gln	Thr	Thr	Arg	Asp	Leu	Ile	Glu	Arg	Lys	Leu	Leu	Lys	Val
65					70					75				80	

Met	Glu	Ser	Phe	Ser	Lys	Ser	Gln	Glu	Ala	Phe	Asp	Leu	Gln	Glu	Ile	
				85					90					95		
Leu	Leu	Arg	Leu	Thr	Phe	Asp	Asn	Ile	Cys	Ile	Ala	Gly	Leu	Gly	Asp	
			100					105					110			
Asp	Pro	Gly	Thr	Leu	Asp	Asp	Asp	Leu	Pro	His	Val	Pro	Phe	Ala	Lys	
			115				120					125				
Ala	Phe	Glu	Glu	Ala	Thr	Glu	Ser	Thr	Leu	Phe	Arg	Phe	Met	Ile	Pro	
			130				135				140					
Pro	Phe	Val	Trp	Lys	Pro	Met	Lys	Phe	Phe	Asp	Ile	Gly	Tyr	Glu	Lys	
			145			150				155					160	
Gly	Leu	Arg	Glu	Ala	Val	Glu	Thr	Val	His	Asn	Phe	Ile	Asp	Lys	Met	
				165					170					175		
Val	Val	Glu	Arg	Ile	Ala	Met	Leu	Lys	Asp	Gln	Gly	Thr	Leu	Ala	Asn	
			180					185					190			
Ser	Lys	Ser	Asp	Val	Leu	Ser	Arg	Leu	Ile	Gln	Ile	Glu	Ser	His	Lys	
			195				200						205			
Arg	Gly	Asp	Glu	Asn	Asp	Arg	Phe	Thr	Ala	Lys	Phe	Phe	Arg	Gln	Phe	
			210				215				220					
Cys	Ser	Ser	Phe	Ile	Leu	Ala	Gly	Arg	Asp	Thr	Ser	Ser	Val	Ala	Leu	
					230				235						240	
Thr	Trp	Phe	Phe	Trp	Leu	Ile	Thr	Lys	His	Pro	Glu	Val	Glu	Thr	Lys	
				245					250					255		
Ile	Leu	His	Glu	Ile	Arg	Glu	Ile	Leu	Ser	Gln	Arg	Glu	Lys	Asn	Asn	
			260					265					270			
Tyr	Lys	Leu	Asp	Glu	Thr	Gly	Glu	Thr	Glu	Ser	Ser	Arg	His	Phe	Thr	
			275				280					285				
Val	Lys	Glu	Leu	Asn	Asp	Met	Val	Tyr	Leu	Gln	Ala	Ala	Leu	Ser	Glu	
			290			295					300					
Ser	Leu	Arg	Leu	Tyr	Pro	Pro	Ile	Pro	Met	Glu	Met	Lys	Gln	Ala	Thr	
					310				315						320	
Glu	Glu	Asp	Val	Phe	Pro	Asp	Gly	Thr	Phe	Leu	Arg	Lys	Gly	Ser	Arg	
				325					330					335		
Val	Tyr	Phe	Ser	Val	Tyr	Ala	Met	Gly	Arg	Met	Glu	Ser	Ile	Trp	Gly	
			340					345					350			
Lys	Asp	Cys	Glu	Met	Phe	Lys	Pro	Glu	Arg	Trp	Ile	Gln	Gly	Gly	Gln	
			355				360					365				
Tyr	Val	Ser	Asp	Asp	Gln	Phe	Lys	Tyr	Val	Val	Phe	Asn	Ala	Gly	Pro	
			370			375					380					
Arg	Leu	Cys	Leu	Gly	Lys	Thr	Phe	Ala	Tyr	Leu	Gln	Met	Lys	Met	Val	
					390				395					400		
Ala	Ala	Ser	Ile	Leu	Leu	Asn	Tyr	Ser	Ile	Lys	Val	Asp	Gln	Asp	His	
				405					410					415		
Val	Val	Val	Pro	Arg	Val	Thr	Thr	Thr	Leu	Tyr	Met	Lys	His	Gly	Leu	
			420					425					430			
Lys	Val	Arg	Ile	Thr	Pro	Arg	Ser	Leu	Glu	Glu	Lys	Lys	Gln	Asp	Ser	
			435				440					445				

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 438 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..438

(D) OTHER INFORMATION: / Ceres Seq. ID 1566800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

Met Leu Lys Thr Asn Phe Lys Asn Phe Pro Lys Gly Glu Phe Tyr Lys

1	5	10	15
Glu Arg Phe Arg	Asp Leu Leu Glu Asp	Gly Ile Phe Asn Ala Asp Asp	
	20	25	30
Glu Ser Trp Lys	Glu Gln Arg Arg Ile Ile Thr Glu Met His Ser		
	35	40	45
Thr Arg Phe Val Asp His Ser	Phe Gln Thr Thr Arg Asp Leu Ile Glu		
	50	55	60
Arg Lys Leu Leu Lys Val Met Glu Ser Phe Ser Lys Ser Gln Glu Ala			
	65	70	75
Phe Asp Leu Gln Glu Ile Leu Leu Arg Leu Thr Phe Asp Asn Ile Cys			
	85	90	95
Ile Ala Gly Leu Gly Asp Asp Pro Gly Thr Leu Asp Asp Asp Leu Pro			
	100	105	110
His Val Pro Phe Ala Lys Ala Phe Glu Glu Ala Thr Glu Ser Thr Leu			
	115	120	125
Phe Arg Phe Met Ile Pro Pro Phe Val Trp Lys Pro Met Lys Phe Phe			
	130	135	140
Asp Ile Gly Tyr Glu Lys Gly Leu Arg Glu Ala Val Glu Thr Val His			
	145	150	155
Asn Phe Ile Asp Lys Met Val Val Glu Arg Ile Ala Met Leu Lys Asp			
	165	170	175
Gln Gly Thr Leu Ala Asn Ser Lys Ser Asp Val Leu Ser Arg Leu Ile			
	180	185	190
Gln Ile Glu Ser His Lys Arg Gly Asp Glu Asn Asp Arg Phe Thr Ala			
	195	200	205
Lys Phe Phe Arg Gln Phe Cys Ser Ser Phe Ile Leu Ala Gly Arg Asp			
	210	215	220
Thr Ser Ser Val Ala Leu Thr Trp Phe Phe Trp Leu Ile Thr Lys His			
	225	230	235
Pro Glu Val Glu Thr Lys Ile Leu His Glu Ile Arg Glu Ile Leu Ser			
	245	250	255
Gln Arg Glu Lys Asn Asn Tyr Lys Leu Asp Glu Thr Gly Glu Thr Glu			
	260	265	270
Ser Ser Arg His Phe Thr Val Lys Glu Leu Asn Asp Met Val Tyr Leu			
	275	280	285
Gln Ala Ala Leu Ser Glu Ser Leu Arg Leu Tyr Pro Pro Ile Pro Met			
	290	295	300
Glu Met Lys Gln Ala Thr Glu Glu Asp Val Phe Pro Asp Gly Thr Phe			
	305	310	315
Leu Arg Lys Gly Ser Arg Val Tyr Phe Ser Val Tyr Ala Met Gly Arg			
	325	330	335
Met Glu Ser Ile Trp Gly Lys Asp Cys Glu Met Phe Lys Pro Glu Arg			
	340	345	350
Trp Ile Gln Gly Gly Gln Tyr Val Ser Asp Asp Gln Phe Lys Tyr Val			
	355	360	365
Val Phe Asn Ala Gly Pro Arg Leu Cys Leu Gly Lys Thr Phe Ala Tyr			
	370	375	380
Leu Gln Met Lys Met Val Ala Ala Ser Ile Leu Leu Asn Tyr Ser Ile			
	385	390	395
Lys Val Asp Gln Asp His Val Val Val Pro Arg Val Thr Thr Thr Leu			
	405	410	415
Tyr Met Lys His Gly Leu Lys Val Arg Ile Thr Pro Arg Ser Leu Glu			
	420	425	430
Glu Lys Lys Gln Asp Ser			
	435		

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1370 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1370

(D) OTHER INFORMATION: / Ceres Seq. ID 1566823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

aaaaagggaaa	aaagaaaaag	aagaagagga	gctaaaaaaa	cgacgtcgta	gaaggagatt	60
cttgccatgg	ccacacatag	tctctccttc	tctctcagag	tctcttctct	ctcttctctt	120
actctctcag	agagaattaa	agggcaagg	gtgggaatca	actacggcca	aatagccaac	180
aaactcccat	ctccgggaag	agtcgcccgt	ctccttcgat	cactaaacat	cacaagagta	240
aaactctcag	acgcagatcc	aaacgtcctc	tctctctctc	caaaactcaa	agtagatttc	300
atgatcgggt	taggcaacga	tatctctcaa	aacatgtcaa	cagatccaac	caaagctcaa	360
gattgggttac	aaacaaagat	tgaaccacat	atctcaaaaa	caagaaatac	ctcaatagtt	420
gtcgccaacg	aaatcttcaa	aaccaatgat	catgtcctca	tccaaagcct	attacggcct	480
atgaaatcgg	tttacgtctc	tttaaccaat	cttggtttag	agaacaagt	aaccgtaact	540
tcagctcatt	cttttagacat	tcttttcaaa	tcttatcctc	cttcttcagg	atcattcaaa	600
gaagaggttta	ttcaatatct	tcaaccactt	cttgattttc	attctcaaat	cgaatcacct	660
ttcttgataa	atgttatatc	cttttttgct	tataaagata	gtcctaaga	agttccattat	720
gagtatgttt	tgtttcaacc	taatacaagg	atggttgatc	caaacactaa	tcttcattat	780
gacaacatgt	tgtttgctca	agttgatgcg	ctttactctg	ccattaaagc	tttgggacat	840
accgatatcg	agggttcggat	atcggaacac	gggtggcctt	ctaaaggaga	tgagaatgag	900
attggaGctt	cgccgggagaa	cgccgctttg	tataatggga	attgttgtaa	gttgatgacg	960
cagaggaaga	gaactccggc	gaagcaatct	gttctattg	atgtttatgt	gtttgctctg	1020
tttaatgaga	atctttaaacc	gggtccgggt	tctgagagga	attatggact	tttttatccg	1080
gaggtgtaaac	cggtttacaa	tgctgggtatg	caaggttatt	tacctgatat	tatctatact	1140
tcaagggcaca	ctacaattaa	gattttgaat	ttgtggagag	tcgtgatggg	ttgtgctgtg	1200
gcttggtgtca	tactcagat	ggcgacaaag	atgaggatga	gataaGcttc	gctgtgtgct	1260
ttgtctgtcc	ttgtaggatt	ttgtttttta	tatgttagtt	gattataggt	gagggtataca	1320
attctttgtc	atgtattgga	ttcacaaaaa	taaaaaaaat	taatttatct		

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..392

(D) OTHER INFORMATION: / Ceres Seq. ID 1566824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

Met	Ala	Thr	His	Ser	Leu	Ser	Phe	Phe	Phe	Arg	Val	Leu	Leu	Leu	Leu
1				5					10				15		
Phe	Leu	Thr	Leu	Ser	Glu	Arg	Ile	Lys	Gly	Gln	Gly	Val	Gly	Ile	Asn
				20				25					30		
Tyr	Gly	Gln	Ile	Ala	Asn	Asn	Leu	Pro	Ser	Pro	Ala	Arg	Val	Ala	Val
				35				40				45			
Leu	Leu	Arg	Ser	Leu	Asn	Ile	Thr	Arg	Val	Lys	Leu	Thr	Asp	Ala	Asp
				50				55			60				
Pro	Asn	Val	Leu	Phe	Ser	Phe	Ser	Asn	Ser	Gln	Val	Asp	Phe	Met	Ile
				70				75					80		
Gly	Leu	Gly	Asn	Glu	Tyr	Leu	Gln	Asn	Met	Ser	Thr	Asp	Pro	Thr	Lys
				85				90				95			
Ala	Gln	Asp	Trp	Leu	Gln	Gln	Arg	Leu	Glu	Pro	His	Ile	Ser	Lys	Thr
				100				105				110			
Arg	Ile	Thr	Ser	Ile	Val	Val	Gly	Asn	Glu	Ile	Phe	Lys	Thr	Asn	Asp
				115				120				125			
His	Val	Leu	Ile	Gln	Ser	Leu	Leu	Pro	Ala	Met	Lys	Ser	Val	Tyr	Ala
				130				135			140				
Ala	Leu	Thr	Asn	Leu	Gly	Leu	Glu	Lys	Gln	Val	Thr	Val	Thr	Ser	Ala
				145				150			155				160

His Ser Leu Asp Ile Leu Ser Thr Ser Tyr Pro Pro Ser Ser Gly Ser
165 170 175
Phe Lys Glu Glu Phe Ile Gln Tyr Leu Gln Pro Leu Leu Asp Phe His
180 185 190
Ser Gln Ile Glu Ser Pro Phe Leu Ile Asn Ala Tyr Pro Phe Ala
195 200 205
Tyr Lys Asp Ser Pro Lys Glu Val Pro Leu Glu Tyr Val Leu Phe Gln
210 215 220
Pro Asn Gln Gly Met Val Asp Pro Asn Thr Asn Leu His Tyr Asp Asn
225 230 235
Met Leu Phe Ala Gln Val Asp Ala Leu Tyr Ser Ala Ile Lys Thr Leu
245 250 255
Gly His Thr Asp Ile Glu Val Arg Ile Ser Glu Thr Gly Trp Pro Ser
260 265 270
Lys Gly Asp Glu Asn Glu Ile Gly Ala Ser Pro Glu Asn Ala Ala Leu
275 280 285
Tyr Asn Gly Asn Leu Leu Lys Leu Ile Gln Gln Arg Lys Gly Thr Pro
290 295 300
Ala Lys Gln Ser Val Pro Ile Asp Val Tyr Val Phe Ala Leu Phe Asn
305 310 315
Glu Asn Leu Lys Pro Gly Pro Val Ser Glu Arg Asn Tyr Gly Leu Phe
325 330 335
Tyr Pro Asp Gly Lys Pro Val Tyr Asn Val Gly Met Gln Gly Tyr Leu
340 345 350
Pro Asp Ile Tyr Thr Ser Arg Ala Thr Thr Ile Lys Ile Leu Asn
355 360 365
Leu Trp Arg Val Val Met Gly Leu Ala Val Ala Trp Phe Ile Leu Asp
370 375 380
Met Gly Asp Lys Met Arg Met Arg
385 390

(2) INFORMATION FOR SEQ ID NO:408:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..314

(D) OTHER INFORMATION: / Ceres Seq. ID 1566825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

Met Ile Gly Leu Gly Asn Glu Tyr Leu Gln Asn Met Ser Thr Asp Pro
1 5 10 15
Thr Lys Ala Gln Asp Trp Leu Gln Gln Arg Leu Glu Pro His Ile Ser
20 25 30
Lys Thr Arg Ile Thr Ser Ile Val Val Gly Asn Glu Ile Phe Lys Thr
35 40 45
Asn Asp His Val Leu Ile Gln Ser Leu Leu Pro Ala Met Lys Ser Val
50 55 60
Tyr Ala Ala Leu Thr Asn Leu Gly Leu Glu Lys Gln Val Thr Val Thr
65 70 75 80
Ser Ala His Ser Leu Asp Ile Leu Ser Thr Ser Tyr Pro Pro Ser Ser
85 90 95
Gly Ser Phe Lys Glu Glu Phe Ile Gln Tyr Leu Gln Pro Leu Leu Asp
100 105 110
Phe His Ser Gln Ile Glu Ser Pro Phe Leu Ile Asn Ala Tyr Pro Phe
115 120 125
Phe Ala Tyr Lys Asp Ser Pro Lys Glu Val Pro Leu Glu Tyr Val Leu
130 135 140
Phe Gln Pro Asn Gln Gly Met Val Asp Pro Asn Thr Asn Leu His Tyr

145 150 155 160
Asp Asn Met Leu Phe Ala Gln Val Asp Ala Leu Tyr Ser Ala Ile Lys
165 170 175
Thr Leu Gly His Thr Asp Ile Glu Val Arg Ile Ser Glu Thr Gly Trp
180 185 190
Pro Ser Lys Gly Asp Glu Asn Glu Ile Gly Ala Ser Pro Glu Asn Ala
195 200 205
Ala Leu Tyr Asn Gly Asn Leu Lys Leu Ile Gln Gln Arg Lys Gly
210 215 220
Thr Pro Ala Lys Gln Ser Val Pro Ile Asp Val Tyr Val Phe Ala Leu
225 230 235 240
Phe Asn Glu Asn Leu Lys Pro Gly Pro Val Ser Glu Arg Asn Tyr Gly
245 250 255
Leu Phe Tyr Pro Asp Gly Lys Pro Val Tyr Asn Val Gly Met Gln Gly
260 265 270
Tyr Leu Pro Asp Ile Ile Tyr Thr Ser Arg Ala Thr Thr Ile Lys Ile
275 280 285
Leu Asn Leu Trp Arg Val Val Met Gly Leu Ala Val Ala Trp Phe Ile
290 295 300
Leu Asp Met Gly Asp Lys Met Arg Met Arg
305 310

(2) INFORMATION FOR SEQ ID NO:409:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..303
(D) OTHER INFORMATION: / Ceres Seq. ID 1566826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

Met Ser Thr Asp Pro Thr Lys Ala Gln Asp Trp Leu Gln Gln Arg Leu
1 5 10 15
Glu Pro His Ile Ser Lys Thr Arg Ile Thr Ser Ile Val Val Gly Asn
20 25 30
Glu Ile Phe Lys Thr Asn Asp His Val Leu Ile Gln Ser Leu Leu Pro
35 40 45
Ala Met Lys Ser Val Tyr Ala Ala Leu Thr Asn Leu Gly Leu Glu Lys
50 55 60
Gln Val Thr Val Thr Ser Ala His Ser Leu Asp Ile Leu Ser Thr Ser
65 70 75 80
Tyr Pro Pro Ser Ser Gly Ser Phe Lys Glu Glu Phe Ile Gln Tyr Leu
85 90 95
Gln Pro Leu Leu Asp Phe His Ser Gln Ile Glu Ser Pro Phe Leu Ile
100 105 110
Asn Ala Tyr Pro Phe Phe Ala Tyr Lys Asp Ser Pro Lys Glu Val Pro
115 120 125
Leu Glu Tyr Val Leu Phe Gln Pro Asn Gln Gly Met Val Asp Pro Asn
130 135 140
Thr Asn Leu His Tyr Asp Asn Met Leu Phe Ala Gln Val Asp Ala Leu
145 150 155 160
Tyr Ser Ala Ile Lys Thr Leu Gly His Thr Asp Ile Glu Val Arg Ile
165 170 175
Ser Glu Thr Gly Trp Pro Ser Lys Gly Asp Glu Asn Glu Ile Gly Ala
180 185 190
Ser Pro Glu Asn Ala Ala Leu Tyr Asn Gly Asn Leu Leu Lys Leu Ile
195 200 205
Gln Gln Arg Lys Gly Thr Pro Ala Lys Gln Ser Val Pro Ile Asp Val
210 215 220

Tyr	Val	Phe	Ala	Leu	Phe	Asn	Glu	Asn	Leu	Lys	Pro	Gly	Pro	Val	Ser
225				230					235					240	
Glu	Arg	Asn	Tyr	Gly	Leu	Phe	Tyr	Pro	Asp	Gly	Lys	Pro	Val	Tyr	Asn
				245					250					255	
Val	Gly	Met	Gln	Gly	Tyr	Leu	Pro	Asp	Ile	Ile	Tyr	Thr	Ser	Arg	Ala
			260					265					270		
Thr	Thr	Ile	Lys	Ile	Leu	Asn	Leu	Trp	Arg	Val	Val	Met	Gly	Leu	Ala
		275					280					285			
Val	Ala	Trp	Phe	Ile	Leu	Asp	Met	Gly	Asp	Lys	Met	Arg	Met	Arg	
	290					295				300					

(2) INFORMATION FOR SEO ID NO:410:

(i) SEQUENCE CHARACTERIST

- (A) LENGTH: 1530 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1530
(D) OTHER INFORMATION: / Ceres Seq. ID 1566827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

gtatattttt	ttgacagcgc	gattacagaaa	tttggaaaag	atcagcttttt	ttttcttcgg	60
ttcttaacctt	ttaaaggctgc	tgaaaattttg	ggaaatcactg	atacaattttg	tttaatatgat	120
ttctctgattt	aggggtttctc	tgcatgcctc	tgagaatcagc	aagtgtaaag	caattaccat	180
gggtgactcgc	aagcagatgc	atttctctctc	ctgtgggtgtg	gtgataactc	cgacgatacc	240
ctctccaccat	gagaaattccc	acggaaattct	tctccaaaagc	gtgctgcgtc	ttctctgcga	300
gcgcagaagcg	gcgaaagagac	tatgaagaag	aaaaaagaag	agaaagaaga	gaattttgggt	360
cccgactgtga	tcgtccggatg	ctggaacgag	gaagatgagc	tctctatctt	aaaggagta	420
gttgattacaa	gagctaaagc	aggattccaat	cccaaaattg	attgggtagt	gtttctacag	480
ttctccggtaa	gttctatcgt	tcgcaaaatt	ctccaggagc	aggtttttgag	taagatcaga	540
aagttgtaaaa	ggagattttca	tgttctattg	gagaaaaatc	gtgaagggaa	tgatccgaaa	600
tttactagatt	ctagtgatttc	tgaagccttg	gtgtttttct	cgatgatttg	gggaacaggt	660
gaattttgta	atgatgatgg	tactgataag	gagatgggtga	aggagcacga	tgtaaaacgga	720
aattggcgacg	ctgaaaatgg	gattgcctga	atagcacagg	aagacgaagc	tgggggagag	780
tgtttaaagg	agcatgagga	aagcttaaat	gagaattggg	cagaggagat	aagagacaac	840
gacgacagat	ctcgaaaagc	acacgacgtc	gagagcgaga	gcgagagaga	gattgtgtaag	900
gagcatgagg	aaccttttaa	tgagaattggt	gcagagaata	taagagacaa	taaccgggac	960
actcaaatagt	cacagcagag	cgagagcagc	agtgaggaga	tgttgtaaga	gcgatgaggaa	1020
gttgGctaat	actgaacttg	taatatgagaa	tggggcagc	aaaaaacacg	agacacggac	1080
tactgtgtga	aaagagagac	atgatgagca	tgatgatgat	gagttatgcg	ctgtgcagga	1140
tgcttttgtag	gcgttaattg	cgcaagtggt	aagtggtttt	caaaagaagc	tcgactgagta	1200
gaagctgatg	aacctttgaa	tcgaaaaaag	aaagagtggt	atgtgatgat	ggaaacgctga	1260
atgtgttgtag	gaagaagaagt	tgaaattcca	gaagctttga	ttttccgcga	aggaatcggtt	1320
ggcagcgaat	gatagttaga	tgaataccat	aagccgcttg	agcattttgt	gttaaatagg	1380
ttcttagttaa	gcctaatagc	ttgctctgtt	cagtgtaatat	ctttgtagtg	tctcttttgt	1440
ctgtttgggc	aagttgtttg	aagacattcc	agtttttaac	gaagtatcca	gaagagccat	1500
ccatgaccat	ttctgaaatc	ataaataattc				

(2) INFORMATION FOR SEQ ID NO:411:

(1) SEQUENCE CHARACTERIST

- (A) LENGTH: 235 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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- (A) NAME/KEY: peptide
(B) LOCATION: 1..235
(D) OTHER INFORMATION: / Ceres Seq. ID 1566828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Asn Leu Gly Pro Pro Leu

1 5 10 15
Ile Val Arg Ile Trp Asn Glu Glu Asp Glu Leu Ser Ile Leu Lys Gly
20 25 30
Leu Val Asp Tyr Arg Ala Lys Thr Gly Phe Asn Pro Lys Ile Asp Trp
35 40 45
Asp Ala Phe Tyr Ser Phe Leu Gly Ser Ser Ile Val Ala Lys Phe Ser
50 55 60
Lys Glu Gln Val Leu Ser Lys Ile Arg Lys Leu Lys Arg Arg Phe His
65 70 75 80
Val His Trp Glu Lys Ile Ser Glu Gly Asn Asp Pro Lys Phe Thr Arg
85 90 95
Ser Ser Asp Ser Glu Ala Phe Gly Phe Ser Ser Met Ile Trp Gly Gln
100 105 110
Gly Glu Phe Gly Asn Asp Asp Gly Met Asp Lys Glu Met Val Lys Glu
115 120 125
His Asp Val Asn Gly Asn Gly Ala Ala Glu Asn Gly Thr Ala Arg Ile
130 135 140
Ala Gln Glu Asn Glu Ser Gly Glu Glu Met Leu Lys Glu His Glu Glu
145 150 155 160
Thr Leu Asn Glu Asn Gly Ala Glu Glu Ile Arg Asp Asn Asp Glu Thr
165 170 175
Ala Arg Lys Ala Gln Gln Leu Glu Ser Glu Ser Glu Glu Glu Met Leu
180 185 190
Lys Glu His Glu Glu Pro Phe Asn Glu Asn Gly Ala Glu Asn Ile Arg
195 200 205
Asp Asn Asn Gly Thr Thr Gln Ile Ala Gln Gln Ser Glu Ser Glu Ser
210 215 220
Glu Glu Met Leu Lys Glu His Glu Glu Val Gly
225 230 235

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1566829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

Met Ile Trp Gly Gln Gly Glu Phe Gly Asn Asp Asp Gly Met Asp Lys
1 5 10 15
Glu Met Val Lys Glu His Asp Val Asn Gly Asn Gly Ala Ala Glu Asn
20 25 30
Gly Thr Ala Arg Ile Ala Gln Glu Asn Glu Ser Gly Glu Glu Met Leu
35 40 45
Lys Glu His Glu Glu Thr Leu Asn Glu Asn Gly Ala Glu Glu Ile Arg
50 55 60
Asp Asn Asp Glu Thr Ala Arg Lys Ala Gln Gln Leu Glu Ser Glu Ser
65 70 75 80
Glu Glu Glu Met Leu Lys Glu His Glu Glu Pro Phe Asn Glu Asn Gly
85 90 95
Ala Glu Asn Ile Arg Asp Asn Asn Gly Thr Thr Gln Ile Ala Gln Gln
100 105 110
Ser Glu Ser Glu Ser Glu Glu Met Leu Lys Glu His Glu Glu Val Gly
115 120 125

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1824 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1824
(D) OTHER INFORMATION: / Ceres Seq. ID 1566838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

attctctttt	ctctctcttc	tctctcacac	aacacaaaca	actcttgaga	gagagaaaca	60
aattcttcc	ttgacacttc	tctccaaatc	ctcatctcat	tctctatctc	aaacatttgc	120
tcactctcac	gatgagccat	aaccacaaac	aacctcacgc	gccagtcocg	gtccatgtca	180
caaacgcgga	gccaaactct	aaccacaaac	acctcccaaa	ctttctatta	tcgctgtctc	240
tcaaatcagt	aaaactcggg	taccactaac	tgatctccaa	cgctctctac	atcctctctc	300
ttctctctct	cgcgcgcaac	atcgctaaac	tctctctctt	caccatcaac	gacctctctc	360
tcctctacaa	cacactcgtg	ttccatttcc	tctccgccac	actcgccacc	gacctcttgc	420
tctctctctc	caccgcttac	ttaccacccc	gtcctgcgcg	tgtcttctct	ctcgactttc	480
cgtgttacaa	accagaccct	tcactgatct	gcactcgtga	aacattccatg	gacagatctc	540
aacgtgttag	catcttcaca	gaAgacaaat	TagtcttccA	acaaaagatc	ctcgaaaAga	600
tcgggtctag	gtcagaaaaa	ttacttccct	gaagctcttc	ttcgtgttcc	tcctaatctc	660
tgtatggtag	aagcgagaaa	agaggcgaaa	acagtattgt	tcggagctat	tgacgcgggt	720
cttgagagaa	cctcgtgtga	acataaagat	attggaatcc	ttgtggtgaa	ttgtagcttg	780
tttaatccaa	caccgtcaat	ttctgctatg	attgtgaata	agtataaagt	tagaggcaac	840
attttgagct	ataattcttg	tgggaatgga	tgtagtgtgc	gccttatctc	catgtatctc	900
gctaaaacaga	tgtcttcagg	gcaaccacaa	tcatacgcac	tgtgtgtgag	cacagagaac	960
ataaccctaa	actggtactt	aggcaacgac	cgatacaatgc	ttctatctaa	ttgtatcttc	1020
cgatgtggcg	gagcgcgggt	acttctctcg	aaccgctcct	ctgatcgcag	ccgttcaaaa	1080
tatcagctca	tccataccgt	ccgtaccccc	aaaggagctg	atgacaacgc	attcggtctg	1140
gtttaccac	gagaaagaaa	caacgcagaa	gaaccgcgca	agatcggagt	ctcactctct	1200
aaaaacctta	tggcaaatgc	cgagagaagt	ctcaagacaa	acatcacaa	ctctcgacca	1260
ctagtctctac	caatgtccga	acaacttctc	tttttcgcga	ctcttgtggc	ccgaaaagtc	1320
ttcaaatgta	agaaaaataa	gccttacatt	ccctgacttca	agctagcttt	cgagcatttc	1380
tgtatccacg	ctggaggtag	agccgtgctt	gacgagattg	agaagaacct	gatttatctc	1440
gaatggcaca	tggagccatc	gaggatgacg	ttgaaccggg	ttgtaaacac	ttcgagttag	1500
tcacttttgt	atgagcttgc	gtatagttaa	gctaaaggaa	ggattaagag	aggagatagg	1560
acttggcgaga	tgtcttttgg	atcgggtttt	aagtgttaaca	gtcgggtttg	gaaagctttg	1620
agaacgattg	atccaatgga	cgagaagact	aatccatgga	ttgatgagat	tgatgacttt	1680
cctgttccaag	tctctaggat	cactccattc	acatcgtcgt	agtgttttta	aattcttttg	1740
gagaactaat	ttgttatggt	ttattaaatg	taataactta	tgtgatgtga	tattttttta	1800
ttatcttaat	atatatgatt	gccg				

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..352
(D) OTHER INFORMATION: / Ceres Seq. ID 1566839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

Met	Glu	Glu	Ala	Arg	Lys	Glu	Ala	Glu	Thr	Val	Met	Phe	Gly	Ala	Ile
1			5						10				15		
Asp	Ala	Val	Leu	Glu	Lys	Thr	Gly	Val	Lys	Pro	Lys	Asp	Ile	Gly	Ile
			20						25				30		
Leu	Val	Val	Asn	Cys	Ser	Leu	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala
			35					40				45			
Met	Ile	Val	Asn	Lys	Tyr	Lys	Leu	Arg	Gly	Asn	Ile	Leu	Ser	Tyr	Asn
			50				55				60				

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Leu Gly Gly Met Gly Cys Ser Ala Gly Leu Ile Ser Ile Asp Leu Ala
65 70 75 80
Lys Gln Met Leu Gln Val Gln Pro Asn Ser Tyr Ala Leu Val Val Ser
85 90 95
Thr Glu Asn Ile Thr Leu Asn Trp Tyr Leu Gly Asn Asp Arg Ser Met
100 105 110
Leu Leu Ser Asn Cys Ile Phe Arg Met Gly Gly Ala Ala Val Leu Leu
115 120 125
Ser Asn Arg Ser Ser Asp Arg Ser Arg Ser Lys Tyr Gln Leu Ile His
130 135 140
Thr Val Arg Thr His Lys Gly Ala Asp Asp Asn Ala Phe Gly Cys Val
145 150 155 160
Tyr Gln Arg Glu Asp Asn Asn Ala Glu Glu Thr Gly Lys Ile Gly Val
165 170 175
Ser Leu Ser Lys Asn Leu Met Ala Ile Ala Gly Glu Ala Leu Lys Thr
180 185 190
Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Met Ser Glu Gln Leu
195 200 205
Leu Phe Phe Ala Thr Leu Val Ala Arg Lys Val Phe Lys Val Lys Lys
210 215 220
Ile Lys Pro Tyr Ile Pro Asp Phe Lys Leu Ala Phe Glu His Phe Cys
225 230 235 240
Ile His Ala Gly Gly Arg Ala Val Leu Asp Glu Ile Glu Lys Asn Leu
245 250 255
Asp Leu Ser Glu Trp His Met Glu Pro Ser Arg Met Thr Leu Asn Arg
260 265 270
Phe Gly Asn Thr Ser Ser Ser Ser Leu Trp Tyr Glu Leu Ala Tyr Ser
275 280 285
Glu Ala Lys Gly Arg Ile Lys Arg Gly Asp Arg Thr Trp Gln Ile Ala
290 295 300
Phe Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp Lys Ala Leu Arg
305 310 315 320
Thr Ile Asp Pro Met Asp Glu Lys Thr Asn Pro Trp Ile Asp Glu Ile
325 330 335
Asp Asp Phe Pro Val Gln Val Pro Arg Ile Thr Pro Ile Thr Ser Ser
340 345 350

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..341
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

Met Phe Gly Ala Ile Asp Ala Val Leu Glu Lys Thr Gly Val Lys Pro
1 5 10 15
Lys Asp Ile Gly Ile Leu Val Val Asn Cys Ser Leu Phe Asn Pro Thr
20 25 30
Pro Ser Leu Ser Ala Met Ile Val Asn Lys Tyr Lys Leu Arg Gly Asn
35 40 45
Ile Leu Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Leu Ile
50 55 60
Ser Ile Asp Leu Ala Lys Gln Met Leu Gln Val Gln Pro Asn Ser Tyr
65 70 75 80
Ala Leu Val Val Ser Thr Glu Asn Ile Thr Leu Asn Trp Tyr Leu Gly

2008年12月10日

(i) SEQUENCE CHARACTERISTICS:

- | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Val | Asn | 5 | Tyr | Lys | Leu | Arg | Gly | 10 | Asn | Ile | Leu | Ser | Tyr | Asn |
| 1 | Leu | Gly | Gly | Met | Gly | Cys | Ser | Ala | Gly | Leu | Ile | Ser | Ile | Asp | Leu | Ala |
| | | | | 20 | | | | | 25 | | | | | 30 | | |
| Lys | Gln | Met | Leu | Gln | Val | Gln | Pro | Asn | Ser | Tyr | Ala | Leu | Val | Val | Ser | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Thr | Glu | Asn | Ile | Thr | Leu | Asn | Trp | Tyr | Leu | Gly | Asn | Asp | Arg | Ser | Met | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Leu | Leu | Ser | Asn | Cys | Ile | Phe | Arg | Met | Gly | Gly | Ala | Ala | Val | Leu | Leu | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Ser | Asn | Arg | Ser | Ser | Asp | Arg | Ser | Arg | Ser | Lys | Tyr | Gln | Leu | Ile | His | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Thr | Val | Arg | Thr | His | Lys | Gly | Ala | Asp | Asp | Asn | Ala | Phe | Gly | Cys | Val | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Tyr | Gln | Arg | Glu | Asp | Asn | Asn | Ala | Glu | Glu | Thr | Gly | Lys | Ile | Gly | Val | |
| | | | 115 | | | | 120 | | | | | 125 | | | | |

Ser Leu Ser Lys Asn Leu Met Ala Ile Ala Gly Glu Ala Leu Lys Thr
130 135 140
Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Met Ser Glu Gln Leu
145 150 155 160
Leu Phe Phe Ala Thr Leu Val Ala Arg Lys Val Phe Lys Val Lys Lys
165 170 175
Ile Lys Pro Tyr Ile Pro Asp Phe Lys Leu Ala Phe Glu His Phe Cys
180 185 190
Ile His Ala Gly Gly Arg Ala Val Leu Asp Glu Ile Glu Lys Asn Leu
195 200 205
Asp Leu Ser Glu Trp His Met Glu Pro Ser Arg Met Thr Leu Asn Arg
210 215 220
Phe Gly Asn Thr Ser Ser Ser Ser Leu Trp Tyr Glu Leu Ala Tyr Ser
225 230 235 240
Glu Ala Lys Gly Arg Ile Lys Arg Gly Asp Arg Thr Trp Gln Ile Ala
245 250 255
Phe Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp Lys Ala Leu Arg
260 265 270
Thr Ile Asp Pro Met Asp Glu Lys Thr Asn Pro Trp Ile Asp Glu Ile
275 280 285
Asp Asp Phe Pro Val Gln Val Pro Arg Ile Thr Pro Ile Thr Ser Ser
290 295 300

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..998
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

aatattcattt	ccattttogat	tcgattcctc	ctttgtgtgg	gagggcctttg	ttcggtcaac	60
ttatgtgttc	tggtttttgtc	tccttttttat	tgattaggga	ccgatctatc	aaggcttcaa	120
gggcaaacag	aaatgggacca	cgacaagaca	ggatgcctga	gcccacctga	aggtcccaag	180
ctatgtacta	acaactgcgg	tttctttgga	agcgctgcc	caatgaacat	gtgttctaag	240
tgtcacaagg	atatgttgtt	ccaacaggag	cagggcgcta	agtttgcata	tcgagtgtct	300
ggaacatcgt	catccagcaa	catcataaag	gaaaccttta	ccgctgcgtt	ggtcgatatt	360
gaaaccaaatt	ccgttgagcc	gatgactgtt	tcgtacagc	catcctctgt	ccaagtctgt	420
cgagagtgat	tagcaccaga	agaagctcgc	aaaccaaagg	gaccaagccg	atgtactact	480
tgcaataaagc	gggttgccct	gactggattc	aaatgtcgtc	gtgggagcct	ctctgtcgga	540
acacacccgct	atgcagacat	acatgactgc	tccttcaatt	accatgctgc	tgccgaagag	600
gcgatagcta	agggcaaacct	ggttgtgaaa	gcagagaagc	ttgacaaaaa	ctgaaaaact	660
aagtaaacact	ctctgtgttc	atcaggtggc	ctggtgtttc	cttctcctgt	ctgtgtctgg	720
ttcaagtatt	ctcatgttaa	aaagggttta	tataaagctg	aatgaaagcg	tgcttgcatt	780
ttagcgtctt	ccatctctct	gcaatatttg	tggtgtggaa	ctttctatta	cttgtgtttg	840
caagcagaga	aactgtctct	taaaaaaaat	gctttgtgtg	tttatctctc	tactattttt	900
gagcactgtg	ttatgtgttc	ctgtttggtc	tgatcatat	tgagattgtc	tctgtagcta	960
catgaagcct	atttaaaaaa	ggcctgtgtt	tgctccttc			

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1566910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

Met	Asp	His	Asp	Lys	Thr	Gly	Cys	Gln	Ser	Pro	Pro	Glu	Gly	Pro	Lys	1
				5						10					15	
Leu	Cys	Thr	Asn	Asn	Cys	Gly	Phe	Phe	Gly	Ser	Ala	Ala	Thr	Met	Asn	
			20					25						30		
Met	Cys	Ser	Lys	Cys	His	Lys	Asp	Met	Leu	Phe	Gln	Gln	Glu	Gln	Gly	
			35				40					45				
Ala	Lys	Phe	Ala	Ser	Ala	Val	Ser	Gly	Thr	Ser	Ser	Ser	Ser	Asn	Ile	
	50					55					60					
Ile	Lys	Glu	Thr	Phe	Thr	Ala	Ala	Leu	Val	Asp	Ile	Glu	Thr	Lys	Ser	
65					70				75					80		
Val	Glu	Pro	Met	Thr	Val	Ser	Val	Gln	Pro	Ser	Ser	Val	Gln	Val	Val	
				85					90					95		
Ala	Glu	Val	Val	Ala	Pro	Glu	Glu	Ala	Ala	Lys	Pro	Lys	Gly	Pro	Ser	
			100					105						110		
Arg	Cys	Thr	Thr	Cys	Asn	Lys	Arg	Val	Gly	Leu	Thr	Gly	Phe	Lys	Cys	
			115				120						125			
Arg	Cys	Gly	Ser	Leu	Phe	Cys	Gly	Thr	His	Arg	Tyr	Ala	Asp	Ile	His	
			130			135					140					
Asp	Cys	Ser	Phe	Asn	Tyr	His	Ala	Ala	Ala	Gln	Glu	Ala	Ile	Ala	Lys	
145				150						155					160	
Ala	Asn	Pro	Val	Val	Lys	Ala	Glu	Lys	Leu	Asp	Lys	Ile				
				165					170							

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1566911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

Met	Asn	Met	Cys	Ser	Lys	Cys	His	Lys	Asp	Met	Leu	Phe	Gln	Gln	Glu	1
				5						10					15	
Gln	Gly	Ala	Lys	Phe	Ala	Ser	Ala	Val	Ser	Gly	Thr	Ser	Ser	Ser	Ser	
			20					25					30			
Asn	Ile	Ile	Lys	Glu	Thr	Phe	Thr	Ala	Ala	Leu	Val	Asp	Ile	Glu	Thr	
			35				40					45				
Lys	Ser	Val	Glu	Pro	Met	Thr	Val	Ser	Val	Gln	Pro	Ser	Ser	Val	Gln	
			50			55					60					
Val	Val	Ala	Glu	Val	Val	Ala	Pro	Glu	Glu	Ala	Ala	Lys	Pro	Lys	Gly	
65				70					75					80		
Pro	Ser	Arg	Cys	Thr	Thr	Cys	Asn	Lys	Arg	Val	Gly	Leu	Thr	Gly	Phe	
			85						90					95		
Lys	Cys	Arg	Cys	Gly	Ser	Leu	Phe	Cys	Gly	Thr	His	Arg	Tyr	Ala	Asp	
			100					105					110			
Ile	His	Asp	Cys	Ser	Phe	Asn	Tyr	His	Ala	Ala	Ala	Gln	Glu	Ala	Ile	
			115				120					125				
Ala	Lys	Ala	Asn	Pro	Val	Val	Lys	Ala	Glu	Lys	Leu	Asp	Lys	Ile		
			130				135					140				

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..141
(D) OTHER INFORMATION: / Ceres Seq. ID 1566912
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:
Met Cys Ser Lys Cys His Lys Asp Met Leu Phe Gln Gln Glu Gln Gly
1 5 10 15
Ala Lys Phe Ala Ser Ala Val Ser Gly Thr Ser Ser Ser Ser Asn Ile
20 25 30
Ile Lys Glu Thr Phe Thr Ala Ala Leu Val Asp Ile Glu Thr Lys Ser
35 40 45
Val Glu Pro Met Thr Val Ser Val Gln Pro Ser Ser Val Gln Val Val
50 55 60
Ala Glu Val Val Ala Pro Glu Glu Ala Ala Lys Pro Lys Gly Pro Ser
65 70 75 80
Arg Cys Thr Thr Cys Asn Lys Arg Val Gly Leu Thr Gly Phe Lys Cys
85 90 95
Arg Cys Gly Ser Leu Phe Cys Gly Thr His Arg Tyr Ala Asp Ile His
100 105 110
Asp Cys Ser Phe Asn Tyr His Ala Ala Gln Glu Ala Ile Ala Lys
115 120 125
Ala Asn Pro Val Val Lys Ala Glu Lys Leu Asp Lys Ile
130 135 140

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..574
(D) OTHER INFORMATION: / Ceres Seq. ID 1566913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

aaacgcagaaa ttaRaaacccc cttttgcctc aaaaAccctg atttcaaatc tccccaaagca 60
caacaatggc gaatacaatg agatgcaga gggatgaagc attgagagca ataagaagag 120
aaatagtga gaaggaatca ttactcttaa cgagagaaga cgccaaatcc gccgctattg 180
aagccgcact cgctgctccg aagttaccag ttogtcaagc cccagtttct ccgtttatgg 240
aagttgcgac gccttctctc gagtctgcat ctgcctccac tacaatgcc aaaaatagtg 300
atgagaaat ggaatgatgag aagaaaaaca agtcgctaaa acctattgg aagaagtga 360
agaagaagtt taagctgggg atgaagaatc gtgctagtaa ggggtgctct cgaggcaaac 420
gaaactaaaa ctggtcttgg cttcttcta ctgggtttgt ttctacttg cataatttat 480
gttctctctt aattttgggg ttcttcaatg tcttagaata tagcatcttt tgtactgtgt 540
tttttccatg agtttcagta ctatagaaac cctg

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..120
(D) OTHER INFORMATION: / Ceres Seq. ID 1566914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

Met Ala Lys Ser Met Arg Cys Lys Arg Val Lys Arg Leu Arg Ala Ile
1 5 10 15

Arg Arg Glu Ile Val Glu Lys Glu Ser Phe Thr Leu Thr Arg Glu Asp
20 25 30
Ala Lys Ser Ala Ala Ile Glu Ala Ala Leu Ala Ala Pro Lys Leu Pro
35 40 45
Val Arg Gln Ala Pro Val Ser Pro Phe Met Glu Val Ala Thr Pro Ser
50 55 60
Ser Glu Ser Ala Ser Ala Ser Thr Thr Ile Ala Lys Asn Ser Asp Glu
65 70 75 80
Glu Met Asp Asp Glu Lys Lys Asn Lys Ser Leu Lys Pro Ile Gly Lys
85 90 95
Lys Leu Lys Lys Lys Phe Lys Leu Gly Met Lys Asn Arg Arg Ser Lys
100 105 110
Gly Val Leu Arg Gly Lys Arg Asn
115 120

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1566915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

Met Arg Cys Lys Arg Val Lys Arg Leu Arg Ala Ile Arg Arg Glu Ile
1 5 10 15
Val Glu Lys Glu Ser Phe Thr Leu Thr Arg Glu Asp Ala Lys Ser Ala
20 25 30
Ala Ile Glu Ala Ala Leu Ala Ala Pro Lys Leu Pro Val Arg Gln Ala
35 40 45
Pro Val Ser Pro Phe Met Glu Val Ala Thr Pro Ser Ser Glu Ser Ala
50 55 60
Ser Ala Ser Thr Thr Ile Ala Lys Asn Ser Asp Glu Glu Met Asp Asp
65 70 75 80
Glu Lys Lys Asn Lys Ser Leu Lys Pro Ile Gly Lys Lys Leu Lys Lys
85 90 95
Lys Phe Lys Leu Gly Met Lys Asn Arg Arg Ser Lys Gly Val Leu Arg
100 105 110
Gly Lys Arg Asn
115

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1566916

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

Met Glu Val Ala Thr Pro Ser Ser Glu Ser Ala Ser Ala Ser Thr Thr
1 5 10 15
Ile Ala Lys Asn Ser Asp Glu Glu Met Asp Asp Glu Lys Lys Asn Lys
20 25 30
Ser Leu Lys Pro Ile Gly Lys Lys Leu Lys Lys Lys Phe Lys Leu Gly
35 40 45
Met Lys Asn Arg Arg Ser Lys Gly Val Leu Arg Gly Lys Arg Asn

50

55

60

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1793

(D) OTHER INFORMATION: / Ceres Seq. ID 1566917

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

aacatctctaa	tcgaaaaaac	aatctatctt	ttgggtccct	aaaaaagctc	cttctcttat	60
cttgttttct	aagtattctt	tttgtatgag	tttcaaagct	tatcattatc	tcactcttct	120
tcctatagcta	tgactacttt	aacgaagatt	caagtgtacc	cacaagctct	ggagcacogt	180
ctctctctca	gagatccgat	acgggtcggg	tcaagattga	cttgtagaga	acgtagtaat	240
aggggtttat	tgcatcgggt	tgagaaaaaa	gttgaagaaa	agagaaaaat	tgagaaaatt	300
aagggaaatg	ggctgtggga	ttctttgaaa	cttgggtttt	taggggttag	taaatttaggg	360
ttcttctcta	aaagttagta	taatcagaaa	gttgaaaact	tggagatggt	ttctctctcg	420
gtttgtgttc	aaattgcgag	atacattgtg	acgatgacaa	gtactggagc	tattcttttg	480
attgggtttc	aattatcagg	tgagatagat	tcgatgaact	cattgtgttg	gtatagttgg	540
cttgggtgaa	tctcatctgg	accatgactc	ggtgctaaca	tggttttgga	agatcattat	600
cgagccggtc	cacggaatgt	tgttataacc	ggaagcacta	ggggactagg	gaaagctctt	660
gctagagagt	ttcttctctc	tgagacacga	gtcattgtca	catctcgcag	ttctgaaatc	720
gttgatagta	ctctcaaaag	gctagagcaa	aatctcaaa	agattatgag	taacgctagc	780
gagtcagcta	gaagaaacct	gagtgatgct	aaggtagtgt	gtattgcctg	tgatgtttgc	840
aaaccogaag	acgtttgagaa	ctctgtcgat	ttcgtgtgaa	aagagcttgg	ttccatcaac	900
atatggataa	acaatgtctg	tactaacaaa	ggttttagac	cgtactctca	attcacggaa	960
gaagatatca	cacagattgt	ctccacaact	ttgattggat	caattctatg	tacacagagg	1020
gctatagatg	tgatgagcag	acagcacagt	ggtggacaca	tttttaacct	ggatgggtct	1080
ggctctggag	gttcaagtac	ttctctcact	gccgtatatg	gttcaacaaa	atgtggagct	1140
agggcatttc	atgggtctat	agtgaagaaa	agccaaaaaa	caaacgttgg	cttccacact	1200
gcactccctg	gcattgttct	gacagaactt	cttctcagtg	gttcgagcat	taaaaaaaag	1260
cagatgttta	acataaatct	tgagcttctc	gagacagtag	ctagaacttt	ggtaccacga	1320
atgcgagttg	tgaaaagttc	gggaaaagcc	gtcaattacc	taactctctc	tcggatatgt	1380
ttagctattg	tcacttctct	gctaaggaga	ggccgatggt	ttgatgacca	aggacgggag	1440
ttatatcgag	cagaagcaga	tagactaagg	aactggggag	agaacaggag	gaggttgtcg	1500
ttaacagacg	cgatggagat	gtatacacag	aatacttggg	ttctgttttt	ctctctttct	1560
gttgttttgc	ctttcatcat	cttacaaaag	acaacacctc	gtcttttttc	aggcacataa	1620
caaacatctt	ctctcgatgt	gttttaagaa	aattgtaaac	gtatcagtta	tgataaaaaa	1680
acatatatat	aacagaacog	atttgttcac	gtaaaacact	cttatagttg	tagaatgtgt	1740
cgttgttgaa	aacaatgaaa	aaaatagatt	gtaataaact	tttatcagat	tgt	

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..496

(D) OTHER INFORMATION: / Ceres Seq. ID 1566918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

Met	Thr	Thr	Leu	Thr	Lys	Ile	Gln	Val	Tyr	Pro	Gln	Val	Leu	Glu	His
1			5				10				15				
Arg	Leu	Phe	Phe	Arg	Asp	Pro	Ile	Arg	Val	Gly	Ser	Arg	Leu	Thr	Cys
			20				25					30			
Arg	Glu	Arg	Ser	Asn	Arg	Val	Tyr	Val	His	Arg	Cys	Glu	Lys	Lys	Val
			35				40					45			

DEPARTMENT OF THE ARMY

(2) INFORMATION FOR SEQ ID NO:427:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 404 amino acids

Met	Val	Phe	Ser	Ser	Val	Ala	Val	Gln	Ile	Ala	Arg	Tyr	Ile	Val	Thr
1			5					10						15	
Met	Thr	Ser	Thr	Gly	Ala	Ile	Leu	Leu	Ile	Gly	Phe	Gln	Leu	Ser	Gly
			20					25					30		
Gly	Asp	Ser	Ser	Met	Asn	Ser	Leu	Val	Trp	Tyr	Ser	Trp	Leu	Gly	Gly
		35					40					45			
Ile	Ile	Ile	Gly	Thr	Met	Thr	Gly	Ala	Asn	Met	Val	Leu	Glu	Asp	His
	50					55					60				
Tyr	Arg	Ala	Gly	Pro	Arg	Asn	Val	Val	Ile	Thr	Gly	Ser	Thr	Arg	Gly
65					70					75				80	
Leu	Gly	Lys	Ala	Leu	Ala	Arg	Glu	Phe	Leu	Leu	Ser	Gly	Asp	Arg	Val
				85					90					95	
Ile	Val	Thr	Ser	Arg	Ser	Ser	Glu	Ser	Val	Asp	Met	Thr	Val	Lys	Glu
			100					105					110		
Leu	Glu	Gln	Asn	Leu	Lys	Glu	Ile	Met	Ser	Asn	Ala	Ser	Glu	Ser	Ala
		115				120						125			
Arg	Lys	Lys	Leu	Ser	Asp	Ala	Lys	Val	Val	Gly	Ile	Ala	Cys	Asp	Val
	130					135					140				
Cys	Lys	Pro	Glu	Asp	Val	Glu	Lys	Leu	Ser	Asn	Phe	Ala	Val	Lys	Glu
145				150						155				160	
Leu	Gly	Ser	Ile	Asn	Ile	Trp	Ile	Asn	Asn	Ala	Gly	Thr	Asn	Lys	Gly
			165					170						175	
Phe	Arg	Pro	Leu	Leu	Lys	Phe	Thr	Glu	Glu	Asp	Ile	Thr	Gln	Ile	Val
			180					185					190		
Ser	Thr	Asn	Leu	Ile	Gly	Ser	Ile	Leu	Cys	Thr	Arg	Gly	Ala	Ile	Asp
		195				200						205			
Val	Met	Ser	Arg	Gln	His	Ser	Gly	Gly	His	Ile	Phe	Asn	Met	Asp	Gly
	210					215					220				
Ala	Gly	Ser	Gly	Gly	Ser	Ser	Thr	Pro	Leu	Thr	Ala	Val	Tyr	Gly	Ser
225				230						235				240	
Thr	Lys	Cys	Gly	Leu	Arg	Gln	Phe	His	Gly	Ser	Ile	Val	Lys	Glu	Ser
			245					250					255		
Gln	Lys	Thr	Asn	Val	Gly	Leu	His	Thr	Ala	Ser	Pro	Gly	Met	Val	Leu
		260						265					270		
Thr	Glu	Leu	Leu	Leu	Ser	Gly	Ser	Ser	Ile	Lys	Asn	Lys	Gln	Met	Phe
		275					280					285			
Asn	Ile	Ile	Cys	Glu	Leu	Pro	Glu	Thr	Val	Ala	Arg	Thr	Leu	Val	Pro
	290					295					300				
Arg	Met	Arg	Val	Val	Lys	Gly	Ser	Gly	Lys	Ala	Val	Asn	Tyr	Leu	Thr
305				310						315				320	
Pro	Pro	Arg	Ile	Leu	Leu	Ala	Ile	Val	Thr	Ser	Trp	Leu	Arg	Arg	Gly
			325						330					335	
Arg	Trp	Phe	Asp	Asp	Gln	Gly	Arg	Ala	Leu	Tyr	Ala	Ala	Glu	Ala	Asp
		340						345					350		
Arg	Leu	Arg	Asn	Trp	Ala	Glu									

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..388

SEQUENCE DESCRIPTION: SEQ ID NO:428:

[illegible]

385

(2) INFORMATION FOR SEQ ID NO:429:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 681 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..681

(D) OTHER INFORMATION: / Ceres Seq. ID 1566921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

acataatcat	cgctattctc	tctctctctc	tctctctctc	tctctctcgc	tctcatattt	60
gcagttgaca	atttgtttctc	tttgggaaat	tagagatgca	ggcatcaaga	gcgcgactgt	120
ttaaagaata	caaagaggta	cagcgagaga	aagtagcaga	tcctgatatt	caattgatct	180
gtgacgatac	caacataattc	aaatggaccg	ctcttatcaa	aggaccttcg	gagactcctt	240
acgaaggcgg	tgtttttcag	cttgcttttt	ctgttctctg	accttatcct	ttgcaacctc	300
ctcaagttcg	attcttgacc	aagatattcc	atcctaattg	tcatttcaag	acaggagaaa	360
tatgtctcga	cattttgaag	aatgcttggg	gtcctgcttg	gacgcttcag	tctgtgtgtg	420
gagctatcat	agcattgatg	gctcatctcg	agcgggacag	tcctcttaac	tgcgactcag	480
ggaatctctc	aagatctggg	gatgtgagag	ggttcaattc	aatggcaca	atgtatacac	540
gcctcgccgc	tatgctcaag	aaaggatgat	gatgatgatg	atcctcttgc	tttttttttg	600
tttttttttt	tgaaatytgt	aatgatattg	attCtgcgag	agtgaataca	ttattaacga	660
gaagaaGgat	gattctctt	t				

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1566922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

Met	Gln	Ala	Ser	Arg	Ala	Arg	Leu	Phe	Lys	Glu	Tyr	Lys	Glu	Val	Gln	
1			5				10						15			
Arg	Glu	Lys	Val	Ala	Asp	Pro	Asp	Ile	Gln	Leu	Ile	Cys	Asp	Asp	Thr	
			20				25						30			
Asn	Ile	Phe	Lys	Trp	Thr	Ala	Leu	Ile	Lys	Gly	Pro	Ser	Glu	Thr	Pro	
			35				40						45			
Tyr	Glu	Gly	Gly	Val	Phe	Gln	Leu	Ala	Phe	Ser	Val	Pro	Glu	Pro	Tyr	
			50				55						60			
Pro	Leu	Gln	Pro	Pro	Gln	Val	Arg	Phe	Leu	Thr	Lys	Ile	Phe	His	Pro	
			65				70						75		80	
Asn	Val	His	Phe	Lys	Thr	Gly	Glu	Ile	Cys	Leu	Asp	Ile	Leu	Lys	Asn	
			85				90						95			
Ala	Trp	Ser	Pro	Ala	Trp	Thr	Leu	Gln	Ser	Val	Cys	Arg	Ala	Ile	Ile	
			100				105						110			
Ala	Leu	Met	Ala	His	Pro	Glu	Pro	Asp	Ser	Pro	Leu	Asn	Cys	Asp	Ser	
			115				120						125			
Gly	Asn	Leu	Leu	Arg	Ser	Gly	Asp	Val	Arg	Gly	Phe	Asn	Ser	Met	Ala	
			130				135						140			
Gln	Met	Tyr	Thr	Arg	Leu	Ala	Ala	Met	Pro	Lys	Lys	Gly				
			145				150					155				

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..429
(D) OTHER INFORMATION: / Ceres Seq. ID 1566936
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:
aaaWacaaa aaaaaaatgc tttaaagat aaagccgggtg gttctcatgt cgttcttgct 60
tctgtttcca ttgtgttctt cggggtttag agaaggccat ggagttaact acacgacca 120
aaatttcotta aacaaggttg aagagatgat tccaacgac atggattatc cggaaccagg 180
tccagaccgg aacacgacgc caacaaaacc cggttatggt ttctctccc caccgccacc 240
gccactgtca ccgccaccgc caccgaatat gaactaagaa tcatgatgaa gcaaaaatat 300
gtaatatcgt taaatcatgc tcgtgagaag aactagtatt catgtgaagc aaaagaaaaa 360
cttaaatatg atgattctat gatattgact atcaaagtaa tcaatcaaat ataaaagagt 420
aaaatttgg

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..91
(D) OTHER INFORMATION: / Ceres Seq. ID 1566937
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:
Xaa Thr Asn Lys Lys Met Leu Ser Lys Ile Lys Pro Val Val Leu Met
1 5 10 15
Ser Phe Leu Leu Phe Pro Leu Cys Ser Ser Gly Phe Arg Glu Gly
20 25 30
His Gly Val Thr His Thr Asp Gln Asn Ser Leu Asn Lys Val Glu Glu
35 40 45
Ser Ile Pro Thr Ile Met Asp Tyr Pro Glu Pro Gly Pro Asp Pro Lys
50 55 60
His Asp Pro Thr Lys Pro Gly Tyr Gly Phe Pro Pro Pro Pro Pro
65 70 75 80
Pro Leu Ser Pro Pro Pro Pro Asn Met Asn
85 90

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..86
(D) OTHER INFORMATION: / Ceres Seq. ID 1566938
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:
Met Leu Ser Lys Ile Lys Pro Val Val Leu Met Ser Phe Leu Leu Leu
1 5 10 15
Phe Pro Leu Cys Ser Ser Gly Phe Arg Glu Gly His Gly Val Thr His
20 25 30
Thr Asp Gln Asn Ser Leu Asn Lys Val Glu Glu Ser Ile Pro Thr Ile
35 40 45
Met Asp Tyr Pro Glu Pro Gly Pro Asp Pro Lys His Asp Pro Thr Lys
50 55 60
Pro Gly Tyr Gly Phe Pro Pro Pro Pro Pro Pro Leu Ser Pro Pro

65 70 75 80
Pro Pro Pro Asn Met Asn
85

(2) INFORMATION FOR SEQ ID NO:434:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..76
(D) OTHER INFORMATION: / Ceres Seq. ID 1566939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Met	Ser	Phe	Leu	Leu	Phe	Pro	Leu	Cys	Ser	Ser	Gly	Phe	Arg	Glu
1			5				10						15	
Gly	His	Gly	Val	Thr	His	Thr	Asp	Gln	Asn	Ser	Leu	Asn	Lys	Val
			20				25						30	
Glu	Ser	Ile	Pro	Thr	Ile	Met	Asp	Tyr	Pro	Glu	Pro	Gly	Pro	Asp
		35					40					45		
Lys	His	Asp	Pro	Thr	Lys	Pro	Gly	Tyr	Gly	Phe	Pro	Pro	Pro	Pro
		50				55					60			
Pro	Pro	Leu	Ser	Pro	Pro	Pro	Pro	Pro	Asn	Met	Asn			
65			70				75							

(2) INFORMATION FOR SEQ ID NO:435:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 716 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..716
(D) OTHER INFORMATION: / Ceres Seq. ID 1566946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

cccttgatca	gatagtga	gagattctct	atattgcaga	tcatctccgc	agtttgctaa	60
atcgccggga	aatttactga	atttggagct	agtcattgct	tcagatccgt	acaaaatgat	120
gtccaaagcc	gacaaaaatga	caaagctcac	gcttactaga	tggagtgcgt	attggagagg	180
tgctactagt	aacacaaata	caccaaataa	aaaaaacag	aaagtaacat	gagatctctc	240
ttattagcgc	tgtgcctggt	tcttgcttta	cactgcggtg	aagcagccgt	gtcttgcaac	300
acgggtgattg	cggatcttta	cccttgctta	tcctactgtg	ctcaggggcg	accggtccca	360
accctctgct	gcaacggctc	cacaacactc	aagagtcagg	ctcaaacctc	tgtggaccgt	420
caggggGctc	gtcgttgcat	caaatctgct	attggaggac	tcactctctc	tcctagaacc	480
atccaaaatg	ctttgggaatt	gccttctaaa	tgtgggtgct	atctccctta	caagttcagc	540
ctttccactg	actgcgacag	tatccagtga	gacaagcaga	aaatctctaa	ggaagctact	600
acaagaacta	taataaccta	ataattaata	aatgaggcca	ttggtttgct	agttgctaatt	660
tgatcagtga	tgtattgtca	ttttgaatgt	tctaataatc	gcaggcactt	atctcc	

(2) INFORMATION FOR SEQ ID NO:436:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..113
(D) OTHER INFORMATION: / Ceres Seq. ID 1566947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

Met Arg Ser Leu Leu Leu Ala Val Cys Leu Val Leu Ala Leu His Cys
1 5 10 15
Gly Glu Ala Ala Val Ser Cys Asn Thr Val Ile Ala Asp Leu Tyr Pro
20 25 30
Cys Leu Ser Tyr Val Thr Gln Gly Gly Pro Val Pro Thr Leu Cys Cys
35 40 45
Asn Gly Leu Thr Thr Leu Lys Ser Gln Ala Gln Thr Ser Val Asp Arg
50 55 60
Gln Gly Val Cys Arg Cys Ile Lys Ser Ala Ile Gly Gly Leu Thr Leu
65 70 75 80
Ser Pro Arg Thr Ile Gln Asn Ala Leu Glu Leu Pro Ser Lys Cys Gly
85 90 95
Val Asp Leu Pro Tyr Lys Phe Ser Pro Ser Thr Asp Cys Asp Ser Ile
100 105 110
Gln

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2928 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2928
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

aaaaactcct	aaaccaaatt	ataattgtta	gtaagttaag	taacagagaa	caaaataata	60
ctcgtaacct	ttgtttccaa	actataacgt	aacttttgtt	catcatcttc	acagttttctg	120
tttctgtttc	taagatttct	aaattttgtg	tttttttttt	ctttttttct	tcgattatttt	180
ttgattttct	gatggaattc	cgcaaacctc	ttaagtctca	tagctcgat	aaacagatta	240
taagcacogg	aatcaaaac	gagaagacaa	agaagaagaa	gaaactggcg	aatcttgacg	300
atggcgacat	tgctaaaaat	cagagctctg	ggtctagtgt	cgatggaaac	agctataagt	360
tctggcaaga	cattgcaaca	gatgattata	caaagagcgg	gagtttcgat	ttccgcgaat	420
accgtgagga	gatcacactc	gatgtaaacg	aagaacaaga	ggaacacag	gagtccaaga	480
acaacaacaa	tttgtccggg	tctaaagaaa	cgagagcttc	tttcaaaaa	aacagttcag	540
gaactaataa	tatgtctcgt	tctgtacgtt	cttgatcatc	ttcgactctg	ttttcatcgg	600
ccacaatcgc	gttaaattta	gagcagcagt	tggaggatga	aggagagggt	gttgtaagat	660
gttcacatcgt	gaggaaaaaca	gagcttgttt	cgagggcgaa	ggcgagatcg	aggttgatag	720
atccgcacaa	agaagaggaa	caacaatact	cgagctggat	cgggacatcg	gatcagttaa	780
gatcaggttt	atctggggaa	caactctgat	atattgatga	agaagatgat	tcttcggctg	840
aaagaagatg	tccagtggaa	tatcgaagt	tgaaaatgga	cgcgataacg	ttgcttcaat	900
ggatgagctt	aatcgcactc	gtagtggcgt	tagtgttgag	tctagcgctt	catacttga	960
gAaaaatgct	actctatgga	gccttcatct	gtggaaaatg	gaagtggctt	tctgtgtctt	1020
catctgcggg	aggctgggtt	ccggatgcgg	aatcacgaatc	atcgtctctt	ttatcgaaag	1080
aaacttctta	ttgaggaaac	gggttcttta	ctctgtatac	ggtgtgaaga	ctcgtgttca	1140
gaactgtctc	ttgctttggcc	tctgtctcgt	cctctggcat	ttctgtctcg	acaagaaagt	1200
agaaaaggaa	acacaaagcg	acgttctctc	tctcgtatct	aaaatattag	tgtgtttctt	1260
gttgagcagc	gtcttatggc	tgatcaagac	actgggtgtg	aaagttttag	catcttcggt	1320
ccagcttagt	acctactttg	atcggattca	agaagctctg	tttcatcatt	acttgatcga	1380
gcagttatct	tgacctccaa	tgcttgagtt	aagcaggatt	gaggagaagg	aagatcggaac	1440
gcaagatgag	atctacaagg	tcagaaaagg	aggagctgat	ttatccaccg	aaactttgtc	1500
cgctgcggtt	ctccaggaaa	aaagtggaa	tacaatgaac	atgaagttct	ctccaatcat	1560
tccgaagacg	gggtggtgata	acggaatcac	aatggatgat	ttacacaaga	tgaatcagaa	1620
aaactgttca	gcttgggaaca	tgaagagact	gtgagaagt	gtgagaata	tttccctgac	1680
tacgttggac	gaacaagcgc	ttcaaaaacac	gatgtgaagt	gaatccactc	gacagatacg	1740
gagcgaaaaa	gaagcttaag	cagctgcaag	gaagattttc	aagaacgtag	ctcaacctgg	1800
cacaaaaacac	atatacctgg	aggacttgat	gaagtttttg	cgagtagacg	aggcgatgaa	1860
gacaatgtgt	ctcttcgaag	gcgccttagt	gacaaaaaag	attactaat	cagccttgaa	1920
gaactggctg	gtaaatgctt	tcagagagag	aagagcactt	gccttaaacac	tacaatgacac	1980

caaaacagca	gtgaacaaac	tccatcacat	gattagtttt	ctcactgcc	ttgtcatcat	2040
agtcataatg	ctgatccctc	ttgaaatcgc	tacttccaag	tatcttttat	ttttaacttc	2100
acaagtgtga	ctcttagcct	tcattgtttg	gaactctctc	aagaccgctc	tcagatcaat	2160
catctctctc	ttcatcattc	acccttaaga	tgttggtgat	cggttactca	tcgacactgt	2220
agagatggtg	gtggaggaaa	tgaacattct	cacaacagtt	ttcttgagag	ctgacaatct	2280
gaagatttgt	tatccaaaata	ttcttctatg	gcagaaagcg	atccacaatt	acaaccgtag	2340
tcgggatatg	ggagatgaag	ttacatgctg	tgtccacatt	actactcctc	ctgaaaagat	2400
tgctgcaatc	aaacaaagaa	tatcaagcta	cattgatagc	aagccagagt	attggtatcc	2460
aaaagctgat	atcattgttaa	aggatgtgga	agatttgaac	attgtgagga	tagcaatatg	2520
gctgtgtcat	aaaatttaacc	atcaaaaacat	gggagagaga	tttacaagaa	gagcggttgt	2580
gatcgaggaa	gtaatcaaaa	tcctctcoga	actcgacatt	caataccoggt	ttcatccact	2640
tgatatcaat	gttaaaaacca	tgccaacagt	tgtctcgagc	agagttccac	acggtgtggt	2700
acaaaaccct	gattcaaggt	aattatagag	atgatgtgaa	ttgtgtttac	tttaactcta	2760
agtggtgttt	agtatgaggt	ttgatttgtg	tatttttttt	ttcttttttt	gtaaacoggt	2820
tggtgtatat	atatgaaggt	gaaagcaaat	agtgggatca	taaaccttgt	ttatagaaac	2880
tttatgaaaa	tagaaactaa	tgatattttt	agtaatgatt	tttttttt		

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 607 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..607

(D) OTHER INFORMATION: / Ceres Seq. ID 1566956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

Met	Asp	Glu	Leu	Asn	Arg	Thr	Arg	Ser	Gly	Val	Ser	Val	Glu	Ser	Ser
1		5						10					15		
Ala	Ser	Tyr	Leu	Glu	Lys	Asn	Ala	Thr	Leu	Trp	Ser	Leu	His	Leu	Trp
		20						25					30		
Lys	Trp	Glu	Val	Val	Leu	Leu	Val	Leu	Ile	Cys	Gly	Arg	Leu	Val	Ser
		35						40				45			
Gly	Cys	Gly	Ile	Arg	Ile	Ile	Val	Phe	Phe	Ile	Glu	Arg	Asn	Phe	Leu
	50					55					60				
Leu	Arg	Lys	Arg	Val	Leu	Tyr	Phe	Val	Tyr	Gly	Val	Lys	Thr	Ala	Val
	65					70					75			80	
Gln	Asn	Cys	Leu	Trp	Leu	Gly	Leu	Val	Leu	Val	Ala	Trp	His	Phe	Leu
		85						90					95		
Phe	Asp	Lys	Lys	Val	Glu	Arg	Glu	Thr	Gln	Ser	Asp	Val	Leu	Leu	Leu
		100						105					110		
Val	Ser	Lys	Ile	Leu	Val	Cys	Phe	Leu	Leu	Ser	Thr	Val	Leu	Trp	Leu
		115						120					125		
Ile	Lys	Thr	Leu	Val	Val	Lys	Val	Leu	Ala	Ser	Ser	Phe	His	Val	Ser
		130				135					140				
Thr	Tyr	Phe	Asp	Arg	Ile	Gln	Glu	Ala	Leu	Phe	His	His	Tyr	Leu	Ile
	145					150				155				160	
Glu	Thr	Leu	Ser	Val	Pro	Pro	Met	Leu	Glu	Leu	Ser	Arg	Ile	Glu	Glu
		165						170					175		
Glu	Glu	Asp	Arg	Thr	Gln	Asp	Glu	Ile	Tyr	Lys	Val	Gln	Lys	Gly	Gly
		180						185					190		
Ala	Asp	Leu	Ser	Pro	Glu	Leu	Cys	Ser	Ala	Ala	Phe	Pro	Gln	Glu	Lys
		195						200					205		
Ser	Gly	Ser	Thr	Met	Asn	Met	Lys	Phe	Ser	Pro	Ile	Ile	Pro	Lys	Thr
	210					215					220				
Gly	Gly	Asp	Asn	Gly	Ile	Thr	Met	Asp	Asp	Leu	His	Lys	Met	Asn	Gln
	225					230				235				240	
Lys	Asn	Val	Ser	Ala	Trp	Asn	Met	Lys	Arg	Leu	Met	Lys	Ile	Val	Arg
		245							250					255	
Asn	Ile	Ser	Leu	Thr	Thr	Leu	Asp	Glu	Gln	Ala	Leu	Gln	Asn	Thr	Cys

260	265	270
Glu Asp Glu Ser Thr Arg Gln Ile Arg Ser Glu Lys Glu Ala Lys Ala		
275	280	285
Ala Ala Arg Lys Ile Phe Lys Asn Val Ala Gln Pro Gly Thr Lys His		
290	295	300
Ile Tyr Leu Glu Asp Leu Met Arg Phe Leu Arg Val Asp Glu Ala Met		
305	310	315
Lys Thr Met Cys Leu Phe Glu Gly Ala Leu Val Thr Lys Lys Ile Thr		
325	330	335
Lys Ser Ala Leu Lys Asn Trp Leu Val Asn Ala Phe Arg Glu Arg Arg		
340	345	350
Ala Leu Ala Leu Thr Leu Asn Asp Thr Lys Thr Ala Val Asn Lys Leu		
355	360	365
His His Met Ile Ser Phe Leu Thr Ala Ile Val Ile Val Ile Trp		
370	375	380
Leu Ile Leu Leu Glu Ile Ala Thr Ser Lys Tyr Leu Leu Phe Leu Thr		
385	390	395
Ser Gln Val Val Leu Leu Ala Phe Met Phe Gly Asn Ser Leu Lys Thr		
405	410	415
Val Phe Glu Ser Ile Ile Phe Leu Phe Ile Ile His Pro Tyr Asp Val		
420	425	430
Gly Asp Arg Leu Leu Ile Asp Thr Val Glu Met Val Val Glu Glu Met		
435	440	445
Asn Ile Leu Thr Thr Val Phe Leu Arg Ala Asp Asn Leu Lys Ile Val		
450	455	460
Tyr Pro Asn Ile Leu Leu Trp Gln Lys Ala Ile His Asn Tyr Asn Arg		
465	470	475
Ser Pro Asp Met Gly Asp Glu Val Thr Cys Cys Val His Ile Thr Thr		
485	490	495
Pro Pro Glu Lys Ile Ala Ala Ile Lys Gln Arg Ile Ser Ser Tyr Ile		
500	505	510
Asp Ser Lys Pro Glu Tyr Trp Tyr Pro Lys Ala Asp Ile Val Lys		
515	520	525
Asp Val Glu Asp Leu Asn Ile Val Arg Ile Ala Ile Trp Leu Cys His		
530	535	540
Lys Ile Asn His Gln Asn Met Gly Glu Arg Phe Thr Arg Arg Ala Leu		
545	550	555
Leu Ile Glu Glu Val Ile Lys Ile Leu Leu Glu Leu Asp Ile Gln Tyr		
565	570	575
Arg Phe His Pro Leu Asp Ile Asn Val Lys Thr Met Pro Thr Val Val		
580	585	590
Ser Ser Arg Val Pro Pro Gly Trp Ser Gln Asn Pro Asp Ser Arg		
595	600	605

(2) INFORMATION FOR SEQ ID NO:439:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 440 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..440
(D) OTHER INFORMATION: / Ceres Seq. ID 1566957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

Met	Leu	Glu	Leu	Ser	Arg	Ile	Glu	Glu	Glu	Asp	Arg	Thr	Gln	Asp
1		5					10						15	
Glu	Ile	Tyr	Lys	Val	Gln	Lys	Gly	Gly	Ala	Asp	Leu	Ser	Pro	Glu
		20					25						30	
Cys	Ser	Ala	Ala	Phe	Pro	Gln	Glu	Lys	Ser	Gly	Ser	Thr	Met	Asn
		35				40							45	

Lys Phe Ser Pro Ile Ile Pro Lys Thr Gly Gly Asp Asn Gly Ile Thr
50 55 60
Met Asp Asp Leu His Lys Met Asn Gln Lys Asn Val Ser Ala Trp Asn
65 70 75 80
Met Lys Arg Leu Met Lys Ile Val Arg Asn Ile Ser Leu Thr Thr Leu
85 90 95
Asp Glu Gln Ala Leu Gln Asn Thr Cys Glu Asp Glu Ser Thr Arg Gln
100 105 110
Ile Arg Ser Glu Lys Glu Ala Lys Ala Ala Ala Arg Lys Ile Phe Lys
115 120 125
Asn Val Ala Gln Pro Gly Thr Lys His Ile Tyr Leu Glu Asp Leu Met
130 135 140
Arg Phe Leu Arg Val Asp Glu Ala Met Lys Thr Met Cys Leu Phe Glu
145 150 155 160
Gly Ala Leu Val Thr Lys Lys Ile Thr Lys Ser Ala Leu Lys Asn Trp
165 170 175
Leu Val Asn Ala Phe Arg Glu Arg Arg Ala Leu Ala Leu Thr Leu Asn
180 185 190
Asp Thr Lys Thr Ala Val Asn Lys Leu His His Met Ile Ser Phe Leu
195 200 205
Thr Ala Ile Val Ile Ile Val Ile Trp Leu Ile Leu Leu Glu Ile Ala
210 215 220
Thr Ser Lys Tyr Leu Leu Phe Leu Thr Ser Gln Val Val Leu Leu Ala
225 230 235 240
Phe Met Phe Gly Asn Ser Leu Lys Thr Val Phe Glu Ser Ile Ile Phe
245 250 255
Leu Phe Ile Ile His Pro Tyr Asp Val Gly Asp Arg Leu Leu Ile Asp
260 265 270
Thr Val Glu Met Val Val Glu Glu Met Asn Ile Leu Thr Thr Val Phe
275 280 285
Leu Arg Ala Asp Asn Leu Lys Ile Val Tyr Pro Asn Ile Leu Leu Trp
290 295 300
Gln Lys Ala Ile His Asn Tyr Asn Arg Ser Pro Asp Met Gly Asp Glu
305 310 315 320
Val Thr Cys Cys Val His Ile Thr Thr Pro Pro Glu Lys Ile Ala Ala
325 330 335
Ile Lys Gln Arg Ile Ser Ser Tyr Ile Asp Ser Lys Pro Glu Tyr Trp
340 345 350
Tyr Pro Lys Ala Asp Ile Ile Val Lys Asp Val Glu Asp Leu Asn Ile
355 360 365
Val Arg Ile Ala Ile Trp Leu Cys His Lys Ile Asn His Gln Asn Met
370 375 380
Gly Glu Arg Phe Thr Arg Arg Ala Leu Leu Ile Glu Glu Val Ile Lys
385 390 395 400
Ile Leu Leu Glu Leu Asp Ile Gln Tyr Arg Phe His Pro Leu Asp Ile
405 410 415
Asn Val Lys Thr Met Pro Thr Val Val Ser Ser Arg Val Pro Pro Gly
420 425 430
Trp Ser Gln Asn Pro Asp Ser Arg
435 440

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..395
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566958

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

Met	Asn	Met	Lys	Phe	Ser	Pro	Ile	Ile	Pro	Lys	Thr	Gly	Gly	Asp	Asn
1			5						10					15	
Gly	Ile	Thr	Met	Asp	Asp	Leu	His	Lys	Met	Asn	Gln	Lys	Asn	Val	Ser
			20					25					30		
Ala	Trp	Asn	Met	Lys	Arg	Leu	Met	Lys	Ile	Val	Arg	Asn	Ile	Ser	Leu
			35				40					45			
Thr	Thr	Leu	Asp	Glu	Gln	Ala	Leu	Gln	Asn	Thr	Cys	Glu	Asp	Glu	Ser
			50			55				60					
Thr	Arg	Gln	Ile	Arg	Ser	Glu	Lys	Glu	Ala	Lys	Ala	Ala	Ala	Arg	Lys
65					70				75					80	
Ile	Phe	Lys	Asn	Val	Ala	Gln	Pro	Gly	Thr	Lys	His	Ile	Tyr	Leu	Glu
			85					90						95	
Asp	Leu	Met	Arg	Phe	Leu	Arg	Val	Asp	Glu	Ala	Met	Lys	Thr	Met	Cys
			100				105						110		
Leu	Phe	Glu	Gly	Ala	Leu	Val	Thr	Lys	Lys	Ile	Thr	Lys	Ser	Ala	Leu
			115				120					125			
Lys	Asn	Trp	Leu	Val	Asn	Ala	Phe	Arg	Glu	Arg	Arg	Ala	Leu	Ala	Leu
			130			135					140				
Thr	Leu	Asn	Asp	Thr	Lys	Thr	Ala	Val	Asn	Lys	Leu	His	His	Met	Ile
145					150				155					160	
Ser	Phe	Leu	Thr	Ala	Ile	Val	Ile	Ile	Val	Ile	Trp	Leu	Ile	Leu	Leu
			165						170					175	
Glu	Ile	Ala	Thr	Ser	Lys	Tyr	Leu	Leu	Phe	Leu	Thr	Ser	Gln	Val	Val
			180				185						190		
Leu	Leu	Ala	Phe	Met	Phe	Gly	Asn	Ser	Leu	Lys	Thr	Val	Phe	Glu	Ser
			195				200					205			
Ile	Ile	Phe	Leu	Phe	Ile	Ile	His	Pro	Tyr	Asp	Val	Gly	Asp	Arg	Leu
			210			215					220				
Leu	Ile	Asp	Thr	Val	Glu	Met	Val	Val	Glu	Glu	Met	Asn	Ile	Leu	Thr
225					230				235					240	
Thr	Val	Phe	Leu	Arg	Ala	Asp	Asn	Leu	Lys	Ile	Val	Tyr	Pro	Asn	Ile
			245					250						255	
Leu	Leu	Trp	Gln	Lys	Ala	Ile	His	Asn	Tyr	Asn	Arg	Ser	Pro	Asp	Met
			260				265						270		
Gly	Asp	Glu	Val	Thr	Cys	Cys	Val	His	Ile	Thr	Thr	Pro	Pro	Glu	Lys
			275				280					285			
Ile	Ala	Ala	Ile	Lys	Gln	Arg	Ile	Ser	Ser	Tyr	Ile	Asp	Ser	Lys	Pro
			290			295					300				
Glu	Tyr	Trp	Tyr	Pro	Lys	Ala	Asp	Ile	Ile	Val	Lys	Asp	Val	Glu	Asp
305					310				315					320	
Leu	Asn	Ile	Val	Arg	Ile	Ala	Ile	Trp	Leu	Cys	His	Lys	Ile	Asn	His
			325						330					335	
Gln	Asn	Met	Gly	Glu	Arg	Phe	Thr	Arg	Arg	Ala	Leu	Leu	Ile	Glu	Glu
			340				345						350		
Val	Ile	Lys	Ile	Leu	Leu	Glu	Leu	Asp	Ile	Gln	Tyr	Arg	Phe	His	Pro
			355			360						365			
Leu	Asp	Ile	Asn	Val	Lys	Thr	Met	Pro	Thr	Val	Val	Ser	Ser	Arg	Val
			370			375					380				
Pro	Pro	Gly	Trp	Ser	Gln	Asn	Pro	Asp	Ser	Arg					
385					390				395						

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 421 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..421

(D) OTHER INFORMATION: / Ceres Seq. ID 1566972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

Met	Ser	Asn	Ile	Val	Val	Leu	Asp	Asn	Gly	Gly	Gly	Leu	Ile	Lys	Ala
1			5						10					15	
Gly	Gln	Gly	Gly	Glu	Arg	Asp	Pro	Thr	Thr	Val	Ile	Pro	Asn	Cys	Leu
		20						25					30		
Tyr	Lys	Pro	Leu	Ser	Ser	Lys	Lys	Phe	Ile	His	Pro	Ser	Pro	Leu	Thr
		35					40					45			
Thr	Leu	Ser	Asp	Glu	Ile	Asp	Leu	Thr	Ser	Ala	Ala	Val	Arg	Arg	Pro
	50					55				60					
Ile	Asp	Arg	Gly	Tyr	Leu	Ile	Asn	Ser	Asp	Leu	Gln	Arg	Glu	Ile	Trp
65				70					75					80	
Ser	His	Leu	Phe	Thr	Ser	Leu	Leu	His	Ile	Ala	Pro	Ser	Ser	Ser	Ser
				85					90					95	
Leu	Leu	Leu	Thr	Glu	Ala	Pro	Leu	Ser	Ile	Pro	Ser	Val	Gln	Arg	Thr
			100					105					110		
Thr	Asp	Glu	Leu	Val	Phe	Glu	Asp	Phe	Gly	Phe	Ser	Ser	Leu	Tyr	Ile
		115				120					125				
Ala	His	Pro	Gln	Ser	Leu	Val	His	Leu	Tyr	Glu	Ala	Ser	Arg	Gln	Gly
	130					135				140					
Asp	Ser	Ile	Leu	Ser	Lys	Thr	Gln	Cys	Ser	Leu	Val	Val	Asp	Cys	Gly
145					150					155				160	
Phe	Ser	Phe	Thr	His	Ala	Val	Pro	Val	Leu	His	Asn	Phe	Thr	Leu	Asn
				165					170					175	

His Ala Ile Lys Arg Ile Asp Leu Gly Gly Lys Ala Phe Thr Asn Tyr
180 185 190
Leu Lys Glu Leu Val Ser Tyr Arg Ser Ile Asn Val Met Asp Glu Thr
195 200 205
Phe Leu Val Asp Asp Ala Lys Glu Lys Leu Cys Phe Val Ser Leu Asp
210 215 220
Leu Leu Arg Asp Leu Arg Leu Ala Arg Asn Gly Asn Thr Leu Ile Lys
225 230 235 240
Ser Thr Tyr Val Leu Pro Asp Gly Val Thr His Thr Lys Gly Tyr Val
245 250 255
Lys Asp Pro Gln Ala Ala Lys Arg Phe Leu Ser Leu Ser Glu Lys Glu
260 265 270
Ser Val Val Val Met Asp Lys Val Gly Glu Arg Lys Lys Ala Asp Met
275 280 285
Asn Lys Asn Glu Ile Asp Leu Thr Asn Glu Arg Phe Leu Val Pro Glu
290 295 300
Thr Leu Phe Gln Pro Ala Asp Leu Gly Met Asn Gln Ala Gly Leu Ala
305 310 315 320
Glu Cys Ile Val Arg Ala Ile Asn Ser Cys His Ser Tyr Leu Gln Pro
325 330 335
Val Leu Tyr Gln Ser Ile Ile Leu Thr Gly Gly Ser Thr Leu Phe Pro
340 345 350
Gln Leu Lys Glu Arg Leu Glu Gly Glu Leu Arg Pro Leu Val Pro Asp
355 360 365
His Phe Asp Val Lys Ile Thr Thr Gln Glu Asp Pro Ile Leu Gly Val
370 375 380
Trp Arg Gly Gly Ser Leu Leu Ala Ser Ser Pro Asp Phe Glu Ser Met
385 390 395 400
Cys Val Thr Lys Ala Glu Tyr Glu Glu Leu Gly Ser Ala Arg Cys Arg
405 410 415
Arg Arg Phe Phe His
420

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..217
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

Met Asp Glu Thr Phe Leu Val Asp Asp Ala Lys Glu Lys Leu Cys Phe
1 5 10 15
Val Ser Leu Asp Leu Leu Arg Asp Leu Arg Leu Ala Arg Asn Gly Asn
20 25 30
Thr Leu Ile Lys Ser Thr Tyr Val Leu Pro Asp Gly Val Thr His Thr
35 40 45
Lys Gly Tyr Val Lys Asp Pro Gln Ala Ala Lys Arg Phe Leu Ser Leu
50 55 60
Ser Glu Lys Glu Ser Val Val Val Met Asp Lys Val Gly Glu Arg Lys
65 70 75 80
Lys Ala Asp Met Asn Lys Asn Glu Ile Asp Leu Thr Asn Glu Arg Phe
85 90 95
Leu Val Pro Glu Thr Leu Phe Gln Pro Ala Asp Leu Gly Met Asn Gln
100 105 110
Ala Gly Leu Ala Glu Cys Ile Val Arg Ala Ile Asn Ser Cys His Ser
115 120 125
Tyr Leu Gln Pro Val Leu Tyr Gln Ser Ile Ile Leu Thr Gly Gly Ser

130	135	140
Thr Leu Phe Pro Gln Leu Lys Glu Arg	Leu Gly Glu Leu Arg Pro	
145	150	155
Leu Val Pro Asp His Phe Asp Val Lys Ile Thr Thr Gln Glu Asp Pro		
	165	170
Ile Leu Gly Val Trp Arg Gly Gly Ser	Leu Leu Ala Ser Ser Pro Asp	
	180	185
Phe Glu Ser Met Cys Val Thr Lys Ala	Glu Tyr Glu Glu Leu Gly Ser	
	195	200
Ala Arg Cys Arg Arg Arg Phe Phe His		205
	210	215

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

attctctagg	cttttttata	ttctgaaagt	tttgattttt	tgtatcttgt	tttgtttctc	60
aatcatcaat	ttgtgtagt	agctcactag	caaacatagg	aggggaggtt	gaataatag	120
tggagggtga	ctgtgaatga	gagcaaatc	gttgaatctg	cgttgcaatc	tgagctcaga	180
gtcgatggtc	gtggccctta	tgattaccgc	aagcttacta	tttaagtttg	caaggaatat	240
ggcagctcac	aagttcaact	gggtcagact	catgtaatgg	cttttgtgac	tgctcagcta	300
gtacaacctt	acaaagacag	acctagtga	gggtcctctc	ctatctctac	cgagttttct	360
ccaatggctg	tccatcggt	tggagccagg	catcctgggtg	aatctgctgt	tgagcttggc	420
cgtattatag	acogtgcctc	acagaaaagc	cgtgcagtag	atacagagtc	gctttgtgtt	480
ctagccgaa	agctggtttg	gtctgttcgc	attgatcttc	acattttgga	caatggaggg	540
aaottggttg	atgctgctaa	tgttgctgcc	ttagccgcac	tcatgacttt	caggagacct	600
gattgcaactg	taggaggggg	caacagtcac	gacgtgatca	tacatccacc	cgaagaaagg	660
Gaaccacttc	ctttgataat	acatcatctc	ccaatagcct	tcacgttttg	attttttaat	720
aaaggcagta	tcttgggtgt	ggaccacaat	tacgttgaa	agcgtgttat	gtgtgggaga	780
atgactgtga	cagtcaatgc	caatggcgat	atatgcgcaa	tcacaaaacc	aggagaagaa	840
ggcgtgaacc	agagtgtaat	ccttcattgc	ctgcgtcttg	cttcttcaag	agcttctgca	900
acaacaaga	taattagaga	tgcagttgaa	gcatacaacc	gtgagaggag	ctcacagaag	960
gtggagcggc	atcatacttt	ggctaagtct	gaagttttgg	gacctattgt	agttgtgtag	1020
gaagagacat	aaataaaaca	tttgcgtgtg	tgcgtcgaatg	taataaaaga	ttttagttgt	1080
agaatctcta	tcagcaacac	taagctataa	aaacgtcgat	atgatcaaga	catgttgaga	1140

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..307
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

Met Glu Gly Arg Leu Asn Asn Met Trp Arg Leu Thr Val Asn Glu Ser	
1	5
Lys Phe Val Glu Ser Ala Leu Gln Ser Glu Leu Arg Val Asp Gly Arg	
20	25
Gly Leu Tyr Asp Tyr Arg Lys Leu Thr Ile Lys Phe Gly Lys Glu Tyr	
35	40
	45

Gly Ser Ser Gln Val Gln Leu Gly Gln Thr His Val Met Ala Phe Val
50 55 60
Thr Ala Gln Leu Val Gln Pro Tyr Lys Asp Arg Pro Ser Glu Gly Ser
65 70 75 80
Phe Ser Ile Phe Thr Glu Phe Ser Pro Met Ala Asp Pro Ser Phe Glu
85 90 95
Pro Gly His Pro Gly Glu Ser Ala Val Glu Leu Gly Arg Ile Ile Asp
100 105 110
Arg Ala Leu Arg Glu Ser Arg Ala Val Asp Thr Glu Ser Leu Cys Val
115 120 125
Leu Ala Gly Lys Leu Val Trp Ser Val Arg Ile Asp Leu His Ile Leu
130 135 140
Asp Asn Gly Gly Asn Leu Val Asp Ala Ala Asn Val Ala Ala Leu Ala
145 150 155 160
Ala Leu Met Thr Phe Arg Arg Pro Asp Cys Thr Val Gly Gly Asp Asn
165 170 175
Ser Gln Asp Val Ile Ile His Pro Pro Glu Glu Arg Glu Pro Leu Pro
180 185 190
Leu Ile Ile His His Leu Pro Ile Ala Phe Thr Phe Gly Phe Phe Asn
195 200 205
Lys Gly Ser Ile Leu Val Met Asp Pro Thr Tyr Val Glu Glu Ala Val
210 215 220
Met Cys Gly Arg Met Thr Val Thr Val Asn Ala Asn Gly Asp Ile Cys
225 230 235 240
Ala Ile Gln Lys Pro Gly Glu Glu Gly Val Asn Gln Ser Val Ile Leu
245 250 255
His Cys Leu Arg Leu Ala Ser Ser Arg Ala Ser Ala Thr Thr Lys Ile
260 265 270
Ile Arg Asp Ala Val Glu Ala Tyr Asn Arg Glu Arg Ser Ser Gln Lys
275 280 285
Val Glu Arg His His Thr Leu Ala Lys Ser Glu Val Leu Gly Pro Ile
290 295 300
Val Val Val
305

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..300
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

Met Trp Arg Leu Thr Val Asn Glu Ser Lys Phe Val Glu Ser Ala Leu
1 5 10
Gln Ser Glu Leu Arg Val Asp Gly Arg Gly Leu Tyr Asp Tyr Arg Lys
20 25 30
Leu Thr Ile Lys Phe Gly Lys Glu Tyr Gly Ser Ser Gln Val Gln Leu
35 40 45
Gly Gln Thr His Val Met Ala Phe Val Thr Ala Gln Leu Val Gln Pro
50 55 60
Tyr Lys Asp Arg Pro Ser Glu Gly Ser Phe Ser Ile Phe Thr Glu Phe
65 70 75 80
Ser Pro Met Ala Asp Pro Ser Phe Glu Pro Gly His Pro Gly Glu Ser
85 90 95
Ala Val Glu Leu Gly Arg Ile Ile Asp Arg Ala Leu Arg Glu Ser Arg
100 105 110
Ala Val Asp Thr Glu Ser Leu Cys Val Leu Ala Gly Lys Leu Val Trp

(2) INFORMATION FOR SEQ ID NO:447:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

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(ix) FEATURE:
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(A) NAME/KEY: peptide

(B) LOCATION: 1..247

(D) OTHER INFORMATION: / Ceres Seq. ID 1566988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

1	Met	Ala	Phe	Val	5	Thr	Ala	Gln	Leu	Val	Gln	Pro	Tyr	Lys	Asp	Arg	Pro
1	Ser	Glu	Gly	Ser	20	Phe	Ser	Ile	Phe	Thr	Glu	Phe	Ser	Pro	Met	Ala	Asp
					35					25					30		
	Pro	Ser	Phe	Glu	Pro	Gly	His	Pro	Gly	Glu	Ser	Ala	Val	Glu	Leu	Gly	
									40					45			
	Arg	Ile	Ile	Asp	Arg	Ala	Leu	Arg	Glu	Ser	Arg	Ala	Val	Asp	Thr	Glu	
		50					55					60					
	Ser	Leu	Cys	Val	Leu	Ala	Gly	Lys	Leu	Val	Trp	Ser	Val	Arg	Ile	Asp	
	65					70					75				80		
	Leu	His	Ile	Leu	Asp	Asn	Gly	Gly	Asn	Leu	Val	Asp	Ala	Ala	Asn	Val	
					85					90					95		
	Ala	Ala	Leu	Ala	Leu	Met	Thr	Phe	Arg	Arg	Pro	Asp	Cys	Thr	Val		
					100				105					110			
	Gly	Gly	Asp	Asn	Ser	Gln	Asp	Val	Ile	Ile	His	Pro	Pro	Glu	Glu	Arg	
					115				120				125				
	Glu	Pro	Leu	Pro	Leu	Ile	Ile	His	His	Leu	Pro	Ile	Ala	Phe	Thr	Phe	
		130				135						140					
	Gly	Phe	Phe	Asn	Lys	Gly	Ser	Ile	Leu	Val	Met	Asp	Pro	Thr	Tyr	Val	
	145					150					155				160		
	Glu	Glu	Ala	Val	Met	Cys	Gly	Arg	Met	Thr	Val	Thr	Val	Asn	Ala	Asn	
					165					170				175			
	Gly	Asp	Ile	Cys	Ala	Ile	Gln	Lys	Pro	Gly	Glu	Glu	Gly	Val	Asn	Gln	
					180				185					190			
	Ser	Val	Ile	Leu	His	Cys	Leu	Arg	Leu	Ala	Ser	Ser	Arg	Ala	Ser	Ala	
					195			200					205				

Thr	Thr	Lys	Ile	Ile	Arg	Asp	Ala	Val	Glu	Ala	Tyr	Asn	Arg	Glu	Arg
	210					215					220				
Ser	Ser	Gln	Lys	Val	Glu	Arg	His	His	Thr	Leu	Ala	Lys	Ser	Glu	Val
	225				230					235				240	
Leu	Gly	Pro	Ile	Val	Val	Val									
				245											

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

atttttctcc	taccgtcgaa	ctaaatccta	gggcacaggt	gaaatcgccg	agtgacgtct	60
agccaccgca	cgcctcctt	ctccggttat	ctcgtacta	atcagactat	tcacacagcta	120
tgctcacagg	agacagcaga	aattcatcag	cagccaagcg	tgctagaact	gacggggggc	180
gtagagaaga	tgattggatc	tgcccaagtt	gtggcaatgt	caacttttca	ttcaggacaa	240
cttgcaatat	gcgttaattgc	actcagccta	gacctgcaga	tcataatgga	aagtcctgctc	300
ccaaacctat	gcaacatcaa	caaggtttct	catcaccccg	ggcatactta	ggatctgggg	360
gtccccctcc	agtatatatg	ggcgggtcac	catatggatc	tcctctcttt	aatggatcgt	420
ctatgcctcc	tatgacgttc	ccattttctg	gggggtcgcc	ttaccatttt	aactataata	480
gcgaatgccc	tgccggagct	cattacagac	cattacatat	gtctggacca	ccaccatacc	540
atggcggtac	tatgatggga	atgggtggta	tgatgggaat	gcctccacca	atagacaggt	600
atggccttgg	tatggcaatg	ggctcctggt	ctgcgcgtcg	catgatgcca	agaccaaggt	660
tttaccocaga	tgaaaaatca	caaaagagag	attcaactcg	cgataatgat	tggtcatgtc	720
cgaatttggtg	taattgtaaac	ttctcattca	gaactgtatg	taacatgagg	aagtgcacaa	780
ctccaaagcc	tggttctcag	cagggtggaa	gctcagataa	aatatccaaa	caaaatgcac	840
cggaaggagag	ctgggaagtgt	gataaactgtg	gaaatataaa	ctaccatttc	aggagcaaat	900
gcaacaggca	aaactgtgga	gctgataagc	ctggggatcg	gtcgaatgga	tctccgtccc	960
gtgcaccaga	agagaacgat	caggtttgta	agatgtatct	atgtgggtcac	aactgtttgt	1020
taataaaatg	tttgctctcg	aaactcgtaa	atgtaacaac	ctgtgtagat	tttatgcctt	1080
gtgaaagcag	aggttatatg	tttatgaaaa	aattgactcc	gaCtactgtt		

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..337
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

Met	Ser	Gln	Val	Asp	Ser	Arg	Asn	Ser	Ser	Ala	Ala	Lys	Arg	Ala	Arg
				5				10						15	
Thr	Asp	Gly	Gly	Arg	Arg	Glu	Asp	Asp	Trp	Ile	Cys	Pro	Ser	Cys	Gly
				20				25					30		
Asn	Val	Asn	Phe	Ser	Phe	Arg	Thr	Thr	Cys	Asn	Met	Arg	Asn	Cys	Thr
				35				40					45		
Gln	Pro	Arg	Pro	Ala	Asp	His	Asn	Gly	Lys	Ser	Ala	Pro	Lys	Pro	Met
				50			55				60				
Gln	His	Gln	Gln	Gly	Phe	Ser	Ser	Pro	Gly	Ala	Tyr	Leu	Gly	Ser	Gly
				65			70			75				80	
Gly	Pro	Pro	Pro	Gly	Tyr	Met	Gly	Gly	Ser	Pro	Tyr	Gly	Ser	Pro	Leu
				85			90							95	

Phe Asn Gly Ser Ser Met Pro Pro Tyr Asp Val Pro Phe Ser Gly Gly
100 105 110
Ser Pro Tyr His Phe Asn Tyr Asn Ser Arg Met Pro Ala Gly Ala His
115 120 125
Tyr Arg Pro Leu His Met Ser Gly Pro Pro Pro Tyr His Gly Gly Ser
130 135 140
Met Met Gly Ser Gly Gly Met Tyr Gly Met Pro Pro Ile Asp Arg
145 150 155 160
Tyr Gly Leu Gly Met Ala Met Gly Pro Gly Ser Ala Ala Ala Met Met
165 170 175
Pro Arg Pro Arg Phe Tyr Pro Asp Glu Lys Ser Gln Lys Arg Asp Ser
180 185 190
Thr Arg Asp Asn Asp Trp Thr Cys Pro Asn Cys Gly Asn Val Asn Phe
195 200 205
Ser Phe Arg Thr Val Cys Asn Met Arg Lys Cys Asn Thr Pro Lys Pro
210 215 220
Gly Ser Gln Gln Gly Gly Ser Ser Asp Lys Ile Ser Lys Gln Asn Ala
225 230 235 240
Pro Glu Gly Ser Trp Lys Cys Asp Asn Cys Gly Asn Ile Asn Tyr Pro
245 250 255
Phe Arg Ser Lys Cys Asn Arg Gln Asn Cys Gly Ala Asp Lys Pro Gly
260 265 270
Asp Arg Ser Asn Gly Ser Pro Ser Arg Ala Pro Glu Glu Asn Asp Gln
275 280 285
Val Cys Lys Met Tyr Leu Cys Gly His Asn Cys Leu Leu Ile Lys Cys
290 295 300
Leu Pro Leu Lys Leu Val Asn Val Thr Thr Cys Val Asp Phe Met Pro
305 310 315 320
Cys Glu Ser Arg Gly Tyr Met Phe Met Lys Lys Leu Thr Pro Thr Thr
325 330 335
Phe

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..294

(D) OTHER INFORMATION: / Ceres Seq. ID 1566991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

Met Arg Asn Cys Thr Gln Pro Arg Pro Ala Asp His Asn Gly Lys Ser
1 5 10 15
Ala Pro Lys Pro Met Gln His Gln Gly Phe Ser Ser Pro Gly Ala
20 25 30
Tyr Leu Gly Ser Gly Gly Pro Pro Val Tyr Met Gly Gly Ser Pro
35 40 45
Tyr Gly Ser Pro Leu Phe Asn Gly Ser Ser Met Pro Pro Tyr Asp Val
50 55 60
Pro Phe Ser Gly Gly Ser Pro Tyr His Phe Asn Tyr Asn Ser Arg Met
65 70 75 80
Pro Ala Gly Ala His Tyr Arg Pro Leu His Met Ser Gly Pro Pro Pro
85 90 95
Tyr His Gly Gly Ser Met Met Gly Ser Gly Gly Met Tyr Gly Met Pro
100 105 110
Pro Pro Ile Asp Arg Tyr Gly Leu Gly Met Ala Met Gly Pro Gly Ser
115 120 125
Ala Ala Ala Met Met Pro Arg Pro Arg Phe Tyr Pro Asp Glu Lys Ser

130 135 140
Gln Lys Arg Asp Ser Thr Arg Asp Asn Asp Trp Thr Cys Pro Asn Cys
145 150 155 160
Gly Asn Val Asn Phe Ser Phe Arg Thr Val Cys Asn Met Arg Lys Cys
165 170 175
Asn Thr Pro Lys Pro Gly Ser Gln Gln Gly Gly Ser Ser Asp Lys Ile
180 185 190
Ser Lys Gln Asn Ala Pro Glu Gly Ser Trp Lys Cys Asp Asn Cys Gly
195 200 205
Asn Ile Asn Tyr Pro Phe Arg Ser Lys Cys Asn Arg Gln Asn Cys Gly
210 215 220
Ala Asp Lys Pro Gly Asp Arg Ser Asn Gly Ser Pro Ser Arg Ala Pro
225 230 235 240
Glu Glu Asn Asp Gln Val Cys Lys Met Tyr Leu Cys Gly His Asn Cys
245 250 255
Leu Leu Ile Lys Cys Leu Pro Leu Lys Leu Val Asn Val Thr Thr Cys
260 265 270
Val Asp Phe Met Pro Cys Glu Ser Arg Gly Tyr Met Phe Met Lys Lys
275 280 285
Leu Thr Pro Thr Thr Phe
290

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..274

(D) OTHER INFORMATION: / Ceres Seq. ID 1566992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

Met Gln His Gln Gln Gly Phe Ser Ser Pro Gly Ala Tyr Leu Gly Ser
1 5 10 15
Gly Gly Pro Pro Val Tyr Met Gly Gly Ser Pro Tyr Gly Ser Pro
20 25 30
Leu Phe Asn Gly Ser Ser Met Pro Pro Tyr Asp Val Pro Phe Ser Gly
35 40 45
Gly Ser Pro Tyr His Phe Asn Tyr Asn Ser Arg Met Pro Ala Gly Ala
50 55 60
His Tyr Arg Pro Leu His Met Ser Gly Pro Pro Tyr His Gly Gly
65 70 75 80
Ser Met Met Gly Ser Gly Gly Met Tyr Gly Met Pro Pro Pro Ile Asp
85 90 95
Arg Tyr Gly Leu Gly Met Ala Met Gly Pro Gly Ser Ala Ala Ala Met
100 105 110
Met Pro Arg Pro Arg Phe Tyr Pro Asp Glu Lys Ser Gln Lys Arg Asp
115 120 125
Ser Thr Arg Asp Asn Asp Trp Thr Cys Pro Asn Cys Gly Asn Val Asn
130 135 140
Phe Ser Phe Arg Thr Val Cys Asn Met Arg Lys Cys Asn Thr Pro Lys
145 150 155 160
Pro Gly Ser Gln Gln Gly Gly Ser Ser Asp Lys Ile Ser Lys Gln Asn
165 170 175
Ala Pro Glu Gly Ser Trp Lys Cys Asp Asn Cys Gly Asn Ile Asn Tyr
180 185 190
Pro Phe Arg Ser Lys Cys Asn Arg Gln Asn Cys Gly Ala Asp Lys Pro
195 200 205
Gly Asp Arg Ser Asn Gly Ser Pro Ser Arg Ala Pro Glu Gly Asn Asp
210 215 220

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Gln Val Cys Lys Met Tyr Leu Cys Gly His Asn Cys Leu Leu Ile Lys
225 230 235 240
Cys Leu Pro Leu Lys Leu Val Asn Val Thr Thr Cys Val Asp Phe Met
245 250 255
Pro Cys Glu Ser Arg Gly Tyr Met Phe Met Lys Lys Leu Thr Pro Thr
260 265 270
Thr Phe

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1717 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1717

(D) OTHER INFORMATION: / Ceres Seq. ID 1566993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

aaaaaaggct	tctctgtgtt	gttctctgtg	tgttctctgt	tggtcattct	tctttctttt	60
cacttctctt	tcttcttcgc	tcttctcttc	actgtcgggt	tcoattttgc	gcgaaaagtt	120
cttcaacttt	tccagctttt	ttttgttctc	tgacagtttt	ttttttgttt	ggtacaaaat	180
aaagatgcca	gtaagtgtgg	cactagtttt	gctgttgaca	ttgagcagtg	taattctgat	240
taatgggaga	agttacggcg	tcggaaacat	atgcgactgt	ggtcggagac	cgagcggagag	300
accacacagt	gtcaaaaatca	ctgatttttg	tgctgtggga	gatgggaaaa	cggtgaacac	360
acttgcgttt	caaaatgctg	tcttttatct	aaagtctttc	gctgataaag	gtggtgtgtca	420
gctttatgtt	cctccgggac	ggtggctcac	cggaagtttc	aacctcacca	gtcatctcac	480
tctctttctc	gagaaagacg	cgttcatact	tgcttcacag	gatccatcgc	attggcaagt	540
cacggatgcc	ttaccgtcat	atgggcgggg	tattgatcta	ccagggaaga	gatacatgat	600
tttgataaac	ggtagacatg	tacatgatgt	agtagtaaca	ggtagataac	gtaccataga	660
tgggcaaggc	cttgttttgt	gggactgggt	taattctcat	tctttagagt	acagtcgccc	720
tcacctgttc	gagtttgtct	ctgcgcaaaa	tgtcattgta	tcaaatctta	cattcttgaa	780
tgctccggct	tatactatcc	attcgtttta	ttgtcgcaat	ttatacatcc	atagagtaac	840
ggctaatact	tgtccagaat	ctccttatac	catcggattt	gtcccagatt	cttctgaaaa	900
tgtgtgtatc	caagaatcta	gtatcaacat	ggggatgat	gccattttct	ttaaaaagtg	960
tgtggatgaa	tacggtttat	cgatgcaaag	acctactgct	aatgtccaga	taagaaatgt	1020
ttaccctaga	gcagcttctg	gttcctccat	ttccttttgt	agtgaatagt	ctggttggtat	1080
atctgatgtt	gaggtcagtg	atgctcacat	acacaactgc	ttatccggga	ttgcctttag	1140
aaacacaaat	ggaagatgtg	gttatattaa	ggagattgat	atttccaaac	tccatattgt	1200
taatgttggt	actgcatttc	tagccaacgc	tagcttcggt	actcatccgg	atttctggtt	1260
cgatgaaagt	gcttaccocg	ttgtgagtca	catcagggtta	catgacattg	ttggagaaaa	1320
cataagcact	gctggaattt	tctttggaac	gaaagagtct	ctttcaactt	cgatttttgt	1380
atcgaaatca	tctctgtcga	ttaaaaactc	ggcttctcct	gctgattctt	ggcaatgctc	1440
atatgttgac	gggtcttcgg	aattcgtagt	ccctgaacgc	tgcttgagtc	tgaagagttt	1500
tgatagttac	tatggtagag	ctgaggccct	atgaaaccaa	acttcattag	gaatgatgat	1560
tcataatttt	taaagagaga	gcaaatgggt	ctgattcttt	tctttccccc	aaaaataaac	1620
cacagttgtg	agaatttata	ctgttcctct	gttggtgttg	ttgtccctgt	tatttgacag	1680
ttgtgagatt	aatatattct	gtacagggtc	atttctt			

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..510

(D) OTHER INFORMATION: / Ceres Seq. ID 1566994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

Lys	Lys	Ala	Ser	Leu	Cys	Cys	Ser	Leu	Cys	Cys	Ser	Leu	Trp	Ser	Phe
1				5					10					15	
Phe	Phe	Leu	Phe	Thr	Ser	Ser	Ser	Ser	Ser	Leu	Phe	Phe	Ser	Leu	Ser
		20						25					30		
Gly	Ser	Ile	Trp	Arg	Glu	Lys	Phe	Phe	Thr	Phe	Ser	Ser	Ser	Phe	Leu
		35					40					45			
Phe	Ser	Asp	Ser	Phe	Phe	Phe	Val	Trp	Leu	Gln	Ile	Lys	Met	Pro	Val
	50					55				60					
Ser	Val	Ala	Leu	Val	Leu	Leu	Leu	Thr	Leu	Ser	Ser	Val	Ile	Leu	Ile
65					70				75					80	
Asn	Gly	Arg	Ser	Tyr	Gly	Val	Gly	Asn	Ile	Cys	Asp	Arg	Gly	Arg	Arg
			85						90				95		
Pro	Ser	Glu	Arg	Pro	His	Ser	Val	Lys	Ile	Thr	Asp	Phe	Gly	Ala	Val
			100					105					110		
Gly	Asp	Gly	Lys	Thr	Leu	Asn	Thr	Leu	Ala	Phe	Gln	Asn	Ala	Val	Phe
		115					120					125			
Tyr	Leu	Lys	Ser	Phe	Ala	Asp	Lys	Gly	Gly	Ala	Gln	Leu	Tyr	Val	Pro
	130					135					140				
Pro	Gly	Arg	Trp	Leu	Thr	Gly	Ser	Phe	Asn	Leu	Thr	Ser	His	Leu	Thr
145					150				155					160	
Leu	Phe	Leu	Glu	Lys	Asp	Ala	Val	Ile	Leu	Ala	Ser	Gln	Asp	Pro	Ser
			165					170						175	
His	Trp	Gln	Val	Thr	Asp	Ala	Leu	Pro	Ser	Tyr	Gly	Arg	Gly	Ile	Asp
		180						185					190		
Leu	Pro	Gly	Lys	Arg	Tyr	Met	Ser	Leu	Ile	Asn	Gly	Asp	Met	Leu	His
	195					200						205			
Asp	Val	Val	Val	Thr	Gly	Asp	Asn	Gly	Thr	Ile	Asp	Gly	Gln	Gly	Leu
	210					215					220				
Val	Trp	Trp	Asp	Arg	Phe	Asn	Ser	His	Ser	Leu	Glu	Tyr	Ser	Arg	Pro
225					230				235					240	
His	Leu	Val	Glu	Phe	Val	Ser	Ala	Glu	Asn	Val	Ile	Val	Ser	Asn	Leu
			245					250						255	
Thr	Phe	Leu	Asn	Ala	Pro	Ala	Tyr	Thr	Ile	His	Ser	Val	Tyr	Cys	Arg
		260						265					270		
Asn	Leu	Tyr	Ile	His	Arg	Val	Thr	Ala	Asn	Thr	Cys	Pro	Glu	Ser	Pro
	275						280					285			
Tyr	Thr	Ile	Gly	Ile	Val	Pro	Asp	Ser	Ser	Glu	Asn	Val	Cys	Ile	Gln
	290					295					300				
Glu	Ser	Ser	Ile	Asn	Met	Gly	Tyr	Asp	Ala	Ile	Ser	Leu	Lys	Ser	Gly
	305				310				315					320	
Trp	Asp	Glu	Tyr	Gly	Leu	Ser	Tyr	Ala	Arg	Pro	Thr	Ala	Asn	Val	Gln
			325						330					335	
Ile	Arg	Asn	Val	Tyr	Leu	Arg	Ala	Ala	Ser	Gly	Ser	Ser	Ile	Ser	Phe
		340						345					350		
Gly	Ser	Glu	Met	Ser	Gly	Gly	Ile	Ser	Asp	Val	Glu	Val	Ser	Asp	Ala
		355					360					365			
His	Ile	His	Asn	Ser	Leu	Ser	Gly	Ile	Ala	Phe	Arg	Thr	Thr	Asn	Gly
	370					375					380				
Arg	Cys	Gly	Tyr	Ile	Lys	Glu	Ile	Asp	Ile	Ser	Asn	Ile	His	Met	Val
385					390				395					400	
Asn	Val	Gly	Thr	Ala	Phe	Leu	Ala	Asn	Gly	Ser	Phe	Gly	Thr	His	Pro
			405						410					415	
Asp	Ser	Gly	Phe	Asp	Glu	Asn	Ala	Tyr	Pro	Leu	Val	Ser	His	Ile	Arg
		420						425					430		
Leu	His	Asp	Ile	Val	Gly	Glu	Asn	Ile	Ser	Thr	Ala	Gly	Tyr	Phe	Phe
	435						440					445			
Gly	Thr	Lys	Glu	Ser	Pro	Phe	Thr	Ser	Ile	Leu	Leu	Ser	Asn	Ile	Ser
	450					455					460				
Leu	Ser	Ile	Lys	Asn	Ser	Ala	Ser	Pro	Ala	Asp	Ser	Trp	Gln	Cys	Ser
465					470				475					480	
Tyr	Val	Asp	Gly	Ser	Ser	Glu	Phe	Val	Val	Pro	Glu	Pro	Cys	Leu	Glu

(2) INFORMATION FOR SEQ ID NO:454:

(1) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

1	Met	Pro	Val	Ser	Val	Ala	Leu	Val	Leu	Leu	Leu	Thr	Leu	Ser	Ser	Val
Ile	Leu	Ile	Asn	5	Gly	Arg	Ser	Tyr	Gly	10	Val	Gly	Asn	Ile	15	Val
			20					25				30				
Gly	Arg	Arg	Pro	Ser	Glu	Arg	Pro	His	Ser	Val	Lys	Ile	Thr	Asp	Phe	
Gly	Ala	Val	Gly	Asp	Gly	Lys	Thr	Leu	Asn	Thr	Leu	Ala	Phe	Gln	Asn	
Ala	Val	Phe	Tyr	Leu	Lys	70	Ser	Phe	Ala	Asp	Lys	Gly	Gly	Ala	Gln	Leu
65										75						80
Tyr	Val	Pro	Pro	Gly	Arg	Trp	Leu	Thr	Gly	Ser	Phe	Asn	Leu	Thr	Ser	
His	Leu	Thr	Leu	Phe	Leu	Glu	Lys	Asp	Ala	Val	Ile	Leu	Ala	Ser	Gln	
Asp	Pro	Ser	His	Trp	Gln	Val	Thr	Asp	Ala	Leu	Pro	Ser	Tyr	Gly	Arg	
Gly	Ile	Asp	Leu	Pro	Gly	Lys	Arg	Tyr	Met	Ser	Leu	Ile	Asn	Gly	Asp	
Met	Leu	His	Asp	Val	Val	Val	Thr	Gly	Asp	Asn	Gly	Thr	Ile	Asp	Gly	160
145										155						160
Gln	Gly	Leu	Val	Trp	Trp	Asp	Arg	Phe	Asn	Ser	His	Ser	Leu	Glu	Tyr	
Ser	Arg	Pro	His	Leu	Val	Glu	Phe	Val	Ser	Ala	Glu	Asn	Val	Ile	Val	
Ser	Asn	Leu	Thr	Phe	Leu	Asn	Ala	Pro	Ala	Tyr	Thr	Ile	His	Ser	Val	
Tyr	Cys	Arg	Asn	Leu	Tyr	Ile	His	Arg	Val	Thr	Ala	Asn	Thr	Cys	Pro	
Ser	Asn	Leu	Thr	Phe	Leu	Asn	Ala	Pro	Ala	Tyr	Thr	Ile	His	Ser	Val	
Tyr	Cys	Arg	Asn	Leu	Tyr	Ile	His	Arg	Val	Thr	Ala	Asn	Thr	Cys	Pro	
Glu	Ser	Pro	Tyr	Thr	Ile	Gly	Ile	Val	Pro	Asp	Ser	Ser	Glu	Asn	Val	
225	Cys	Ile	Gln	Glu	Ser	Ser	Ile	Asn	Met	Gly	Tyr	Asp	Ala	Ile	Ser	Leu
Glu	Ser	Pro	Tyr	Thr	Ile	Gly	Ile	Val	Pro	Asp	Ser	Ser	Glu	Asn	Val	
225	Cys	Ile	Gln	Glu	Ser	Ser	Ile	Asn	Met	Gly	Tyr	Asp	Ala	Ile	Ser	Leu
Lys	Ser	Gly	Trp	Asp	Glu	Tyr	Gly	Leu	Ser	Tyr	Ala	Arg	Pro	Thr	Ala	
Asn	Val	Gln	Ile	Arg	Asn	Val	Tyr	Leu	Arg	Ala	Ala	Ser	Gly	Ser	Ser	
Ile	Ser	Phe	Gly	Ser	Glu	Met	Ser	Gly	Gly	Ile	Ser	Asp	Val	Glu	Val	
Ser	Asp	Ala	His	Ile	His	Asn	Ser	Leu	Ser	Gly	Ile	Ala	Phe	Arg	Thr	
Thr	Asn	Gly	Arg	Cys	Gly	Tyr	Ile	Lys	Glu	Ile	Asp	Ile	Ser	Asn	Ile	

His	Ile	Arg	Leu	His	Asp	Ile	Val	Gly	Glu	Asn	Ile	Ser	Thr	Ala	Gly	
	370				375					380						
Tyr	Phe	Phe	Gly	Thr	Lys	Glu	Ser	Pro	Phe	Thr	Ser	Ile	Leu	Leu	Ser	
	385				390					395					400	
Asn	Ile	Ser	Leu	Ser	Ile	Lys	Asn	Ser	Ala	Ser	Pro	Ala	Asp	Ser	Trp	
			405						410						415	
Gln	Cys	Ser	Tyr	Val	Asp	Gly	Ser	Ser	Glu	Phe	Val	Val	Pro	Glu	Pro	
			420						425						430	
Cys	Leu	Glu	Leu	Lys	Ser	Phe	Asp	Ser	Tyr	Tyr	Gly	Arg	Ala	Glu	Ala	
		435					440								445	
Leu																

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

Met	Ser	Leu	Ile	Asn	Gly	Asp	Met	Leu	His	Asp	Val	Val	Thr	Gly	
1				5				10					15		
Asp	Asn	Gly	Thr	Ile	Asp	Gly	Gln	Gly	Leu	Val	Trp	Trp	Asp	Arg	Phe
			20					25					30		
Asn	Ser	His	Ser	Leu	Glu	Tyr	Ser	Arg	Pro	His	Leu	Val	Glu	Phe	Val
			35				40						45		
Ser	Ala	Glu	Asn	Val	Ile	Val	Ser	Asn	Leu	Thr	Phe	Leu	Asn	Ala	Pro
			50				55				60				
Ala	Tyr	Thr	Ile	His	Ser	Val	Tyr	Cys	Arg	Asn	Leu	Tyr	Ile	His	Arg
			65				70				75				80
Val	Thr	Ala	Asn	Thr	Cys	Pro	Glu	Ser	Pro	Tyr	Thr	Ile	Gly	Ile	Val
				85						90				95	
Pro	Asp	Ser	Ser	Glu	Asn	Val	Cys	Ile	Gln	Glu	Ser	Ser	Ile	Asn	Met
			100					105						110	
Gly	Tyr	Asp	Ala	Ile	Ser	Leu	Lys	Ser	Gly	Trp	Asp	Glu	Tyr	Gly	Leu
			115				120						125		
Ser	Tyr	Ala	Arg	Pro	Thr	Ala	Asn	Val	Gln	Ile	Arg	Asn	Val	Tyr	Leu
			130				135					140			
Arg	Ala	Ala	Ser	Gly	Ser	Ser	Ile	Ser	Phe	Gly	Ser	Glu	Met	Ser	Gly
				145			150			155					160
Gly	Ile	Ser	Asp	Val	Glu	Val	Ser	Asp	Ala	His	Ile	His	Asn	Ser	Leu
				165					170					175	
Ser	Gly	Ile	Ala	Phe	Arg	Thr	Thr	Asn	Gly	Arg	Cys	Gly	Tyr	Ile	Lys
			180					185						190	
Glu	Ile	Asp	Ile	Ser	Asn	Ile	His	Met	Val	Asn	Val	Gly	Thr	Ala	Phe
			195				200						205		
Leu	Ala	Asn	Gly	Ser	Phe	Gly	Thr	His	Pro	Asp	Ser	Gly	Phe	Asp	Glu
			210				215						220		
Asn	Ala	Tyr	Pro	Leu	Val	Ser	His	Ile	Arg	Leu	His	Asp	Ile	Val	Gly
			225				230				235				240
Glu	Asn	Ile	Ser	Thr	Ala	Gly	Tyr	Phe	Phe	Gly	Thr	Lys	Glu	Ser	Pro
				245					250					255	
Phe	Thr	Ser	Ile	Leu	Leu	Ser	Asn	Ile	Ser	Leu	Ser	Ile	Lys	Asn	Ser
			260					265						270	
Ala	Ser	Pro	Ala	Asp	Ser	Trp	Gln	Cys	Ser	Tyr	Val	Asp	Gly	Ser	Ser
			275				280						285		
Glu	Phe	Val	Val	Pro	Glu	Pro	Cys	Leu	Glu	Leu	Lys	Ser	Phe	Asp	Ser

290
Tyr Tyr Gly Arg Ala Glu Ala Leu
305 310

295

300

(2) INFORMATION FOR SEQ ID NO:456:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 719 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..719
(D) OTHER INFORMATION: / Ceres Seq. ID 1567007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

cttttcgcgt	ggtcgaccaa	acctaaaaacc	ccccaaaaaga	gaaaaatcaa	agaccattcg	60
ctatttcgct	cgctactcag	ttgcagaaga	agatgccgac	actcacaaag	ctttattcca	120
tggaagaagc	cgcaactcac	aacaagcaag	atgactgctg	ggctgcctac	gacggcaagg	180
tctatgatgt	atcctcttat	atggatgagc	atcctggagg	agatgatgtg	cttcttgctg	240
tcgcaggcaa	agatgcaacg	gatgattttg	aagacgcagg	gcacagcaaa	gatgctaggg	300
aacttatgga	gaagtatttt	attggcgagc	tagatgaatc	ttctttaccg	gaaataacctg	360
agcttaagat	ctacaagaag	gaccagccac	aagactctgt	tcagaagcgt	tttgacttga	420
caaacgcagta	ttggggtggt	cctgtctcca	ttatcccat	ctctgtagcg	gttagtgtct	480
tgttctctcg	caagacttaa	taagttagtag	tctcttctct	accttgatat	gctctgggat	540
attgaattac	ttggggaatc	aactttacac	ccccattata	gattttttga	ataacagata	600
tgatagagag	ataattgtta	tttttcatt	ttatcagatt	ttgagttgag	atcatgtttc	660
ataacactta	ttactcgata	tgattatatc	atgattaatg	gatggtttgg	tttgctggcg	

(2) INFORMATION FOR SEQ ID NO:457:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..110
(D) OTHER INFORMATION: / Ceres Seq. ID 1567008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

Leu	Phe	Ala	Trp	Ser	Thr	Lys	Pro	Lys	Thr	Pro	Lys	Lys	Arg	Lys	Ile	
1			5					10					15			
Lys	Asp	His	Ser	Leu	Phe	Arg	Ser	Leu	Leu	Ser	Cys	Arg	Arg	Arg	Cys	
			20					25					30			
Arg	His	Ser	Gln	Ser	Phe	Ile	Pro	Trp	Lys	Lys	Pro	Gln	Leu	Thr	Thr	
			35				40					45				
Ser	Lys	Met	Thr	Ala	Gly	Ser	Ser	Ser	Thr	Ala	Arg	Ser	Met	Met	Tyr	
			50				55					60				
Pro	Leu	Ile	Trp	Met	Ser	Ile	Leu	Glu	Glu	Met	Met	Cys	Phe	Leu	Leu	
			65				70			75				80		
Ser	Gln	Ala	Lys	Met	Gln	Arg	Met	Ile	Leu	Lys	Thr	Gln	Gly	Thr	Ala	
			85					90					95			
Lys	Met	Leu	Gly	Asn	Leu	Trp	Arg	Ser	Ile	Leu	Leu	Ala	Ser			
			100				105					110				

(2) INFORMATION FOR SEQ ID NO:458:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..135
(D) OTHER INFORMATION: / Ceres Seq. ID 1567009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

Met Pro Thr Leu Thr Lys Leu Tyr Ser Met Glu Glu Ala Ala Thr His
1 5 10 15
Asn Lys Gln Asp Asp Cys Trp Val Val Ile Asp Gly Lys Val Tyr Asp
20 25 30
Val Ser Ser Tyr Met Asp Glu His Pro Gly Gly Asp Asp Val Leu Leu
35 40 45
Ala Val Ala Gly Lys Asp Ala Thr Asp Asp Phe Glu Asp Ala Gly His
50 55 60
Ser Lys Asp Ala Arg Glu Leu Met Glu Lys Tyr Phe Ile Gly Glu Leu
65 70 75 80
Asp Glu Ser Ser Leu Pro Glu Ile Pro Glu Leu Lys Ile Tyr Lys Lys
85 90 95
Asp Gln Pro Gln Asp Ser Val Gln Lys Leu Phe Asp Leu Thr Lys Gln
100 105 110
Tyr Trp Val Val Pro Val Ser Ile Ile Thr Ile Ser Val Ala Val Ser
115 120 125
Val Leu Phe Ser Arg Lys Thr
130 135

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..126
(D) OTHER INFORMATION: / Ceres Seq. ID 1567010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

Met Glu Glu Ala Ala Thr His Asn Lys Gln Asp Asp Cys Trp Val Val
1 5 10 15
Ile Asp Gly Lys Val Tyr Asp Val Ser Ser Tyr Met Asp Glu His Pro
20 25 30
Gly Gly Asp Asp Val Leu Leu Ala Val Ala Gly Lys Asp Ala Thr Asp
35 40 45
Asp Phe Glu Asp Ala Gly His Ser Lys Asp Ala Arg Glu Leu Met Glu
50 55 60
Lys Tyr Phe Ile Gly Glu Leu Asp Glu Ser Ser Leu Pro Glu Ile Pro
65 70 75 80
Glu Leu Lys Ile Tyr Lys Lys Asp Gln Pro Gln Asp Ser Val Gln Lys
85 90 95
Leu Phe Asp Leu Thr Lys Gln Tyr Trp Val Val Pro Val Ser Ile Ile
100 105 110
Thr Ile Ser Val Ala Val Ser Val Leu Phe Ser Arg Lys Thr
115 120 125

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1124
(D) OTHER INFORMATION: / Ceres Seq. ID 1567015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

acgacggaga	gaaaacgtct	tccaaagacg	aattgagcgc	gtggaagaag	aaaaaaaaa	60
atcaaaatcc	aatttgtatc	tcaaagtagt	gaagaagaag	gagaagcaat	cgaattctc	120
tgacgatgtt	gttacaaccc	caaagatcct	cttatcgatt	atcgtaattc	gtagaaaaag	180
aagcagagag	aaaatggggg	gcgaagatga	taaagataag	aaatgggaatc	ctccaccacc	240
gcagcagaag	coggactcaa	ggccttggga	agtctctcgc	gcttttgtaa	tctgcgcaac	300
cgctactact	tctgcgcttc	atcagctcgc	aagaaatctt	gattgggtct	ataccagcat	360
aactagaaca	cogtggcgcg	gaagaggaac	tttccgaaca	tcttttcagg	cgaagcatg	420
gagaagggtac	aacaaacgga	tgcaagagga	gtatgaggat	gaattggaga	gagtggcacg	480
tattaggcgt	atgcaaacgc	tttccaacag	agagagggaat	aaatttagaa	ggggctacga	540
gaactggacg	gaaaatgatc	ctgGtgacac	gcaataccat	cagcagtttc	agcgcacatg	600
ttggtactcg	aaaactgagt	cttcgcakag	aaaccaaagg	accaatcacc	aggagccttc	660
agaccagaga	agagtatatc	cactatcaca	ccattactct	gttttagggc	tcagcaggtc	720
cccgacaact	ccatacacag	aagctgagat	taagaaagca	ttcagggaaa	aggctttgga	780
attccatcca	gaccaaatac	aggataacaa	aattgtagct	gaagcaaaat	tcaaaagaggt	840
gttactttca	tatgaagcta	taaaacagga	aataaaaagg	aagtgtatct	ttttggtaag	900
cgagatcaat	ctctttttcca	tgcgctctaa	agaaattgga	atattgtcta	caatatcgat	960
caacaggtttt	tttgggtgtc	ttcccatctt	ataagtttat	tttaaatgct	tttgtgtttg	1020
ctttttttac	tcagtttaag	ttctttgttg	taatatgtaa	taaaaccaat	ccacagctta	1080
aatatgttga	agagagagaat	ttgggacaga	tggtccattg	attc		

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..294

(D) OTHER INFORMATION: / Ceres Seq. ID 1567016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

Arg	Arg	Arg	Glu	Asn	Val	Phe	Gln	Arg	Arg	Ile	Glu	Ala	Val	Glu	Glu
1			5						10				15		
Glu	Lys	Lys	Lys	Ser	Lys	Ser	Asn	Leu	Ile	Phe	Lys	Val	Val	Lys	Lys
			20					25				30			
Glu	Glu	Lys	Gln	Ser	Lys	Phe	Ser	Asp	Asp	Val	Val	Thr	Thr	Pro	Lys
			35				40				45				
Ile	Leu	Leu	Ser	Ile	Ile	Val	Ile	Arg	Arg	Lys	Arg	Ser	Arg	Glu	Lys
			50			55					60				
Met	Gly	Gly	Glu	Asp	Asp	Lys	Asp	Lys	Lys	Trp	Asn	Pro	Pro	Pro	Pro
65				70					75					80	
Gln	Gln	Lys	Pro	Asp	Ser	Arg	Pro	Trp	Glu	Val	Leu	Ala	Ala	Phe	Val
			85					90					95		
Ile	Cys	Ala	Thr	Ala	Thr	Thr	Phe	Ala	Val	His	Gln	Leu	Arg	Arg	Asn
			100					105					110		
Phe	Asp	Trp	Val	Tyr	Thr	Gln	Leu	Thr	Arg	Thr	Pro	Ser	Ala	Gly	Arg
			115					120				125			
Gly	Thr	Phe	Arg	Thr	Ser	Phe	Gln	Glu	Glu	Ala	Trp	Arg	Arg	Tyr	Asn
			130			135					140				
Lys	Arg	Met	Gln	Glu	Glu	Tyr	Glu	Asp	Glu	Leu	Glu	Arg	Val	Ala	Arg
145				150						155				160	
Ile	Arg	Arg	Met	Gln	Ser	Val	Phe	Asn	Arg	Glu	Arg	Asn	Lys	Phe	Arg
			165					170					175		
Arg	Gly	Tyr	Glu	Asn	Trp	Thr	Glu	Asn	Asp	Pro	Gly	Ala	Gln	Gln	Tyr
			180					185					190		
His	Gln	Gln	Phe	Gln	Arg	His	Asp	Trp	Tyr	Trp	Lys	Thr	Glu	Ser	Ser
			195				200					205			
Xaa	Arg	Asn	Gln	Arg	Thr	Asn	His	Gln	Glu	Pro	Ser	Asp	Gln	Arg	Arg
			210			215					220				
Val	Tyr	Pro	Leu	Ser	His	His	Tyr	Ser	Val	Leu	Gly	Leu	Ser	Arg	Ser

(2) INFORMATION FOR SEO ID NO:462:

(A) LENGTH: 230 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..230

(D) OTHER INFORMATION: / Ceres Seq. ID 1567017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

(2) INFORMATION FOR SEQ ID NO:464:

(A) LENGTH: 1518 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1518

(D) OTHER INFORMATION: / Ceres Seq. ID 1567045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..145
(D) OTHER INFORMATION: / Ceres Seq. ID 1567046
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

Met	Gly	His	Ala	Thr	Ser	Leu	Ser	His	Phe	Leu	Ile	Leu	Ser	Ser	Ser	
1				5					10					15		
Arg	Phe	Ser	Arg	Leu	Gly	Ser	Leu	Thr	Arg	Leu	Leu	Ser	Lys	Pro	Thr	
			20					25					30			
Ser	Leu	Ser	Gly	Ser	Leu	Ser	Ser	Ile	Ser	Val	Thr	Gly	Gln	Gly	Phe	
			35					40				45				
Arg	Cys	Cys	Cys	Ser	Ala	Ala	Thr	Asp	Asp	Thr	Ser	Pro	Ser	Val	Lys	
	50					55					60					
Lys	Arg	Val	Val	Ser	Gly	Val	Gln	Pro	Thr	Gly	Ser	Ile	His	Leu	Gly	
65					70					75					80	
Asn	Tyr	Leu	Gly	Ala	Ile	Lys	Asn	Trp	Val	Ala	Phe	Gln	Asp	Thr	Tyr	
				85					90				95			
Glu	Thr	Leu	Phe	Ile	Ile	Val	Asp	His	His	Ala	Ile	Thr	Leu	Pro	Tyr	
			100					105					110			
Asp	Thr	Arg	Gln	Leu	Gly	Lys	Ala	Thr	Thr	Asp	Thr	Ala	Ala	Leu	Tyr	
			115				120					125				
Leu	Ala	Cys	Glu	Asn	Asp	Ser	Val	Gln	Arg	Glu	Ile	Thr	Gln	Gly	Gly	
			130			135					140					

Gly
145

(2) INFORMATION FOR SEQ ID NO:466:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..148
(D) OTHER INFORMATION: / Ceres Seq. ID 1567047
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

Met	Ser	Leu	Thr	Asp	Gly	Leu	Ser	Lys	Met	Ser	Lys	Ser	Ala	Pro	Ser	
1				5					10				15			
Asp	Gln	Ser	Arg	Ile	Asn	Leu	Leu	Asp	Ser	Lys	Asp	Leu	Ile	Val	Asp	
			20					25					30			
Lys	Ile	Lys	Arg	Cys	Lys	Thr	Asp	Ser	Phe	Ala	Gly	Leu	Glu	Phe	Asp	
			35				40					45				
Asn	Ala	Glu	Arg	Pro	Glu	Cys	Asn	Asn	Leu	Leu	Ser	Ile	Tyr	Gln	Ile	
	50					55					60					
Val	Ser	Gly	Lys	Thr	Lys	Glu	Glu	Val	Val	Glu	Glu	Cys	Lys	Asp	Met	
65					70					75					80	
Ser	Trp	Gly	Thr	Phe	Lys	Pro	Leu	Leu	Ala	Asp	Ala	Leu	Ile	Asp	His	
			85					90					95			
Leu	Ser	Pro	Ile	Gln	Val	Arg	Tyr	Gln	Glu	Ile	Ile	Ala	Glu	Pro	Glu	
			100				105					110				
Tyr	Leu	Asp	Lys	Ile	Leu	Ser	Glu	Gly	Ala	Asp	Arg	Ala	Glu	Glu	Leu	
			115				120					125				
Gly	Ala	Val	Thr	Met	Arg	Asn	Met	Tyr	Gln	Ala	Met	Gly	Tyr	Tyr	Gln	
			130			135						140				

Arg Arg Arg Tyr

145

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1567048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

Met	Ser	Lys	Ser	Ala	Pro	Ser	Asp	Gln	Ser	Arg	Ile	Asn	Leu	Leu	Asp
1				5					10					15	
Ser	Lys	Asp	Leu	Ile	Val	Asp	Lys	Ile	Lys	Arg	Cys	Lys	Thr	Asp	Ser
			20					25					30		
Phe	Ala	Gly	Leu	Glu	Phe	Asp	Asn	Ala	Glu	Arg	Pro	Glu	Cys	Asn	Asn
			35				40					45			
Leu	Leu	Ser	Ile	Tyr	Gln	Ile	Val	Ser	Gly	Lys	Thr	Lys	Glu	Glu	Val
			50			55					60				
Val	Glu	Glu	Cys	Lys	Asp	Met	Ser	Trp	Gly	Thr	Phe	Lys	Pro	Leu	Leu
65				70					75					80	
Ala	Asp	Ala	Leu	Ile	Asp	His	Leu	Ser	Pro	Ile	Gln	Val	Arg	Tyr	Gln
			85						90					95	
Glu	Ile	Ile	Ala	Glu	Pro	Glu	Tyr	Leu	Asp	Lys	Ile	Leu	Ser	Glu	Gly
			100				105						110		
Ala	Asp	Arg	Ala	Glu	Glu	Leu	Gly	Ala	Val	Thr	Met	Arg	Asn	Met	Tyr
			115				120						125		
Gln	Ala	Met	Gly	Tyr	Tyr	Gln	Arg	Arg	Arg	Tyr					
			130				135								

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..465

(D) OTHER INFORMATION: / Ceres Seq. ID 1567082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

agaaatctaa	tgggattggt	gaggaagcta	cagaggaaga	gttgatggat	gcaacagctc	60
ttgtgtgattc	tactgtgtat	tttatatgtc	cacatactgg	tgttgcattg	acggcggtga	120
tgaagctgag	aaagtcagga	gttattggag	cgaatgatcg	gactgtgggtg	gtgagtagac	180
ctcatggatt	gaagtattaca	cagagtaaga	ttgattatca	ttctaagaac	ataaaggaga	240
tggcttgtag	attggcgaat	ccaccagtg	aggttaaggc	aaagtttggt	tcagttatgtg	300
atgttctcaa	ggagctattt	aagagcaatg	ataaataagc	tttgtgtgtt	tgttctctca	360
aagctcttca	cgctcatatg	tgatattgtt	ggctttgtta	ttagaggaag	taatgaaatt	420
tcgtttcttt	ggactgtgtg	aataaaaacg	ctggGttggt	tccgt		

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1567083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

Lys	Ser	Asn	Gly	Ile	Val	Glu	Glu	Ala	Thr	Glu	Glu	Glu	Leu	Met	Asp
1		5							10				15		
Ala	Thr	Ala	Leu	Ala	Asp	Ser	Thr	Gly	Met	Phe	Ile	Cys	Pro	His	Thr
		20						25				30			
Gly	Val	Ala	Leu	Thr	Ala	Leu	Met	Lys	Leu	Arg	Lys	Ser	Gly	Val	Ile
		35					40				45				
Gly	Ala	Asn	Asp	Arg	Thr	Val	Val	Val	Ser	Thr	Ala	His	Gly	Leu	Lys
		50				55					60				
Phe	Thr	Gln	Ser	Lys	Ile	Asp	Tyr	His	Ser	Lys	Asn	Ile	Lys	Glu	Met
		65				70				75				80	
Ala	Cys	Arg	Leu	Ala	Asn	Pro	Pro	Val	Lys	Val	Lys	Ala	Lys	Phe	Gly
			85						90					95	
Ser	Val	Met	Asp	Val	Leu	Lys	Glu	Tyr	Leu	Lys	Ser	Asn	Asp	Lys	
			100					105						110	

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1567084

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

Met	Asp	Ala	Thr	Ala	Leu	Ala	Asp	Ser	Thr	Gly	Met	Phe	Ile	Cys	Pro
1		5							10					15	
His	Thr	Gly	Val	Ala	Leu	Thr	Ala	Leu	Met	Lys	Leu	Arg	Lys	Ser	Gly
		20					25					30			
Val	Ile	Gly	Ala	Asn	Asp	Arg	Thr	Val	Val	Val	Ser	Thr	Ala	His	Gly
		35					40				45				
Leu	Lys	Phe	Thr	Gln	Ser	Lys	Ile	Asp	Tyr	His	Ser	Lys	Asn	Ile	Lys
		50				55					60				
Glu	Met	Ala	Cys	Arg	Leu	Ala	Asn	Pro	Pro	Val	Lys	Val	Lys	Ala	Lys
		65				70				75				80	
Phe	Gly	Ser	Val	Met	Asp	Val	Leu	Lys	Glu	Tyr	Leu	Lys	Ser	Asn	Asp
			85						90					95	

Lys

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1567085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

Met	Phe	Ile	Cys	Pro	His	Thr	Gly	Val	Ala	Leu	Thr	Ala	Leu	Met	Lys
1			5							10				15	
Leu	Arg	Lys	Ser	Gly	Val	Ile	Gly	Ala	Asn	Asp	Arg	Thr	Val	Val	
			20				25					30			
Ser	Thr	Ala	His	Gly	Leu	Lys	Phe	Thr	Gln	Ser	Lys	Ile	Asp	Tyr	His
			35				40					45			

Ser Lys Asn Ile Lys Glu Met Ala Cys Arg Leu Ala Asn Pro Pro Val
50 55 60
Lys Val Lys Ala Lys Phe Gly Ser Val Met Asp Val Leu Lys Glu Tyr
65 70 75 80
Leu Lys Ser Asn Asp Lys
85

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1216
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

ccgtagGaaa	agaaaaagg	cggctgatga	agaagtgcga	aacagctgcg	acataaggcc	60
ctacaccttt	agttactcag	aactcagaca	tgcaactcaa	gattttgatc	cttccaacaa	120
gctttggggg	ggaggatttg	gacctgtttt	taagggaata	ctgaacgacg	gaagagagat	180
agccgtgaag	caattgtcag	tgtcatccag	gcaaggaaa	ggtaaatgtg	ttgcggagat	240
tgccactata	tcacctgttc	agcatcgcaa	ccttgtaaaa	ttgtatggat	gctgcattga	300
gggaaatcag	cgcgatgttg	tatatgaata	cctctcaaac	aagagcttag	atcaagctct	360
attcgaggaa	aagagtttgc	agcttggttg	gtcacagcgt	ttcgagatat	gcttggggagt	420
agcaaaaggt	ttagcatata	tgcatagaga	gtcaaatccc	cgtatagtag	atagggaagt	480
gaaggcaagc	aatattcttc	tggactcgga	tctggtcccc	aaactctcag	attttggggt	540
ggccaaacta	tatgatgata	agaagaccga	cataagtaac	cgagtgcag	ggacgatagg	600
atatctgtca	ccagagtagc	tgatgcttgg	acatctttac	gagaagacgg	atgtgtttgc	660
cttttgatata	gtggccttgc	aaattgtcag	cggaaggcct	aactcctctc	cagaattaga	720
tgatgacaaa	caataccctc	tcgaatgggc	atggagccca	caccaagagc	agcgtgatat	780
ggaagtagta	gcacggatc	tgacagaatt	tgacaaggaa	gaagtgaac	gtgtaatagg	840
agtagcgctt	ttgtgcacac	aaacagatca	tgcaatacga	ccaactatgt	cccagtggtg	900
aggtatgttg	accggtgatg	tggagataac	ggaagccaat	gccaagccag	ggtacgtctc	960
tgagagaaca	tttgagaatg	caatgagcct	catgagtgtg	tcaacgagct	cgagctggat	1020
attgactgaa	actccaaaag	attcttccaa	gtcccaagtg	gaagaacatg	gacgacgaca	1080
ttgaaacttg	aaaactttgt	gtttttctat	ttttttctct	tacataaaaa	aaaagaagtc	1140
aatatagaaa	tcgtttgttg	taaataacac	atatacatat	tcgtttgacc	aaaattggat	1200
ttgactgttt	ctcctcg					

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..360
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

Arg Arg Lys Arg Lys Arg Ala Ala Asp Glu Glu Val Leu Asn Ser Leu	
1 5 10 15	
His Ile Arg Pro Tyr Thr Phe Ser Tyr Ser Glu Leu Arg Thr Ala Thr	
20 25 30	
Gln Asp Phe Asp Pro Ser Asn Lys Leu Gly Glu Gly Phe Gly Pro	
35 40 45	
Val Phe Lys Gly Lys Leu Asn Asp Gly Arg Glu Ile Ala Val Lys Gln	
50 55 60	
Leu Ser Val Ala Ser Arg Gln Gly Lys Gly Gln Phe Val Ala Glu Ile	
65 70 75 80	

Ala Thr Ile Ser Pro Val Gln His Arg Asn Leu Val Lys Leu Tyr Gly
85 90 95
Cys Cys Ile Glu Gly Asn Gln Arg Met Leu Val Tyr Glu Tyr Leu Ser
100 105 110
Asn Lys Ser Leu Asp Gln Ala Leu Phe Glu Glu Lys Ser Leu Gln Leu
115 120 125
Gly Trp Ser Gln Arg Phe Glu Ile Cys Leu Gly Val Ala Lys Gly Leu
130 135 140
Ala Tyr Met His Glu Glu Ser Asn Pro Arg Ile Val His Arg Asp Val
145 150 155 160
Lys Ala Ser Asn Ile Leu Leu Asp Ser Asp Leu Val Pro Lys Leu Ser
165 170 175
Asp Phe Gly Leu Ala Lys Leu Tyr Asp Asp Lys Lys Thr His Ile Ser
180 185 190
Thr Arg Val Ala Gly Thr Ile Gly Tyr Leu Ser Pro Glu Tyr Val Met
195 200 205
Leu Gly His Leu Thr Glu Lys Thr Asp Val Phe Ala Phe Gly Ile Val
210 215 220
Ala Leu Glu Ile Val Ser Gly Arg Pro Asn Ser Ser Pro Glu Leu Asp
225 230 235 240
Asp Asp Lys Gln Tyr Leu Leu Glu Trp Ala Trp Ser Leu His Gln Glu
245 250 255
Gln Arg Asp Met Glu Val Val Asp Pro Asp Leu Thr Glu Phe Asp Lys
260 265 270
Glu Glu Val Lys Arg Val Ile Gly Val Ala Phe Leu Cys Thr Gln Thr
275 280 285
Asp His Ala Ile Arg Pro Thr Met Ser Arg Val Val Gly Met Leu Thr
290 295 300
Gly Asp Val Glu Ile Thr Glu Ala Asn Ala Lys Pro Gly Tyr Val Ser
305 310 315 320
Glu Arg Thr Phe Glu Asn Ala Met Ser Phe Met Ser Gly Ser Thr Ser
325 330 335
Ser Ser Trp Ile Leu Pro Glu Thr Pro Lys Asp Ser Ser Lys Ser Gln
340 345 350
Val Glu Glu His Gly Arg Arg His
355 360

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..256
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

Met Leu Val Tyr Glu Tyr Leu Ser Asn Lys Ser Leu Asp Gln Ala Leu
1 5 10 15
Phe Glu Glu Lys Ser Leu Gln Leu Gly Trp Ser Gln Arg Phe Glu Ile
20 25 30
Cys Leu Gly Val Ala Lys Gly Leu Ala Tyr Met His Glu Glu Ser Asn
35 40 45
Pro Arg Ile Val His Arg Asp Val Lys Ala Ser Asn Ile Leu Leu Asp
50 55 60
Ser Asp Leu Val Pro Lys Leu Ser Asp Phe Gly Leu Ala Lys Leu Tyr
65 70 75 80
Asp Asp Lys Lys Thr His Ile Ser Thr Arg Val Ala Gly Thr Ile Gly
85 90 95
Tyr Leu Ser Pro Glu Tyr Val Met Leu Gly His Leu Thr Glu Lys Thr

100	105	110
Asp Val Phe Ala Phe Gly Ile Val Ala Leu Glu Ile Val Ser Gly Arg		
115	120	125
Pro Asn Ser Ser Pro Glu Leu Asp Asp Lys Gln Tyr Leu Leu Glu		
130	135	140
Trp Ala Trp Ser Leu His Gln Glu Gln Arg Asp Met Glu Val Val Asp		
145	150	155
Pro Asp Leu Thr Glu Phe Asp Lys Glu Glu Val Lys Arg Val Ile Gly		
165	170	175
Val Ala Phe Leu Cys Thr Gln Thr Asp His Ala Ile Arg Pro Thr Met		
180	185	190
Ser Arg Val Val Gly Met Leu Thr Gly Asp Val Glu Ile Thr Glu Ala		
195	200	205
Asn Ala Lys Pro Gly Tyr Val Ser Glu Arg Thr Phe Glu Asn Ala Met		
210	215	220
Ser Phe Met Ser Gly Ser Thr Ser Ser Ser Trp Ile Leu Pro Glu Thr		
225	230	235
Pro Lys Asp Ser Ser Lys Ser Gln Val Glu Glu His Gly Arg Arg His		
245	250	255

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1567091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

Met His Glu Glu Ser Asn Pro Arg Ile Val His Arg Asp Val Lys Ala	
1	5
Ser Asn Ile Leu Leu Asp Ser Asp Leu Val Pro Lys Leu Ser Asp Phe	
20	25
Gly Leu Ala Lys Leu Tyr Asp Asp Lys Lys Thr His Ile Ser Thr Arg	
35	40
Val Ala Gly Thr Ile Gly Tyr Leu Ser Pro Glu Tyr Val Met Leu Gly	
50	55
His Leu Thr Glu Lys Thr Asp Val Phe Ala Phe Gly Ile Val Ala Leu	
65	70
Glu Ile Val Ser Gly Arg Pro Asn Ser Ser Pro Glu Leu Asp Asp Asp	
85	90
Lys Gln Tyr Leu Leu Glu Trp Ala Trp Ser Leu His Gln Glu Gln Arg	
100	105
Asp Met Glu Val Val Asp Pro Asp Leu Thr Glu Phe Asp Lys Glu Glu	
115	120
Val Lys Arg Val Ile Gly Val Ala Phe Leu Cys Thr Gln Thr Asp His	
130	135
Ala Ile Arg Pro Thr Met Ser Arg Val Val Gly Met Leu Thr Gly Asp	
145	150
Val Glu Ile Thr Glu Ala Asn Ala Lys Pro Gly Tyr Val Ser Glu Arg	
165	170
Thr Phe Glu Asn Ala Met Ser Phe Met Ser Gly Ser Thr Ser Ser	
180	185
Trp Ile Leu Pro Glu Thr Pro Lys Asp Ser Ser Lys Ser Gln Val Glu	
195	200
Glu His Gly Arg Arg His	
210	

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1192
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

```
aaaatctctc gctctgttac gccattttcg tgagtgaagaa gaagaaaccc taagagtctc 60
tcccacaaac ctcaaaccat ggccagggga ctcgattga agggcattat gcgcgccacc 120
accgacattg tcacgggccat ggctacgccc atcgacaatt cgcacatcat cgtcacacgg 180
tcgctgacaa aatcaatcat cctctggaaa ctcacaaagg acgagaagtc ttacgggtgt 240
gctcagcgta ggctcacagg tcactctcac ttctgtggaag atgttgtctt ctcactcgga 300
ggtcagtttg cactctccgg aagttgggac ggtgagctcc gtctctggga tctcgccacg 360
ggagaaacaa ctcgctgatt cgttggtcac acgaaagatg tgctctctgt tgccttctct 420
actgataacc gtcagatcgt gtctgcttct cgtgatcgta cgattaagct ttggaacaca 480
cttggtgagt gcaagtatac catctctgaa ggtgatggtc acaaggaaatg ggtagttgt 540
gttaggttta gtcctaatac tcttgtacca actattgtat ctgcttcttg ggataaaaat 600
gtgaaagtgt ggaatctcca gaactgtaag ctgaggaact ctcttggttg tcaactctgt 660
tacctcaaca ctgttgtgtg ctgcctgatg ggttcgctat gcgccagtag tgggaaagat 720
gggtgtatct tggtgtggga tttggctgaa ggaagaagac ttactcgtct tgaggctgtg 780
tcgattatct acNtcgcttt gcttcagctc taacagatag tggttgtgtg ctgctactga 840
gaatagcatt aggatttggt atcttgagag caagtctgtt gttgaggact tgaaggttga 900
tctcaagctt gaggcagaga agaatagaag ttggtgttga actggttaac agaagaaggt 960
tatctactgc acaagcttga actggagtcg agatggaagc acattgttca gtggttacac 1020
tgatggagtt gtcagggtct ggggtatttg tcgttactag agatcacac aagatgaaga 1080
agaagtcaacg aaatctccgg aaaaaagtag ctgcttttaa tttttccaga Ctgcgtcagt 1140
attgtattag tctctcgcaa acctctattt tggcaatttt tgtttaattt cc
```

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..244
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

```
Met Ala Glu Gly Leu Val Leu Lys Gly Ile Met Arg Ala His Thr Asp
1 5 10 15
Ile Val Thr Ala Ile Ala Thr Pro Ile Asp Asn Ser Asp Ile Ile Val
20 25 30
Thr Ala Ser Arg Asp Lys Ser Ile Ile Leu Trp Lys Leu Thr Lys Asp
35 40 45
Glu Lys Ser Tyr Gly Val Ala Gln Arg Arg Leu Thr Gly His Ser His
50 55 60
Phe Val Glu Asp Val Val Leu Ser Ser Asp Gly Gln Phe Ala Leu Ser
65 70 75 80
Gly Ser Trp Asp Gly Glu Leu Arg Leu Trp Asp Leu Ala Thr Gly Glu
85 90 95
Thr Thr Arg Arg Phe Val Gly His Thr Lys Asp Val Leu Ser Val Ala
100 105 110
Phe Ser Thr Asp Asn Arg Gln Ile Val Ser Ala Ser Arg Asp Arg Thr
115 120 125
Ile Lys Leu Trp Asn Thr Leu Gly Glu Cys Lys Tyr Thr Ile Ser Glu
```

(2) INFORMATION FOR SEQ ID NO:478:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

(A) NAME

(B) LOCATION: 1 234

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:478:

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:478:
Arg Ala His Thr Asp Ile Val Thr Ala Ile A

1	Met	Arg	Ala	His	5	His	Asp	Ile	Val	Thr	Ala	Ile	Ala	Thr	Pro	15	Asp
Asn	Ser	Asp	Ile	20	Ile	Val	Thr	Ala	Ser	Arg	Asp	Lys	Ser	Ile	30	Ile	Leu
Trp	Lys	Leu	Thr	35	Lys	Asp	Glu	Lys	Ser	Tyr	Gly	Val	Ala	Gln	Arg	Arg	
Leu	Thr	Gly	His	50	Ser	His	Phe	Val	Glu	Asp	Val	Val	Leu	Ser	Ser	Asp	
Gly	Gln	Phe	Ala	65	Leu	Ser	Gly	Ser	Trp	Asp	Gly	Glu	Leu	Arg	Leu	Trp	
Asp	Leu	Ala	Thr	85	Gly	Glu	Thr	Thr	Arg	Arg	Phe	Val	Gly	His	Thr	Lys	
Asp	Val	Leu	Ser	100	Val	Ala	Phe	Ser	Thr	Asp	Asn	Arg	Gln	Ile	Val	Ser	
Ala	Ser	Arg	Asp	115	Arg	Thr	Ile	Lys	Leu	Trp	Asn	Thr	Leu	Gly	Glu	Cys	
Lys	Tyr	Thr	Ile	130	Ser	Glu	Gly	Asp	Gly	His	Lys	Glu	Trp	Val	Ser	Cys	
Val	Arg	Phe	Ser	145	Pro	Asn	Thr	Leu	Val	Pro	Thr	Ile	Val	Ser	Ala	Ser	
Trp	Asp	Lys	Thr	165	Val	Lys	Val	Trp	Asn	Leu	Gln	Asn	Cys	Lys	Leu	Arg	
Asn	Ser	Leu	Val	180	Gly	His	Ser	Gly	Tyr	Leu	Asn	Thr	Val	Ala	Val	Ser	
Pro	Asp	Gly	Ser	195	Leu	Cys	Ala	Ser	Gly	Gly	Lys	Asp	Gly	Val	Ile	Leu	
Leu	Trp	Asp	Leu	210	Ala	Glu	Gly	Lys	Lys	Leu	Tyr	Ser	Leu	Glu	Ala	Gly	
Ser	Ile	Ile	His	225	Xaa	Ala	Leu	Leu	Gln	Ser							

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..123
(D) OTHER INFORMATION: / Ceres Seq. ID 1567095
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:
Met Val Arg Tyr Ala Pro Val Val Gly Lys Met Val Leu Ser Cys Cys
1 5 10 15
Gly Ile Trp Leu Lys Glu Arg Ser Phe Thr Arg Leu Arg Leu Val Arg
20 25 30
Leu Phe Xaa Ser Leu Cys Phe Ser Pro Asn Arg Tyr Trp Leu Cys Ala
35 40 45
Ala Thr Glu Asn Ser Ile Arg Ile Trp Asp Leu Glu Ser Lys Ser Val
50 55 60
Val Glu Asp Leu Lys Val Asp Leu Lys Ser Glu Ala Glu Lys Asn Glu
65 70 75 80
Gly Gly Val Gly Thr Gly Asn Gln Lys Lys Val Ile Tyr Cys Thr Ser
85 90 95
Leu Asn Trp Ser Ala Asp Gly Ser Thr Leu Phe Ser Gly Tyr Thr Asp
100 105 110
Gly Val Val Arg Val Trp Gly Ile Gly Arg Tyr
115 120

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1290
(D) OTHER INFORMATION: / Ceres Seq. ID 1567096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

atcttaccct	aaaaaccaca	tttcttaact	tcttcaataa	aaaaaagaaa	agcttcacc	60
tttaatttta	ccctcaacc	caaaacaaaa	accccttctc	ccacgagggc	atacagaat	120
atcaagacc	caatctttct	tctacttccc	caatctctag	atgacaatct	aacgatacag	180
tctcttttag	atcgattacc	aaatacaaa	gatcaatttt	tcttacatga	acactctgtt	240
gtaattggac	aggagaatct	agaactgagt	cttttatgta	cagagagcaa	cgttgatgat	300
gagggcagta	tgtgtgacga	aactccgatt	gaattttcga	ttcctcagat	gggtttttct	360
caatcgagga	gtgaggagat	tatcatggag	atgggtggaga	aggagaagca	gcatttgcca	420
agtgatgatt	acatcaagag	acttagaagt	ggagatttgg	atttgaatgt	tggagaagaa	480
gatgcctcca	attggatttg	gaaggcttgg	gaagtacacc	agtttggacc	attgtgtttt	540
tgcttagcaa	tgaactactt	ggatcgattc	ttatcggttc	atgatttggc	tagtggcaaa	600
ggttggtat	tgacgtttgt	ggctgtggct	tgtttatcat	tgccagccaa	aattgaagaa	660
actgaagtt	caatgttgat	agacttctag	gttggagatc	ctcagtttgt	gtttgagctt	720
aaatcagttc	aaagataagg	gccttttggt	ttgaacagat	tgaattggag	attgagagca	780
ataactccat	gctcatatcat	aagatatctc	ctgagaaaga	tgagttaaat	tgatcaagaa	840
ccatccaaga	cattgatata	tagatcatta	caagtgaatg	ccagcacaca	caaaggtatt	900
gacttttttg	agtttagacc	ttctgaagtt	gctgtgctgt	tgccactttc	tgtttctcgt	960
gaattgcaga	gagtagactt	tgacaactct	tcttctctct	ctctttttct	actacttcaa	1020
aaaggagagag	tgaagaagat	aggggaaatg	atagagagtg	atggctcaga	cttattttca	1080
caaacaccca	atgggggttt	agaagtatcg	gcttgttgtt	tcagctttta	gacccatgat	1140
tcttcttctt	cttatcacga	tctttcttaa	aaaaaaaact	gtttttttct	tacattatta	1200
taatcagtat	gagtgtctgt	gagaggttga	aaaaagagga	caataaatca	aagcaaaaa	1260
tttaaaaaa	caataaaagt	tattatttt				

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..308
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567097
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:
Met Ala Glu Glu Asn Leu Glu Leu Ser Leu Leu Cys Thr Glu Ser Asn
1 5 10 15
Val Asp Asp Glu Gly Met Ile Val Asp Glu Thr Pro Ile Glu Ile Ser
 20 25 30
Ile Pro Gln Met Gly Phe Ser Gln Ser Glu Glu Ile Ile Met
 35 40 45
Glu Met Val Glu Lys Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile
 50 55 60
Lys Arg Leu Arg Ser Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp
65 70 75 80
Ala Leu Asn Trp Ile Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro
 85 90 95
Leu Cys Phe Cys Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val
 100 105 110
His Asp Leu Pro Ser Gly Lys Gly Trp Ile Leu Gln Leu Leu Ala Val
 115 120 125
Ala Cys Leu Ser Leu Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met
 130 135 140
Leu Ile Asp Leu Gln Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys
145 150 155 160
Ser Val Gln Arg Met Glu Leu Leu Val Leu Asn Arg Leu Lys Trp Arg
 165 170 175
Leu Arg Ala Ile Thr Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys
 180 185 190
Met Ser Lys Cys Asp Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser
 195 200 205
Leu Gln Val Ile Ala Ser Thr Lys Gly Ile Asp Phe Leu Glu Phe
 210 215 220
Arg Pro Ser Glu Val Ala Ala Val Ala Leu Ser Val Ser Gly Glu
225 230 235 240
Leu Gln Arg Val His Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser
 245 250 255
Leu Leu Gln Lys Glu Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser
 260 265 270
Asp Gly Ser Asp Leu Phe Ser Gln Thr Pro Asn Gly Val Leu Glu Val
 275 280 285
Ser Ala Cys Cys Phe Ser Phe Lys Thr His Asp Ser Ser Ser Ser Tyr
290 295 300
Thr His Leu Ser
305
(2) INFORMATION FOR SEQ ID NO:482:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 287 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..287
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567098
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

```

Met Ile Val Asp Glu Thr Pro Ile Glu Ile Ser Ile Pro Gln Met Gly
1      5      10      15
Phe Ser Gln Ser Glu Ser Glu Glu Ile Met Glu Met Val Glu Lys
20      25      30
Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile Lys Arg Leu Arg Ser
35      40      45
Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp Ala Leu Asn Trp Ile
50      55      60
Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro Leu Cys Phe Cys Leu
65      70      75      80
Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val His Asp Leu Pro Ser
85      90      95
Gly Lys Gly Trp Trp Ile Leu Gln Leu Leu Ala Val Ala Cys Leu Ser Leu
100      105      110
Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met Leu Ile Asp Leu Gln
115      120      125
Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys Ser Val Gln Arg Met
130      135      140
Glu Leu Leu Val Leu Asn Arg Leu Lys Trp Arg Leu Arg Ala Ile Thr
145      150      155      160
Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys Met Ser Lys Cys Asp
165      170      175
Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser Leu Gln Val Ile Ala
180      185      190
Ser Thr Thr Lys Gly Ile Asp Phe Leu Glu Phe Arg Pro Ser Glu Val
195      200      205
Ala Ala Ala Val Ala Leu Ser Val Ser Gly Glu Leu Gln Arg Val His
210      215      220
Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser Leu Leu Gln Lys Glu
225      230      235      240
Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser Asp Gly Ser Asp Leu
245      250      255
Phe Ser Gln Thr Pro Asn Gly Val Leu Glu Val Ser Ala Cys Cys Phe
260      265      270
Ser Phe Lys Thr His Asp Ser Ser Ser Ser Tyr Thr His Leu Ser
275      280      285

```

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..273

(D) OTHER INFORMATION: / Ceres Seq. ID 1567099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

```

Met Gly Phe Ser Gln Ser Glu Ser Glu Glu Ile Ile Met Glu Met Val
1      5      10      15
Glu Lys Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile Lys Arg Leu
20      25      30
Arg Ser Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp Ala Leu Asn
35      40      45
Trp Ile Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro Leu Cys Phe
50      55      60
Cys Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val His Asp Leu
65      70      75      80
Pro Ser Gly Lys Gly Trp Ile Leu Gln Leu Leu Ala Val Ala Cys Leu
85      90      95
Ser Leu Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met Leu Ile Asp

```


100	105	110
Leu Gln Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys Ser Val Gln		
115	120	125
Arg Met Glu Leu Leu Val Leu Asn Arg Leu Lys Trp Arg Leu Arg Ala		
130	135	140
Ile Thr Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys Met Ser Lys		
145	150	155
Cys Asp Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser Leu Gln Val		
165	170	175
Ile Ala Ser Thr Thr Lys Gly Ile Asp Phe Leu Glu Phe Arg Pro Ser		
180	185	190
Glu Val Ala Ala Ala Val Ala Leu Ser Val Ser Gly Glu Leu Gln Arg		
195	200	205
Val His Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser Leu Leu Gln		
210	215	220
Lys Glu Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser Asp Gly Ser		
225	230	235
Asp Leu Phe Ser Gln Thr Pro Asn Gly Val Leu Glu Val Ser Ala Cys		
245	250	255
Cys Phe Ser Phe Lys Thr His Asp Ser Ser Ser Tyr Thr His Leu		
260	265	270
Ser		

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

gagagaaaga	gagagatatg	atattattaa	gtagtagtat	aagcctctca	agaccagttt	60
cttctcaaaag	cttctctccca	ctgctgcca	cttcaacaag	gagatctcat	tcctctgtca	120
cagctcaagtg	ctgctgtttct	tccagaagtg	tggtgaagaa	tcctgagtta	aaatgttctt	180
tggaagatct	ctttgaaatc	caggctttga	gggaagtgtt	tggttcaggg	tttgacagta	240
ttttctctct	ctctcaggca	ggccagggtta	tagcgttgga	tcctctcatct	ggttatcaga	300
acatttgcca	actaggagtg	gctgctgctg	tggaagaaaa	caagctgact	cttccatctg	360
atggttgactc	ggaatcaatg	atgatgatga	tgatgagagg	catgactgct	aagaactttg	420
accctgttag	gtactctgga	agatgggttg	aagtactctc	tcctaaagcg	ggatttgcaq	480
gtcaaggcca	agaagactgt	cattgcactc	agggagatata	cacgtttgat	atgaaggaat	540
cagccattag	agtatagata	ttttgtgttc	atggcagccc	tgatggatat	ataacaggaa	600
tcagagggaa	agttcaatgc	gtgggagcgg	aagacctcga	gaaaaagcag	actgacttag	660
aaaaagcaaga	gatgattaaa	gagaagtgtt	tcctacagat	tcaccacatt	ctttttatcc	720
ccaagtgtcc	ttatgatgtc	atagccacag	actacgacaa	ctacgcactt	gtttctggag	780
ctaaagacaa	gggtcttggt	caggtatact	caaggacgcc	aaatccagga	cttgagttca	840
tcgcaaaagta	caagaactac	ttggcacaat	ttggctatga	cccgaaaaaa	ataaaggata	900
caccacagga	ctgtgaagtg	actgatgctg	agctagcagc	catgatgtcc	atgccaggtta	960
tgagagcaaac	actgaccaac	cagtttccag	atcttggtat	aaAgaaagtc	agtcacagtt	1020
gatcccttcca	caagtgtgtt	tgaacacctg	aagaaacttg	taccgtctca	tttcaaatag	1080
agcaagcttc	tttgctcaaa	tcttatgta	gactataatc	actgtccata	tatacatatc	1140
ttccagaatc	aaaacactct	tctg				

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..339
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567117
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:
Glu Lys Glu Arg Asp Met Ile Leu Leu Ser Ser Ser Ile Ser Leu Ser
1 5 10 15
Arg Pro Val Ser Ser Gln Ser Phe Ser Pro Pro Ala Ala Thr Ser Thr
 20 25 30
Arg Arg Ser His Ser Ser Val Thr Val Lys Cys Cys Cys Ser Ser Arg
 35 40 45
Arg Leu Leu Lys Asn Pro Glu Leu Lys Cys Ser Leu Glu Asn Leu Phe
50 55 60 65
Glu Ile Gln Ala Leu Arg Lys Cys Phe Val Ser Gly Phe Ala Ala Ile
65 70 75 80
Leu Leu Leu Ser Gln Ala Gly Gln Gly Ile Ala Leu Asp Leu Ser Ser
 85 90 95
Gly Tyr Gln Asn Ile Cys Gln Leu Gly Ser Ala Ala Ala Val Gly Glu
 100 105 110
Asn Lys Leu Thr Leu Pro Ser Asp Gly Asp Ser Glu Ser Met Met Met
115 120 125
Met Met Met Arg Gly Met Thr Ala Lys Asn Phe Asp Pro Val Arg Tyr
130 135 140
Ser Gly Arg Trp Phe Glu Val Ala Ser Leu Lys Arg Gly Phe Ala Gly
145 150 155 160
Gln Gly Gln Glu Asp Cys His Cys Thr Gln Gly Val Tyr Thr Phe Asp
 165 170 175
Met Lys Glu Ser Ala Ile Arg Val Asp Thr Phe Cys Val His Gly Ser
180 185 190
Pro Asp Gly Tyr Ile Thr Gly Ile Arg Gly Lys Val Gln Cys Val Gly
195 200 205
Ala Glu Asp Leu Glu Lys Ser Glu Thr Asp Leu Glu Lys Gln Glu Met
210 215 220
Ile Lys Glu Lys Cys Phe Leu Arg Phe Pro Thr Ile Pro Phe Ile Pro
225 230 235
Lys Leu Pro Tyr Asp Val Ile Ala Thr Asp Tyr Asp Asn Tyr Ala Leu
 245 250 255
Val Ser Gly Ala Lys Asp Lys Gly Phe Val Gln Val Tyr Ser Arg Thr
260 265 270
Pro Asn Pro Gly Pro Glu Phe Ile Ala Lys Tyr Lys Asn Tyr Leu Ala
275 280 285
Gln Phe Gly Tyr Asp Pro Glu Lys Ile Lys Asp Thr Pro Gln Asp Cys
290 295 300
Glu Val Thr Asp Ala Glu Leu Ala Ala Met Met Ser Met Pro Gly Met
305 310 315 320
Glu Gln Thr Leu Thr Asn Gln Phe Pro Asp Leu Gly Leu Lys Lys Val
 325 330 335
Ser Pro Val

(2) INFORMATION FOR SEQ ID NO:486:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 334 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..334
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567118

Met	Ile	Leu	Leu	5	Ser	Ser	Ile	Ser	Leu	Ser	Arg	Pro	Val	Ser	Ser
1	Gln	Ser	Phe	20	Pro	Ala	Ala	Thr	Ser	Thr	Arg	Arg	Ser	His	Ser
Ser	Val	Thr	Val	Lys	Cys	Cys	Cys	Ser	Ser	Arg	Arg	Leu	Leu	Lys	Asn
Pro	Glu	Leu	Lys	Cys	Ser	Leu	Glu	Asn	Leu	Phe	Glu	Ile	Gln	Ala	Leu
Arg	Lys	Cys	Phe	Val	Ser	Gly	Phe	Ala	Ala	Ile	Leu	Leu	Leu	Ser	Gln
65	Ala	Gly	Gln	Gly	Ile	Ala	Leu	Asp	Leu	Ser	Gly	Tyr	Gln	Asn	Ile
Cys	Gln	Leu	Gly	Ser	Ala	Ala	Ala	Val	Gly	Glu	Asn	Lys	Leu	Thr	Leu
Pro	Ser	Asp	Gly	Asp	Ser	Glu	Ser	Met	Met	Met	Met	Met	Met	Arg	Gly
Met	Thr	Ala	Lys	Asn	Phe	Asp	Pro	Val	Arg	Tyr	Ser	Gly	Arg	Trp	Phe
Glu	Val	Ala	Ser	Leu	Lys	Arg	Gly	Phe	Ala	Gly	Gln	Gly	Gln	Glu	Asp
145	Cys	His	Cys	Thr	Gln	Gly	Val	Tyr	Thr	Phe	Asp	Met	Lys	Glu	Ser
Ile	Arg	Val	Asp	Thr	Phe	Cys	Val	His	Gly	Ser	Pro	Asp	Gly	Tyr	Ile
Thr	Gly	Ile	Arg	Gly	Lys	Val	Gln	Cys	Val	Gly	Ala	Glu	Asp	Leu	Glu
Lys	Ser	Glu	Thr	Asp	Leu	Glu	Lys	Gln	Glu	Met	Ile	Lys	Glu	Lys	Cys
210	Phe	Leu	Arg	Phe	Pro	Thr	Ile	Pro	Phe	Ile	Pro	Lys	Leu	Pro	Tyr
225	Val	Ile	Ala	Thr	Asp	Tyr	Asp	Asn	Tyr	Ala	Leu	Val	Ser	Gly	Ala
Val	Ile	Ala	Thr	Asp	Tyr	Asp	Asn	Tyr	Ala	Leu	Val	Ser	Gly	Ala	Lys
Asp	Lys	Gly	Phe	Val	Gln	Val	Tyr	Asn	Arg	Thr	Pro	Asn	Pro	Gly	Pro
Glu	Phe	Ile	Ala	Lys	Tyr	Lys	Asn	Tyr	Leu	Ala	Gln	Phe	Gly	Tyr	Asp
Pro	Glu	Lys	Ile	Lys	Asp	Thr	Pro	Gln	Asp	Cys	Glu	Val	Thr	Asp	Ala
305	Glu	Leu	Ala	Ala	Met	Met	Ser	Met	Pro	Gly	Met	Glu	Gln	Thr	Leu
Asn	Gln	Phe	Pro	Asp	Leu	Gly	Leu	Lys	Lys	Val	Ser	Pro	Val		

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: / Ceres Seq. ID 1567119

Met	Met	Met	Met	Met	Arg	Gly	Met	Thr	Ala	Lys	Asn	Phe	Asp	Pro	
1			5					10					15		
Val	Arg	Tyr	Ser	Gly	Arg	Trp	Phe	Glu	Val	Ala	Ser	Leu	Lys	Arg	Gly
			20					25					30		
Phe	Ala	Gly	Gln	Gly	Gln	Glu	Asp	Cys	His	Cys	Thr	Gln	Gly	Val	Tyr
		35					40					45			

Thr	Phe	Asp	Met	Lys	Glu	Ser	Ala	Ile	Arg	Val	Asp	Thr	Phe	Cys	Val	
	50					55					60					
His	Gly	Ser	Pro	Asp	Gly	Tyr	Ile	Thr	Gly	Ile	Arg	Gly	Lys	Val	Gln	
65					70				75					80		
Cys	Val	Gly	Ala	Glu	Asp	Leu	Glu	Lys	Ser	Glu	Thr	Asp	Leu	Glu	Lys	
				85					90					95		
Gln	Glu	Met	Ile	Lys	Glu	Lys	Cys	Phe	Leu	Arg	Phe	Pro	Thr	Ile	Pro	
				100					105					110		
Phe	Ile	Pro	Lys	Leu	Pro	Tyr	Asp	Val	Ile	Ala	Thr	Asp	Tyr	Asp	Asn	
				115				120						125		
Tyr	Ala	Leu	Val	Ser	Gly	Ala	Lys	Asp	Lys	Gly	Phe	Val	Gln	Val	Tyr	
				130				135						140		
Ser	Arg	Thr	Pro	Asn	Pro	Gly	Pro	Glu	Phe	Ile	Ala	Lys	Tyr	Lys	Asn	
145					150				155					160		
Tyr	Leu	Ala	Gln	Phe	Gly	Tyr	Asp	Pro	Glu	Lys	Ile	Lys	Asp	Thr	Pro	
				165					170					175		
Gln	Asp	Cys	Glu	Val	Thr	Asp	Ala	Glu	Leu	Ala	Ala	Met	Met	Ser	Met	
				180				185						190		
Pro	Gly	Met	Glu	Gln	Thr	Leu	Thr	Asn	Gln	Phe	Pro	Asp	Leu	Gly	Leu	
				195				200						205		
Lys	Lys	Val	Ser	Pro	Val											
				210												

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1223
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

gaccacatca	attctGstca	tatctctctc	tcactttcga	atatatctta	agataacaga	60
gacacatact	cttaagtttg	gtgaagaata	agaagacaat	gacgaaggaa	gtgggttggtg	120
ataagagatc	tttctccggg	aaagactatc	aagaccacac	acctgaacct	ctattcgacg	180
ctactgagct	tggggaagtgg	tctttctaca	gagctctcat	cgctgagttc	atagccaactc	240
tccttttctc	ctatgtcaat	attatgactg	tcctcggtta	caagagccag	accgatccag	300
ccctgaatcc	tgaccagtgt	acaggcggtg	cgctccttgg	tatcgcatgg	gccttttggtg	360
gcgatgatct	catctcgtgc	tactgcaccg	cggcatcttc	tggtgggcat	attaatccgg	420
cagtgacttt	tggtcgtgtg	ttgtgctcga	aagtgcagtt	ggtgagagca	gtgatgtaca	480
tggtggctca	gtgcctcggt	gccatttggg	gtgtggcttt	ggtcaaggcc	ttccagctcg	540
cttacttcaac	ccgtactcgt	ggtggcgcaa	atggtctctc	tgacggttac	agcatcgcca	600
ccgggtgtgc	agccagagat	attggtacat	tcgtcttagt	ctacaccgtc	ttctctgcca	660
ctgatcccaa	gaggagtgcg	cgtgactctc	acgttctctg	attggctcca	tttccaattg	720
gatttgcaat	gttcatcggt	cacttagcta	caatcccaat	cacggggcact	gggtacaacc	780
ctgcaagaag	tctcggagct	gcaatcatct	acaacaagga	caaatgcttg	gaccatcatt	840
ggatattctg	gggtgggtccg	tttgcctggt	cagccatcgc	agctttctac	catcagtttg	900
tggtgagggc	tggtgcgatt	aaggcgctcg	ggtctttcag	gagccagcct	cacgtttaac	960
tttgatatgc	tcttccctga	gtacatcaaa	gagagaaaaa	gagaagataa	taagagagggc	1020
ttgtaatatt	atcttctgtg	gacggttgga	gccaaagtgc	gtgtagtact	agtatctaat	1080
ttctagcttt	gggtgaggga	gatatattga	agtgctcgct	gcggggccaa	tttgaattgc	1140
tacttctatg	attaaatcta	tgtctctact	cttgactat	taagattgct	ctatttatta	1200
gtactaaata	ttccttatat	atg				

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..286

SEQUENCE DESCRIPTION: SEQ ID NO:489:

5 10 15

(2) INFORMATION FOR SEQ ID NO:490:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1567122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

Met	Thr	Val	Ile	Gly	Tyr	Lys	Ser	Gln	Thr	Asp	Pro	Ala	Leu	Asn	Pro
1			5						10				15		
Asp	Gln	Cys	Thr	Gly	Val	Gly	Val	Leu	Gly	Ile	Ala	Trp	Ala	Phe	Gly
		20						25					30		
Gly	Met	Ile	Phe	Ile	Leu	Val	Tyr	Cys	Thr	Ala	Gly	Ile	Ser	Gly	Gly
		35					40					45			
His	Ile	Asn	Pro	Ala	Val	Thr	Phe	Glv	Leu	Leu	Leu	Ala	Arg	Lys	Val

(2) INFORMATION FOR SEQ ID NO:491:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..198

(D) OTHER INFORMATION: / Ceres Seq. ID 1567123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

[illegible]

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

```
aaaatttgcg aaactaattt ttctcaattt ttcttcgttg atctctctga aagcttctct 60
tctttctctc accatgtctg gttatcctcc atcaagccaa gggttaagggtt acggcggttaa 120
tccaacacct cctcagccac cgtacggatc aaccggcaat aacctctctc cgtgogggatc 180
atccggcagc aatctctctc ctccgtacgg atcatcagcc tctcaccgtc acgcagttcc 240
ctacggagct cagccgcgtc ctacgggtgc accaccgtca gcaccgtacg cgtctctctc 300
aggagaccat aataagccgc acaaagagaa accctcagcg gcctctctac gatctccatc 360
tcccgggtgc tacgggtctc atccatcgtc tggaccttcc gactacggtg gttacggagg 420
agcgccgagc cagttctggc atggaggagg ttacggagga ggcgcgcagc agtctggaca 480
tggaggagggt tacggagctc ctctctccga agcttcttat ggaagtccgt ttgcgtctct 540
ggttcgcgtc cagtttctct ccggaacaga tccgaacatt gtggttctgt tccaagctgc 600
ggatcgggac aaatgtggat tcactcgatg taaggagctt caaggagctc tatcttcgta 660
taatcagagc ttcagcatal gaactgttca tctcttatg tatctattca ccaacagcaa 720
tgtcaggagc attggaccaa aagagtgtac ttcaactttc Tkkagtcttc agaattggag 780
gtctatcttt gagaggtttg ataaggacag aagcggtaga atagatacaa acgagctgag 840
agatgaactc atgagccttg ggttttctgt gctctctgtg attttgatc tgctggttcc 900
aaagtgttgc aaaaagcggag gcaggaacag ggctatcgaa tatgacaatt tcatcgatg 960
ttgtttgact gtaaaagggc tcaccgagaa gttcaaggag aggatgacgg cgtttatcag 1020
ctcagctact ttcaattacg agaacttcac gctcactgtt ttaccattcc tcgtcgtct 1080
agtgaattgt tttttttttt ttgttgaccA aasagattgt tttctaactc tattttcttt 1140
gtgagctttt ggatatttta ttgttgtctt tttt
```

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..359
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

```
Lys Phe Arg Lys Leu Ile Phe Ser Leu Ser Ser Ser Leu Ile Ser Leu
1 5 10
Lys Ala Ser Leu Leu Leu Leu Thr Met Ser Gly Tyr Pro Pro Ser Ser
20 25 30
Gln Gly Tyr Gly Tyr Gly Gly Asn Pro Pro Pro Pro Gln Pro Pro Tyr
35 40 45
Gly Ser Thr Gly Asn Asn Pro Pro Pro Cys Gly Ser Ser Gly Ser Asn
50 55 60
Pro Pro Pro Pro Tyr Gly Ser Ser Ala Ser Ser Pro Tyr Ala Val Pro
65 70 75 80
Tyr Gly Ala Gln Pro Ala Pro Tyr Gly Ala Pro Pro Ser Ala Pro Tyr
85 90 95
Ala Ser Pro Pro Gly Asp His Asn Lys Pro His Lys Glu Lys Pro His
100 105 110
Gly Ala Ser Tyr Gly Ser Pro Ser Pro Gly Gly Tyr Gly Ala His Pro
115 120 125
Ser Ser Gly Pro Ser Asp Tyr Gly Gly Tyr Gly Gly Ala Pro Gln Gln
```

130	135	140
Ser Gly His Gly Gly Gly Tyr Gly Gly Ala Pro Gln Gln Ser Gly His	150	160
145	155	170
Gly Gly Gly Tyr Gly Ala Pro Pro Pro Gln Ala Ser Tyr Gly Ser Pro	165	175
Phe Ala Ser Leu Val Pro Ser Ala Phe Pro Pro Gly Thr Asp Pro Asn	180	190
Ile Val Ala Cys Phe Gln Ala Ala Asp Arg Asp Asn Ser Gly Phe Ile	195	205
Asp Asp Lys Glu Leu Gln Gly Ala Leu Ser Ser Tyr Tyr Gln Ser Phe	210	220
Ser Ile Arg Thr Val His Leu Leu Met Tyr Leu Phe Thr Asn Ser Asn	215	230
225	235	240
Val Arg Lys Ile Gly Pro Lys Glu Phe Thr Ser Leu Phe Xaa Ser Leu	245	255
Gln Asn Trp Arg Ser Ile Phe Glu Arg Phe Asp Lys Asp Arg Ser Gly	260	270
Arg Ile Asp Thr Asn Glu Leu Arg Asp Ala Leu Met Ser Leu Gly Phe	275	285
Ser Val Ser Pro Val Ile Leu Asp Leu Leu Val Ser Lys Phe Asp Lys	290	300
Ser Gly Gly Arg Asn Arg Ala Ile Glu Tyr Asp Asn Phe Ile Glu Cys	295	310
305	315	320
Cys Leu Thr Val Lys Gly Leu Thr Glu Lys Phe Lys Glu Lys Asp Thr	325	330
Ala Leu Ser Gly Ser Ala Thr Phe Asn Tyr Glu Asn Phe Met Leu Thr	335	345
Val Leu Pro Phe Leu Val Ala	340	350
355		

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..335
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

Met Ser Gly Tyr Pro Pro Ser Ser Gln Gly Tyr Gly Tyr Gly Gly Asn
1 5 10 15
Pro Pro Pro Pro Gln Pro Pro Tyr Gly Ser Thr Gly Asn Asn Pro Pro
20 25 30
Pro Cys Gly Ser Ser Gly Ser Asn Pro Pro Pro Tyr Gly Ser Ser
35 40 45
Ala Ser Ser Pro Tyr Ala Val Pro Tyr Gly Ala Gln Pro Ala Pro Tyr
50 55 60
Gly Ala Pro Pro Ser Ala Pro Tyr Ala Ser Pro Pro Gly Asp His Asn
65 70 75 80
Lys Pro His Lys Glu Lys Pro His Gly Ala Ser Tyr Gly Ser Pro Ser
85 90 95
Pro Gly Gly Tyr Gly Ala His Pro Ser Ser Gly Pro Ser Asp Tyr Gly
100 105 110
Gly Tyr Gly Gly Ala Pro Gln Gln Ser Gly His Gly Gly Tyr Gly Tyr Gly
115 120 125
Gly Ala Pro Gln Gln Ser Gly His Gly Gly Tyr Gly Ala Pro Pro
130 135 140
Pro Gln Ala Ser Tyr Gly Ser Pro Phe Ala Ser Leu Val Pro Ser Ala
145 150 155 160


```

Phe Pro Pro Gly Thr Asp Pro Asn Ile Val Ala Cys Phe Gln Ala Ala
      165      170      175
Asp Arg Asp Asn Ser Gly Phe Ile Asp Asp Lys Glu Leu Gln Gly Ala
      180      185      190
Leu Ser Ser Tyr Asn Gln Ser Phe Ser Ile Arg Thr Val His Leu Leu
      195      200      205
Met Tyr Leu Phe Thr Asn Ser Asn Val Arg Lys Ile Gly Pro Lys Glu
      210      215      220
Phe Thr Ser Leu Phe Xaa Ser Leu Gln Asn Trp Arg Ser Ile Phe Glu
      225      230      235
Arg Phe Asp Lys Asp Arg Ser Gly Arg Ile Asp Thr Asn Glu Leu Arg
      245      250      255
Asp Ala Leu Met Ser Leu Gly Phe Ser Val Ser Pro Val Ile Leu Asp
      260      265      270
Leu Leu Val Ser Lys Phe Asp Lys Ser Gly Gly Arg Asn Arg Ala Ile
      275      280      285
Glu Tyr Asp Asn Phe Ile Glu Cys Cys Leu Thr Val Lys Gly Leu Thr
      290      295      300
Glu Lys Phe Lys Glu Lys Asp Thr Ala Leu Ser Gly Ser Ala Thr Phe
      305      310      315      320
Asn Tyr Glu Asn Phe Met Leu Thr Val Leu Pro Phe Leu Val Ala
      325      330      335

```

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1572
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

```

ctctctctct ctctcacttc atctatggct tctctctctc tgcagtctct ctctctctctg      60
ttttgccttg ctctgtttct tcttctctct atcgctctct ccatcggcac caactatggc      120
caggctgccta acaaccttcc tccccctaaa aacgtcatcc ctctctctcaa gtctgtggga      180
gctacaaaag tcaagctcta tgacgcgcat ccacaagccc tacgtgcctt cgcgggctcc      240
ggcttcgagc tcaccgtggc cctcggtaac gagtacctgg ctcatgatgag gcacctatt      300
aaagcccaag gctgggtgaa ggagaacgct caagcttacc tcccaaacac caagatcgtg      360
gcactcgtag tgggaacgaa agTcttcacc tcaaaccaag cagccctcac ggcagccctc      420
ttcccggtcta tgcaaacgat ccacgggtgt ctggtggatt gtggcctaaa caagcagatc      480
tttgtacgca cggctcactc actagccatc ttggatgtat ctaccctcc cgtgcgcaact      540
tccttcgcgc ggcactctct cggctccctc actccatctc tggacttcca cgtcaagact      600
ggctccacca tctcatcaca cgcctaccct tctctgcctc acgaagaaaa ccccaaacac      660
gtttctctcg actctgtact ctcccaacca aatcaaggct tcaccgctcc tggctctaatt      720
ttccactacg acaacatgct ctctgctcag gtccagcgac tctatcacgc tcttgacgct      780
gtccgcatca gctacaagaa agttcccatc gtctgtctcg agaccgggat gccttccaac      840
ggtagaccgc aagaagtcgg agccacctgc gacaatgctc gcaagtacaa ttgggaatctc      900
atcaagatga tgatgagcaa gaagatgagg acgctatttc gacttgagtg cgtactcaac      960
tactgtctct ttgtctctct taacgagaac atgaagcctg Gaccaaacctc cgagaggaaa      1020
tacggtctct tcaaccCtga cggaaactcc gtttactcac ttgggatcaa gacctcttcc      1080
actcatagta gtggtatggt tagcagcaac tccactgggt gtagttagcag tggcgggtggc      1140
ggtaaacact gtgctctctc cgcgggtggt ggcactatc agccagtcaac gggtaaccca      1200
tcaccggatt acatgtocat ttctctcgcc gggggaaaaa gcagattcgt tgagtgtgtg      1260
ttgttctctt tcttgctttt catcatcaag cttcggttgt aaaaagctct ccaactagatc      1320
tcgtgcgctt tgtactttta cggggttgat gacgtgatat agcccccaaa tttaatttaa      1380
ttagttttgt gttggtgttt tggctggagg atgatttagg agacatacca tctttgttgt      1440
gccacattgc tctccaactc ttttcttttt tccattccat ctctctttta      1500
catagattat ttaaataatg aatcttagtt gattagattt ttctaaagaa gatgatgatt      1560
ttcgataaaa gc

```

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..433
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

Leu	Ser	Leu	Ser	Leu	Thr	Ser	Ser	Met	Ala	Ser	Ser	Ser	Leu	Gln	Ser
1			5						10				15		
Leu	Phe	Ser	Leu	Phe	Cys	Leu	Ala	Leu	Phe	Ser	Leu	Pro	Leu	Ile	Val
			20						25				30		
Ser	Ser	Ile	Gly	Ile	Asn	Tyr	Gly	Gln	Val	Ala	Asn	Asn	Leu	Pro	Pro
			35					40				45			
Pro	Lys	Asn	Val	Ile	Pro	Leu	Leu	Lys	Ser	Val	Gly	Ala	Thr	Lys	Val
			50				55				60				
Lys	Leu	Tyr	Asp	Ala	Asp	Pro	Gln	Ala	Leu	Arg	Ala	Phe	Ala	Gly	Ser
			65				70			75				80	
Gly	Phe	Glu	Leu	Thr	Val	Ala	Leu	Gly	Asn	Glu	Tyr	Leu	Ala	Gln	Met
			85					90						95	
Ser	Asp	Pro	Ile	Lys	Ala	Gln	Gly	Trp	Val	Lys	Glu	Asn	Val	Gln	Ala
			100					105					110		
Tyr	Leu	Pro	Asn	Thr	Lys	Ile	Val	Ala	Ile	Val	Val	Gly	Asn	Glu	Val
			115				120					125			
Leu	Thr	Ser	Asn	Gln	Ser	Ala	Leu	Thr	Ala	Ala	Leu	Phe	Pro	Ala	Met
			130				135				140				
Gln	Ser	Ile	His	Gly	Ala	Leu	Val	Asp	Cys	Gly	Leu	Asn	Lys	Gln	Ile
			145				150			155				160	
Phe	Val	Thr	Thr	Ala	His	Ser	Leu	Ala	Ile	Leu	Asp	Val	Ser	Tyr	Pro
			165					170						175	
Pro	Ser	Ala	Thr	Ser	Phe	Arg	Arg	Asp	Leu	Leu	Gly	Ser	Leu	Thr	Pro
			180					185						190	
Ile	Leu	Asp	Phe	His	Val	Lys	Thr	Gly	Ser	Pro	Ile	Leu	Ile	Asn	Ala
			195				200					205			
Tyr	Pro	Phe	Phe	Ala	Tyr	Glu	Glu	Asn	Pro	Lys	His	Val	Ser	Leu	Asp
			210				215				220				
Phe	Val	Leu	Phe	Gln	Pro	Asn	Gln	Gly	Phe	Thr	Asp	Pro	Gly	Ser	Asn
			225				230			235				240	
Phe	His	Tyr	Asp	Asn	Met	Leu	Phe	Ala	Gln	Val	Asp	Ala	Val	Tyr	His
			245					250						255	
Ala	Leu	Asp	Ala	Val	Gly	Ile	Ser	Tyr	Lys	Lys	Val	Pro	Ile	Val	Val
			260					265					270		
Ser	Glu	Thr	Gly	Trp	Pro	Ser	Asn	Gly	Asp	Pro	Gln	Glu	Val	Gly	Ala
			275				280					285			
Thr	Cys	Asp	Asn	Ala	Arg	Lys	Tyr	Asn	Gly	Asn	Leu	Ile	Lys	Met	Met
			290				295				300				
Met	Ser	Lys	Lys	Met	Arg	Thr	Pro	Ile	Arg	Pro	Glu	Cys	Asp	Leu	Thr
			305				310			315				320	
Ile	Phe	Val	Phe	Ala	Leu	Phe	Asn	Glu	Asn	Met	Lys	Pro	Gly	Pro	Thr
			325					330						335	
Ser	Glu	Arg	Asn	Tyr	Gly	Leu	Phe	Asn	Pro	Asp	Gly	Thr	Pro	Val	Tyr
			340					345					350		
Ser	Leu	Gly	Ile	Lys	Thr	Ser	Ser	Thr	His	Ser	Ser	Gly	Ser	Gly	Ser
			355					360				365			
Ser	Asn	Ser	Thr	Gly	Gly	Ser	Ser	Gly	Gly	Gly	Gly	Asn	Thr	Gly	
			370				375				380				
Gly	Ser	Ser	Ser	Gly	Gly	Gly	Ile	Tyr	Gln	Pro	Val	Thr	Gly	Asn	Pro

385				390					395				400
Ser	Pro	Asp	Tyr	Met	Ser	Ile	Ser	Ser	Ala	Gly	Gly	Lys	Gly
				405					410				415
Val	Glu	Cys	Val	Leu	Phe	Phe	Phe	Phe	Leu	Leu	Cys	Ile	Ile
			420						425				430
Leu													

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 425 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..425

(D) OTHER INFORMATION: / Ceres Seq. ID 1567135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

Met	Ala	Ser	Ser	Ser	Leu	Gln	Ser	Leu	Phe	Ser	Leu	Phe	Cys	Leu	Ala
1				5					10				15		
Leu	Phe	Ser	Leu	Pro	Leu	Ile	Val	Ser	Ser	Ile	Gly	Ile	Asn	Tyr	Gly
			20					25					30		
Gln	Val	Ala	Asn	Asn	Leu	Pro	Pro	Pro	Lys	Asn	Val	Ile	Pro	Leu	Leu
			35				40					45			
Lys	Ser	Val	Gly	Ala	Thr	Lys	Val	Lys	Leu	Tyr	Asp	Ala	Asp	Pro	Gln
			50			55				60					
Ala	Leu	Arg	Ala	Phe	Ala	Gly	Ser	Gly	Phe	Glu	Leu	Thr	Val	Ala	Leu
			65		70				75				80		
Gly	Asn	Glu	Tyr	Leu	Ala	Gln	Met	Ser	Asp	Pro	Ile	Lys	Ala	Gln	Gly
			85					90					95		
Trp	Val	Lys	Glu	Asn	Val	Gln	Ala	Tyr	Leu	Pro	Asn	Thr	Lys	Ile	Val
			100					105					110		
Ala	Ile	Val	Val	Gly	Asn	Glu	Val	Leu	Thr	Ser	Asn	Gln	Ser	Ala	Leu
			115				120					125			
Thr	Ala	Ala	Leu	Phe	Pro	Ala	Met	Gln	Ser	Ile	His	Gly	Ala	Leu	Val
			130			135					140				
Asp	Cys	Gly	Leu	Asn	Lys	Gln	Ile	Phe	Val	Thr	Thr	Ala	His	Ser	Leu
			145		150					155				160	
Ala	Ile	Leu	Asp	Val	Ser	Tyr	Pro	Pro	Ser	Ala	Thr	Ser	Phe	Arg	Arg
			165						170					175	
Asp	Leu	Leu	Gly	Ser	Leu	Thr	Pro	Ile	Leu	Asp	Phe	His	Val	Lys	Thr
			180					185					190		
Gly	Ser	Pro	Ile	Leu	Ile	Asn	Ala	Tyr	Pro	Phe	Phe	Ala	Tyr	Glu	Glu
		195					200					205			
Asn	Pro	Lys	His	Val	Ser	Leu	Asp	Phe	Val	Leu	Phe	Gln	Pro	Asn	Gln
		210				215					220				
Gly	Phe	Thr	Asp	Pro	Gly	Ser	Asn	Phe	His	Tyr	Asp	Asn	Met	Leu	Phe
		225			230					235				240	
Ala	Gln	Val	Asp	Ala	Val	Tyr	His	Ala	Leu	Asp	Ala	Val	Gly	Ile	Ser
			245					250					255		
Tyr	Lys	Lys	Val	Pro	Ile	Val	Val	Ser	Glu	Thr	Gly	Trp	Pro	Ser	Asn
			260				265					270			
Gly	Asp	Pro	Gln	Glu	Val	Gly	Ala	Thr	Cys	Asp	Asn	Ala	Arg	Lys	Tyr
		275				280					285				
Asn	Gly	Asn	Leu	Ile	Lys	Met	Met	Met	Ser	Lys	Lys	Met	Arg	Thr	Pro
		290				295					300				
Ile	Arg	Pro	Glu	Cys	Asp	Leu	Thr	Ile	Phe	Val	Phe	Ala	Leu	Phe	Asn
		305			310				315					320	
Glu	Asn	Met	Lys	Pro	Gly	Pro	Thr	Ser	Glu	Arg	Asn	Tyr	Gly	Leu	Phe
			325						330					335	

Asn Pro Asp Gly Thr Pro Val Tyr Ser Leu Gly Ile Lys Thr Ser Ser
340 345 350
Thr His Ser Ser Gly Ser Gly Ser Ser Asn Ser Thr Gly Gly Ser Ser
355 360 365
Ser Gly Gly Gly Gly Asn Thr Gly Gly Ser Ser Ser Gly Gly Gly Ile
370 375 380
Tyr Gln Pro Val Thr Gly Asn Pro Ser Pro Asp Tyr Met Ser Ile Ser
385 390 395 400
Ser Ala Gly Gly Lys Gly Arg Phe Val Glu Cys Val Leu Phe Phe Phe
405 410 415
Leu Leu Cys Ile Ile Lys Leu Arg Leu
420 425

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..338

(D) OTHER INFORMATION: / Ceres Seq. ID 1567136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

Met Ser Asp Pro Ile Lys Ala Gln Gly Trp Val Lys Glu Asn Val Gln
1 5 10 15
Ala Tyr Leu Pro Asn Thr Lys Ile Val Ala Ile Val Val Gly Asn Glu
20 25 30
Val Leu Thr Ser Asn Gln Ser Ala Leu Thr Ala Ala Leu Phe Pro Ala
35 40 45
Met Gln Ser Ile His Gly Ala Leu Val Asp Cys Gly Leu Asn Lys Gln
50 55 60
Ile Phe Val Thr Thr Ala His Ser Leu Ala Ile Leu Asp Val Ser Tyr
65 70 75 80
Pro Pro Ser Ala Thr Ser Phe Arg Arg Asp Leu Leu Gly Ser Leu Thr
85 90 95
Pro Ile Leu Asp Phe His Val Lys Thr Gly Ser Pro Ile Leu Ile Asn
100 105 110
Ala Tyr Pro Phe Phe Ala Tyr Glu Glu Asn Pro Lys His Val Ser Leu
115 120 125
Asp Phe Val Leu Phe Gln Pro Asn Gln Gly Phe Thr Asp Pro Gly Ser
130 135 140
Asn Phe His Tyr Asp Asn Met Leu Phe Ala Gln Val Asp Ala Val Tyr
145 150 155 160
His Ala Leu Asp Ala Val Gly Ile Ser Tyr Lys Lys Val Pro Ile Val
165 170 175
Val Ser Glu Thr Gly Trp Pro Ser Asn Gly Asp Pro Gln Glu Val Gly
180 185 190
Ala Thr Cys Asp Asn Ala Arg Lys Tyr Asn Gly Asn Leu Ile Lys Met
195 200 205
Met Met Ser Lys Lys Met Arg Thr Pro Ile Arg Pro Glu Cys Asp Leu
210 215 220
Thr Ile Phe Val Phe Ala Leu Phe Asn Glu Asn Met Lys Pro Gly Pro
225 230 235 240
Thr Ser Glu Arg Asn Tyr Gly Leu Phe Asn Pro Asp Gly Thr Pro Val
245 250 255
Tyr Ser Leu Gly Ile Lys Thr Ser Ser Thr His Ser Ser Gly Ser Gly
260 265 270
Ser Ser Asn Ser Thr Gly Gly Ser Ser Ser Gly Gly Gly Asn Thr
275 280 285
Gly Gly Ser Ser Ser Gly Gly Ile Tyr Gln Pro Val Thr Gly Asn

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

Met Gly Phe Ile Gly Lys Ser Val Leu Val Ser Leu Val Ala Leu Trp
1 5 10 15
Cys Phe Thr Ser Ser Val Phe Thr Glu Glu Val Asn His Lys Thr Gln
20 25 30
Thr Pro Ser Leu Ala Pro Gly Lys Asp Thr Ala Val Glu Val Ala Val
35 40 45
Glu Asp Val Leu Trp Ile Val Arg Arg Ser Val Ser Leu Ile Val Lys
50 55 60

Ile
65

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1560

(D) OTHER INFORMATION: / Ceres Seq. ID 1567164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

aaaagctctgt	ttattcaaga	ttattccgat	aatgcagtc	ctctccacc	cacacaccat	60
ctctctctct	ctccccagaa	ctctccgtc	tcgtctttt	ccctctcttc	actcccttgc	120
tttccccact	cgattaccgt	ctcttttcta	ttctttctca	acgtcgatcc	cccccgatgc	180
cgccgatgat	ttcattgtcg	gtgactgtct	cgctctacgag	gacggcgctt	tcgaagaccc	240
ttaccttgat	aaggaggtca	ctcaggttgc	gaagcaggag	cgcaagaaga	atcgccgtgg	300
cggggctaag	agatttagat	aatccgagat	tgagcccgag	aacctctgtc	cgagggaagt	360
gagggtatt	caggcggagg	tgaatctgac	gaagaaggac	aagcgcaaaa	tagcgcagga	420
gatggagttc	ggggttcggg	tggagaaaga	gaggcaagg	ctaattccgc	tagggaaagt	480
tgacttgaa	gactttctca	cgtaacaaga	agccaagtgt	gctcaattga	ggcctgtcat	540
ctctgataaa	ccgggaatt	ttctccgacg	cagtggagcg	tcaagcgatg	gagagaccgc	600
tgatatcatc	ccagcgcagc	gagtggtccc	taagaacctc	agatgggcag	tttacggaaa	660
gggatttcgc	acggttgcca	agttcttcaa	tagcgacaag	tacgatccca	gcgacaagaa	720
atcccgacgc	ctctgaaagc	tgctttcaaa	agaagagaag	tttatgtcta	atagccggaa	780
tcctgacctc	gcggttgcca	catcaaaaaa	atggcttctc	cttcacacac	tggcagcatg	840
tggaagagtt	tatctggttg	attccttgct	aaagcacaat	cttgatatca	atgcaaccga	900
tggtggcgcc	ttgacagtat	ttcaccgagc	aatcatttgt	aagaagcagg	ctattactaa	960
ctacctgctg	agggaaatcgg	caaatccatt	tggttttgat	gacgaagggt	cgaccttgat	1020
gcactatgct	gtgcaaacag	catcagctcc	cacaataaaa	cttctctcat	tgtataaacg	1080
tgataaaac	gctcaggaca	ggcagcgggt	gactccactg	cacgttgtag	tacaggccag	1140
agaagaagac	attgtaaagc	ttcttttgat	aaaagggcgc	gacatagaag	tgaagaacaa	1200
ggatgggtta	actccgcttg	ggctttgcct	ctaccttgga	agagagatga	ggacgtatgc	1260
agggtgatgaa	gctgttgaaa	gagtttccac	ttagcagaca	caagaagaga	tttgtaacaa	1320
cagCatgaag	atatttgata	gtcctttcaa	tttcagcttg	agatacctc	acttatgaga	1380
acctgagaaa	aggagatgga	ggtaaaagtg	atgattaggg	cattggaacc	tcggagtcgg	1440
atgtgggtcca	ctgtctcact	tccttaaat	tggtttgctg	ttagtcttat	ccatcgattt	1500
tggtatattt	tcacaaactg	atccattctt	aaagaaaata	tctgaaaata	aataaaaagt	1560

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..430

(D) OTHER INFORMATION: / Ceres Seq. ID 1567165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..420

(D) OTHER INFORMATION: / Ceres Seq. ID 1567166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

Met	Gln	Ser	Leu	Ser	Thr	Pro	His	Thr	Ile	Ser	Leu	Leu	Leu	Pro	Arg
1			5						10					15	
Thr	Ser	Pro	Ser	Arg	Leu	Ser	Pro	Ser	Ser	Leu	His	Ser	Leu	Ala	Phe
			20					25						30	
Thr	Arg	Leu	Arg	Ser	Leu	Ser	Tyr	Ser	Ser	Gln	Thr	Ser	Ile	Leu	Pro
			35				40					45			
Asp	Ala	Gly	Asp	Asp	Phe	Ile	Val	Gly	Asp	Cys	Leu	Val	Tyr	Glu	Asp
			50			55					60				
Gly	Val	Phe	Glu	Asp	Pro	Tyr	Leu	Asp	Lys	Glu	Val	Thr	Gln	Val	Ala
			65			70			75					80	
Lys	Gln	Glu	Arg	Lys	Lys	Asn	Arg	Arg	Gly	Gly	Ala	Lys	Arg	Leu	Asp
			85						90					95	
Glu	Ser	Glu	Ile	Glu	Pro	Glu	Asn	Leu	Val	Pro	Glu	Glu	Trp	Arg	Asp
			100					105					110		
Ile	Gln	Ala	Glu	Val	Asn	Leu	Thr	Lys	Lys	Asp	Lys	Arg	Lys	Ile	Ala
			115				120						125		
Gln	Glu	Met	Glu	Phe	Gly	Val	Arg	Val	Glu	Lys	Lys	Arg	Gln	Gly	Leu
			130			135						140			
Ile	Pro	Leu	Arg	Lys	Val	Asp	Leu	Asn	Asp	Phe	Leu	Thr	Tyr	Lys	Glu
			145			150				155				160	
Ala	Lys	Leu	Ala	Gln	Leu	Arg	Pro	Val	Ile	Leu	Asp	Lys	Pro	Gly	Asn
			165					170						175	
Phe	Ser	Asp	Asp	Ser	Gly	Ala	Ser	Ser	Asp	Gly	Glu	Thr	Ala	Val	Ser
			180					185					190		
Ser	Pro	Ser	Glu	Arg	Val	Ala	Pro	Lys	Asn	Pro	Arg	Trp	Ala	Val	Tyr
			195				200					205			
Gly	Lys	Gly	Phe	Asp	His	Val	Ala	Lys	Phe	Phe	Asn	Ser	Asp	Lys	Tyr
			210			215					220				
Asp	Pro	Ser	Asp	Lys	Lys	Ser	Asp	Gly	Pro	Arg	Lys	Leu	Leu	Ser	Lys
			225			230				235				240	
Glu	Glu	Lys	Phe	Met	Leu	Asn	Ser	Arg	Asn	Pro	Asp	Leu	Ala	Val	Ala
			245						250					255	
Thr	Ser	Lys	Lys	Trp	Leu	Pro	Leu	His	Thr	Leu	Ala	Ala	Cys	Gly	Glu
			260					265					270		
Phe	Tyr	Leu	Val	Asp	Ser	Leu	Leu	Lys	His	Asn	Leu	Asp	Ile	Asn	Ala
			275				280					285			
Thr	Asp	Val	Gly	Gly	Leu	Thr	Val	Leu	His	Arg	Ala	Ile	Ile	Gly	Lys
			290			295					300				
Lys	Gln	Ala	Ile	Thr	Asn	Tyr	Leu	Leu	Arg	Glu	Ser	Ala	Asn	Pro	Phe
			305			310				315				320	
Val	Leu	Asp	Asp	Glu	Gly	Ala	Thr	Leu	Met	His	Tyr	Ala	Val	Gln	Thr
			325						330					335	
Ala	Ser	Ala	Pro	Thr	Ile	Lys	Leu	Leu	Leu	Leu	Tyr	Asn	Ala	Asp	Ile
			340					345					350		
Asn	Ala	Gln	Asp	Arg	Asp	Gly	Trp	Thr	Pro	Leu	His	Val	Ala	Val	Gln
			355				360					365			
Ala	Arg	Arg	Ser	Asp	Ile	Val	Lys	Leu	Leu	Leu	Ile	Lys	Gly	Ala	Asp
			370			375					380				
Ile	Glu	Val	Lys	Asn	Lys	Asp	Gly	Leu	Thr	Pro	Leu	Gly	Leu	Cys	Leu
			385			390				395				400	
Tyr	Leu	Gly	Glu	Ile	Arg	Thr	Tyr	Ala	Gly	Asp	Glu	Ala	Val	Glu	
			405					410					415		
Arg	Val	Ser	Thr												
			420												

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..290
(D) OTHER INFORMATION: / Ceres Seq. ID 1567167
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:
Met Glu Phe Gly Val Arg Val Glu Lys Lys Arg Gln Gly Leu Ile Pro
1 5 10 15
Leu Arg Lys Val Asp Leu Asn Asp Phe Leu Thr Tyr Lys Glu Ala Lys
20 25 30
Leu Ala Gln Leu Arg Pro Val Ile Leu Asp Lys Pro Gly Asn Phe Ser
35 40 45
Asp Asp Ser Gly Ala Ser Ser Asp Gly Glu Thr Ala Val Ser Ser Pro
50 55 60
Ser Glu Arg Val Ala Pro Lys Asn Pro Arg Trp Ala Val Tyr Gly Lys
65 70 75 80
Gly Phe Asp His Val Ala Lys Phe Phe Asn Ser Asp Lys Tyr Asp Pro
85 90 95
Ser Asp Lys Lys Ser Asp Gly Pro Arg Lys Leu Leu Ser Lys Glu Glu
100 105 110
Lys Phe Met Leu Asn Ser Arg Asn Pro Asp Leu Ala Val Ala Thr Ser
115 120 125
Lys Lys Trp Leu Pro Leu His Thr Leu Ala Ala Cys Gly Glu Phe Tyr
130 135 140
Leu Val Asp Ser Leu Leu Lys His Asn Leu Asp Ile Asn Ala Thr Asp
145 150 155 160
Val Gly Gly Leu Thr Val Leu His Arg Ala Ile Ile Gly Lys Lys Gln
165 170 175
Ala Ile Thr Asn Tyr Leu Leu Arg Glu Ser Ala Asn Pro Phe Val Leu
180 185 190
Asp Asp Glu Gly Ala Thr Leu Met His Tyr Ala Val Gln Thr Ala Ser
195 200 205
Ala Pro Thr Ile Lys Leu Leu Leu Leu Tyr Asn Ala Asp Ile Asn Ala
210 215 220
Gln Asp Arg Asp Gly Trp Thr Pro Leu His Val Ala Val Gln Ala Arg
225 230 235 240
Arg Ser Asp Ile Val Lys Leu Leu Leu Ile Lys Gly Ala Asp Ile Glu
245 250 255
Val Lys Asn Lys Asp Gly Leu Thr Pro Leu Gly Leu Cys Leu Tyr Leu
260 265 270
Gly Arg Glu Ile Arg Thr Tyr Ala Gly Asp Glu Ala Val Glu Arg Val
275 280 285
Ser Thr
290

(2) INFORMATION FOR SEQ ID NO:506:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1257

(D) OTHER INFORMATION: / Ceres Seq. ID 1567168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

agattctttc ttctaaaccc attcgctctc tccgatcaac acaacatttg atctaacggt

ttaattttct	cgagaaacgg	aagGaaaaca	aacagagcaa	tggcgctgat	gggacggtgc	120
ctgagctgaa	attgagagtc	gaagaagatt	cggataatgg	tgattatctg	aaattgagag	180
gaggatcaaa	tgaagaagat	gaagatcatc	cggcggaatc	atcgagatgt	ccgataggat	240
cggttaacttc	tgtctgggttc	tgggtgaaat	tgatctcctt	ggtogtttgt	ttgggttcat	300
tggcctttgt	tatcatcaaa	tgggttgggtc	cctttttgat	tgaaggagg	ctgattccat	360
ttataaatgt	gggtgagaaac	acattcagca	taccggttct	cggtctctca	ctatttgtct	420
cagtggcatt	gtttccaagc	attcttcttc	cttctctccc	ttccatgtgg	atggctgggtc	480
ttacatttgg	ttatggaaaa	gggtttcttc	tgattttatc	agctgcttcc	atcggttgta	540
ctcttctttt	cttaattgga	catctcttcc	tccacaagat	gcaagaatgg	ttgaagaaat	600
accctaaaaa	agcagccata	cttagagctg	ctggggaagg	aacctgggtt	catcagtttc	660
aagcagctac	actaatccgt	gtctctccat	ttccttacct	catttacaac	tactgcgctt	720
tagcgactgg	agtttcattat	ggtccttata	tcttaggctc	tcttgttgga	atggttcctg	780
agatctttgt	ctcaatttac	acgggtataa	tgctaaggac	actagcagtt	gcactagaca	840
cgagacacac	actttcgggt	gtggagatag	tgtggaatgt	tcttggcttc	tgtgtaactg	900
cgagcgcgac	tatagtcttg	acaatctatg	cgaagaagaa	gctaagtcg	atgcaatcag	960
aggacgtaga	gacattacaa	aatccaatac	tttattaact	cttttcacca	tgaccacaa	1020
ataccatcat	ctaacacgat	cttgaaattg	ataatatata	atgttttttt	tttttttttt	1080
ttattcttat	tcaattgaaa	atgaatattt	atgtcttttt	ctctgtgata	tatgatattg	1140
atcaattgaa	ttttgaaaa	ttccaatgta	tatttattag	atcatctaa	ttcttttctt	1200
tccttgcata	taattccact	tatgtatcat	ggaacaatgt	ctgtgtgggt	ttgtgttc	

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..177

(D) OTHER INFORMATION: / Ceres Seq. ID 1567169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

Met	Trp	Met	Ala	Gly	Leu	Thr	Phe	Gly	Tyr	Gly	Lys	Gly	Phe	Leu	Leu
1			5						10					15	
Ile	Leu	Ser	Ala	Ala	Ser	Ile	Gly	Val	Thr	Leu	Pro	Phe	Leu	Ile	Gly
			20						25					30	
His	Leu	Phe	Leu	His	Lys	Met	Gln	Glu	Trp	Leu	Lys	Lys	Tyr	Pro	Lys
			35						40					45	
Lys	Ala	Ala	Ile	Leu	Arg	Ala	Ala	Gly	Glu	Gly	Thr	Trp	Phe	His	Gln
			50						55					60	
Phe	Gln	Ala	Val	Thr	Leu	Ile	Arg	Val	Ser	Pro	Phe	Pro	Tyr	Ile	Ile
			65						70					75	
Tyr	Asn	Tyr	Cys	Ala	Leu	Ala	Thr	Gly	Val	His	Tyr	Gly	Pro	Tyr	Ile
			85						90					95	
Leu	Gly	Ser	Leu	Val	Gly	Met	Val	Pro	Glu	Ile	Phe	Val	Ser	Ile	Tyr
			100						105					110	
Thr	Gly	Ile	Met	Leu	Arg	Thr	Leu	Ala	Val	Ala	Ser	Asp	Thr	Arg	His
			115						120					125	
Thr	Leu	Ser	Val	Val	Glu	Ile	Val	Val	Asn	Val	Leu	Gly	Phe	Cys	Val
			130						135					140	
Thr	Ala	Ser	Ala	Thr	Ile	Val	Cys	Thr	Ile	Tyr	Ala	Lys	Lys	Lys	Leu
			145						150					155	
Ser	Ala	Met	Gln	Ser	Glu	Asp	Val	Glu	Thr	Leu	Gln	Asn	Pro	Ile	Leu
			165						170					175	

Tyr

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1567170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

Met	Ala	Gly	Leu	Thr	Phe	Gly	Tyr	Gly	Lys	Gly	Phe	Leu	Leu	Ile	Leu	
1			5					10						15		
Ser	Ala	Ala	Ser	Ile	Gly	Val	Thr	Leu	Pro	Phe	Leu	Ile	Gly	His	Leu	
			20					25					30			
Phe	Leu	His	Lys	Met	Gln	Glu	Trp	Leu	Lys	Lys	Tyr	Pro	Lys	Lys	Ala	
			35				40					45				
Ala	Ile	Leu	Arg	Ala	Ala	Gly	Glu	Gly	Thr	Trp	Phe	His	Gln	Phe	Gln	
			50			55					60					
Ala	Val	Thr	Leu	Ile	Arg	Val	Ser	Pro	Phe	Pro	Tyr	Ile	Ile	Tyr	Asn	
			65			70					75				80	
Tyr	Cys	Ala	Leu	Ala	Thr	Gly	Val	His	Tyr	Gly	Pro	Tyr	Ile	Leu	Gly	
			85						90					95		
Ser	Leu	Val	Gly	Met	Val	Pro	Glu	Ile	Phe	Val	Ser	Ile	Tyr	Thr	Gly	
			100					105					110			
Ile	Met	Leu	Arg	Thr	Leu	Ala	Val	Ala	Ser	Asp	Thr	Arg	His	Thr	Leu	
			115				120					125				
Ser	Val	Val	Glu	Ile	Val	Val	Asn	Val	Leu	Gly	Phe	Cys	Val	Thr	Ala	
			130				135				140					
Ser	Ala	Thr	Ile	Val	Cys	Thr	Ile	Tyr	Ala	Lys	Lys	Lys	Leu	Ser	Ala	
			145			150				155					160	
Met	Gln	Ser	Glu	Asp	Val	Glu	Thr	Leu	Gln	Asn	Pro	Ile	Leu	Tyr		
			165					170						175		

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1567171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

Met	Gln	Glu	Trp	Leu	Lys	Lys	Tyr	Pro	Lys	Lys	Ala	Ala	Ile	Leu	Arg	
1			5					10					15			
Ala	Ala	Gly	Glu	Gly	Thr	Trp	Phe	His	Gln	Phe	Gln	Ala	Val	Thr	Leu	
			20					25					30			
Ile	Arg	Val	Ser	Pro	Phe	Pro	Tyr	Ile	Ile	Tyr	Asn	Tyr	Cys	Ala	Leu	
			35				40				45					
Ala	Thr	Gly	Val	His	Tyr	Gly	Pro	Tyr	Ile	Leu	Gly	Ser	Leu	Val	Gly	
			50			55					60					
Met	Val	Pro	Glu	Ile	Phe	Val	Ser	Ile	Tyr	Thr	Gly	Ile	Met	Leu	Arg	
			65			70				75				80		
Thr	Leu	Ala	Val	Ala	Ser	Asp	Thr	Arg	His	Thr	Leu	Ser	Val	Val	Glu	
			85					90					95			
Ile	Val	Val	Asn	Val	Leu	Gly	Phe	Cys	Val	Thr	Ala	Ser	Ala	Thr	Ile	
			100				105						110			
Val	Cys	Thr	Ile	Tyr	Ala	Lys	Lys	Lys	Leu	Ser	Ala	Met	Gln	Ser	Glu	
			115				120					125				
Asp	Val	Glu	Thr	Leu	Gln	Asn	Pro	Ile	Leu	Tyr						
			130			135										

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1592 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1592
(D) OTHER INFORMATION: / Ceres Seq. ID 1567172
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

gtagtctctc	ttttataaac	cacttctcga	aaactgaaac	ctttgtagag	agaaccata	60
gttcgataaa	acattctttt	tgcacctgag	acttgccaac	ttggttttac	tcaaatgaag	120
atcttctctt	gttgatgggt	ataagttcaa	tatgatgaaa	agtittggcta	gtgcggttgg	180
agggaaagcg	gcgaggcgat	gtgatagctg	cgtaagagg	cgggcacgtt	ggtattgcgc	240
agctgatgat	gcctttcttt	gccatgcttg	tgacgggttg	gtccactcgg	caaaccctct	300
tgctcgtaga	cacgagagag	ttcgcttgaa	atcggtcagc	gcgggaaaaa	atcgccatgc	360
ctcgccgcct	caccaagcca	cgtggcatca	gggattttac	cgtaaacgtc	ggaccaccacg	420
tggaggcaag	aagagccaca	cgatggtttt	tcatgatctt	gtgccggaga	tgagccaggga	480
ggatcaagcg	gagagttacg	aggtggaaga	gcagctcata	tttgaggtgc	cggtgatgaa	540
ctcgatgggt	gaggagcaat	gctttaacca	atccctggag	aaacagaaat	agtttccaat	600
gatgccctta	agttttcaaga	gtagtgaacg	agaagatgac	gacaacgctg	agagtgtgtc	660
gaatgggttt	ttcccaaccg	acatggaact	agctcagttc	acagctgacg	tggagactct	720
actcgggtga	ggggatcgag	agtttcatc	catagaagaa	ctagggttag	gtgaagtgtt	780
aaagatcgaa	aaagaggagg	tggaggaaga	ggaaggaggt	gtgacaagag	aagtgcatac	840
tcaagatgaa	ggtgatgaga	catccccatt	tgaataaagc	tttgactacg	agtaacacga	900
caagaccaca	ttcgatgaag	gagaagaaga	tgagaaagaa	gacgtgatga	agaaatgtgat	960
ggagatggga	gtgaatgaga	tgagtgggtg	gattaaagaa	gagaagaagg	agaaagctct	1020
tatgcttaga	ttggactatg	aatcagtcac	ttccacttgg	ggaggccaa	ggagcccatg	1080
gaccgcocgg	gtgccatctg	aaatagacct	cgacatggtt	tgtttcccaa	cccatccatt	1140
gggtgaaagt	ggagcagagg	ctcatcatca	caaccacttc	gcggcctcag	ggttacacct	1200
aggagatgct	ggggatggag	gaagagagcg	taggttttca	agataccogag	agaaaaaggag	1260
gacaaggttg	ttctccaaga	agataaggta	cgaggtacgt	aaattgaaag	cagataaaag	1320
gcctcgcatg	aaaggaagggt	tcgtcaagag	atcttcaatt	ggtgttgctc	actaaagaac	1380
ttaatttaatt	atggatatta	aattactttg	ctctcatctt	gctttttgtg	tgctatagtt	1440
ttggtgattg	ttagctttct	ttttctgcat	tcatagagaa	ttttgcacgt	ttttgtgagc	1500
tacgtatgta	cataaatata	tcacaaaaaa	atgtgacat	cttgtaagca	ctgatttata	1560
tagtcgat	aacgtgaatt	ttgattgctg	gt			

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 407 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..407

(D) OTHER INFORMATION: / Ceres Seq. ID 1567173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

Met	Met	Lys	Ser	Leu	Ala	Ser	Ala	Val	Gly	Gly	Lys	Thr	Ala	Arg	Ala
1				5					10					15	
Cys	Asp	Ser	Cys	Val	Lys	Arg	Arg	Ala	Arg	Thr	Tyr	Cys	Ala	Ala	Asp
				20				25					30		
Asp	Ala	Phe	Leu	Cys	His	Ala	Cys	Asp	Gly	Ser	Val	His	Ser	Ala	Asn
				35				40				45			
Pro	Leu	Ala	Arg	Arg	His	Glu	Arg	Val	Arg	Leu	Lys	Ser	Ala	Ser	Ala
				50			55				60				
Gly	Lys	Tyr	Arg	His	Ala	Ser	Pro	Pro	His	Gln	Ala	Thr	Trp	His	Gln
				65		70				75				80	
Gly	Phe	Thr	Arg	Lys	Lys	Ala	Thr	Pro	Arg	Gly	Gly	Lys	Lys	Ser	His
				85				90						95	

Thr Met Val Phe His Asp Leu Val Pro Glu Met Ser Thr Glu Asp Gln
100 105 110
Ala Glu Ser Tyr Glu Val Glu Glu Gln Leu Ile Phe Glu Val Pro Val
115 120 125
Met Asn Ser Met Val Glu Glu Gln Cys Phe Asn Gln Ser Leu Glu Lys
130 135 140
Gln Asn Glu Phe Pro Met Met Pro Leu Ser Phe Lys Ser Ser Asp Glu
145 150 155 160
Glu Asp Asp Asp Asn Ala Glu Ser Cys Leu Asn Gly Leu Phe Pro Thr
165 170 175
Asp Met Glu Leu Ala Gln Phe Thr Ala Asp Val Glu Thr Leu Leu Gly
180 185 190
Gly Gly Asp Arg Glu Phe His Ser Ile Glu Glu Leu Gly Leu Gly Glu
195 200 205
Met Leu Lys Ile Glu Lys Glu Glu Val Glu Glu Glu Glu Gly Val Val
210 215 220
Thr Arg Glu Val His Asp Gln Asp Glu Gly Asp Glu Thr Ser Pro Phe
225 230 235 240
Glu Ile Ser Phe Asp Tyr Glu Tyr Thr His Lys Thr Thr Phe Asp Glu
245 250 255
Gly Glu Glu Asp Glu Lys Glu Asp Val Met Lys Asn Val Met Glu Met
260 265 270
Gly Val Asn Glu Met Ser Gly Gly Ile Lys Glu Glu Lys Lys Glu Lys
275 280 285
Ala Leu Met Leu Arg Leu Asp Tyr Glu Ser Val Ile Ser Thr Trp Gly
290 295 300
Gly Gln Gly Ile Pro Trp Thr Ala Arg Val Pro Ser Glu Ile Asp Leu
305 310 315 320
Asp Met Val Cys Phe Pro Thr His Thr Met Gly Glu Ser Gly Ala Glu
325 330 335
Ala His His His Asn His Phe Arg Gly Leu Gly Leu His Leu Gly Asp
340 345 350
Ala Gly Asp Gly Gly Arg Glu Ala Arg Val Ser Arg Tyr Arg Glu Lys
355 360 365
Arg Arg Thr Arg Leu Phe Ser Lys Lys Ile Arg Tyr Glu Val Arg Lys
370 375 380
Leu Asn Ala Asp Lys Arg Pro Arg Met Lys Gly Arg Phe Val Lys Arg
385 390 395 400
Ser Ser Ile Gly Val Ala His
405

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 406 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..406

(D) OTHER INFORMATION: / Ceres Seq. ID 1567174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

Met Lys Ser Leu Ala Ser Ala Val Gly Gly Lys Thr Ala Arg Ala Cys
1 5 10 15
Asp Ser Cys Val Lys Arg Arg Ala Arg Trp Tyr Cys Ala Ala Asp Asp
20 25 30
Ala Phe Leu Cys His Ala Cys Asp Gly Ser Val His Ser Ala Asn Pro
35 40 45
Leu Ala Arg Arg His Glu Arg Val Arg Leu Lys Ser Ala Ser Ala Gly
50 55 60
Lys Tyr Arg His Ala Ser Pro His Gln Ala Thr Trp His Gln Gly

65				70				75				80
Phe	Thr	Arg	Lys	Ala	Arg	Thr	Pro	Arg	Gly	Gly	Lys	Lys
				85				90				95
Met	Val	Phe	His	Asp	Leu	Val	Pro	Glu	Met	Ser	Thr	Glu
				100				105				110
Glu	Ser	Tyr	Glu	Val	Glu	Glu	Gln	Leu	Ile	Phe	Glu	Val
				115				120				125
Asn	Ser	Met	Val	Glu	Glu	Gln	Cys	Phe	Asn	Gln	Ser	Leu
				130				135				140
Asn	Glu	Phe	Pro	Met	Met	Pro	Leu	Ser	Phe	Lys	Ser	Ser
				145				150				155
Asp	Asp	Asp	Asn	Ala	Glu	Ser	Cys	Leu	Asn	Gly	Leu	Phe
				165				170				175
Met	Glu	Leu	Ala	Gln	Phe	Thr	Ala	Asp	Val	Glu	Thr	Leu
				180				185				190
Gly	Asp	Arg	Glu	Phe	His	Ser	Ile	Glu	Glu	Leu	Gly	Leu
				195				200				205
Leu	Lys	Ile	Glu	Lys	Glu	Glu	Val	Glu	Glu	Glu	Gly	Val
				210				215				220
Arg	Glu	Val	His	Asp	Gln	Asp	Glu	Gly	Asp	Glu	Thr	Ser
				225				230				235
Ile	Ser	Phe	Asp	Tyr	Glu	Tyr	Thr	His	Lys	Thr	Thr	Phe
				245				250				255
Glu	Glu	Asp	Glu	Lys	Glu	Asp	Val	Met	Lys	Asn	Val	Met
				260				265				270
Val	Asn	Glu	Met	Ser	Gly	Gly	Ile	Lys	Glu	Glu	Lys	Lys
				275				280				285
Leu	Met	Leu	Arg	Leu	Asp	Tyr	Glu	Ser	Val	Ile	Ser	Thr
				290				295				300
Gln	Gly	Ile	Pro	Trp	Thr	Ala	Arg	Val	Pro	Ser	Glu	Ile
				305				310				315
Met	Val	Cys	Phe	Pro	Thr	His	Thr	Met	Gly	Glu	Ser	Gly
				325				330				335
His	His	His	Asn	His	Phe	Arg	Gly	Leu	Gly	Leu	His	Leu
				340				345				350
Gly	Asp	Gly	Gly	Arg	Glu	Ala	Arg	Val	Ser	Arg	Tyr	Arg
				355				360				365
Arg	Thr	Arg	Leu	Phe	Ser	Lys	Lys	Ile	Arg	Tyr	Glu	Val
				370				375				380
Asn	Ala	Asp	Lys	Arg	Pro	Arg	Met	Lys	Gly	Arg	Phe	Val
				385				390				395
Ser	Ile	Gly	Val	Ala	His							400
				405								

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..310

(D) OTHER INFORMATION: / Ceres Seq. ID 1567175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

Met	Val	Phe	His	Asp	Leu	Val	Pro	Glu	Met	Ser	Thr	Glu	Asp	Gln	Ala
1				5				10				15			
Glu	Ser	Tyr	Glu	Val	Glu	Glu	Gln	Leu	Ile	Phe	Glu	Val	Pro	Val	Met
				20				25				30			
Asn	Ser	Met	Val	Glu	Glu	Gln	Cys	Phe	Asn	Gln	Ser	Leu	Glu	Lys	Gln
				35				40				45			

```

Asn Glu Phe Pro Met Met Pro Leu Ser Phe Lys Ser Ser Asp Glu Glu
  50          55          60
Asp Asp Asp Asn Ala Glu Ser Cys Leu Asn Gly Leu Phe Pro Thr Asp
  65          70          75          80
Met Glu Leu Ala Gln Phe Thr Ala Asp Val Glu Thr Leu Leu Gly Gly
  85          90          95
Gly Asp Arg Glu Phe His Ser Ile Glu Leu Gly Leu Gly Glu Met
  100         105         110
Leu Lys Ile Glu Lys Glu Glu Val Glu Glu Glu Gly Val Val Thr
  115         120         125
Arg Glu Val His Asp Gln Asp Glu Gly Asp Glu Thr Ser Pro Phe Glu
  130         135         140
Ile Ser Phe Asp Tyr Glu Tyr Thr His Lys Thr Thr Phe Asp Glu Gly
  145         150         155         160
Glu Glu Asp Glu Lys Glu Asp Val Met Lys Asn Val Met Glu Met Gly
  165         170         175
Val Asn Glu Met Ser Gly Gly Ile Lys Glu Glu Lys Lys Glu Lys Ala
  180         185         190
Leu Met Leu Arg Leu Asp Tyr Glu Ser Val Ile Ser Thr Trp Gly Gly
  195         200         205
Gln Gly Ile Pro Trp Thr Ala Arg Val Pro Ser Glu Ile Asp Leu Asp
  210         215         220
Met Val Cys Phe Pro Thr His Thr Met Gly Glu Ser Gly Ala Glu Ala
  225         230         235         240
His His His Asn His Phe Arg Gly Leu Gly Leu His Leu Gly Asp Ala
  245         250         255
Gly Asp Gly Gly Arg Glu Ala Arg Val Ser Arg Tyr Arg Glu Lys Arg
  260         265         270
Arg Thr Arg Leu Phe Ser Lys Lys Ile Arg Tyr Glu Val Arg Lys Leu
  275         280         285
Asn Ala Asp Lys Arg Pro Arg Met Lys Gly Arg Phe Val Lys Arg Ser
  290         295         300
Ser Ile Gly Val Ala His
  305         310

```

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1071 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1071
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

```

attgtgttag tggtaaatcaa atccgggtgaa aatggagcgg aGccgagtga ccagagaagc      60
accgaccgga accaggatcc tgcttgcttc actctctgcg atggttgacg agtcaagtac      120
gtttccgatt gatctcaaca agactagaat gcagctccat gggtccggat ccgcttctgg      180
tcgcgatcgg attggcgctt tcggagtcgt atcggagatt cgcgagaaag aaggagtgat      240
tggtctctac aaaggctctat ctccggcgat tatcagacac ctgttctaca cgctatcag      300
aatcatttga tacgagaatt tgaaaggact catcgtcaga tctgaaacta acaatagcga      360
gtctctcttc ctccgccaca aggtctctct cggaggattt tctggtgtta tagctcaggt      420
agtgtcagtg ccagctgatt tggtcaaagt gagaatgcac gcagattgta gattgggtgag      480
ccaaggcctg aaaccggagt actcgggacc aatcgaggct ttaccaaaaa tctacaatc      540
agaaggagta aaagggttat ggaaagggtg tcttccaaac atccagagag catttctagt      600
gaatatggga gaactagctt gctatgatca cgcctcaaac tttgtcatcg ataagaagat      660
tgctgaggat aactattttg cgcacactct tgctcttata atgtccggtc ttgcttcgac      720
aagtttgagt tgtccagctg atgtggtgaa gacgaggatg atgaaccagg gtgaaaaatg      780
tgtgtacaga aattcttaac actgtttggc gaagacggtt aagtttgaa gaaataagag      840
tttgtgtaaa ggttctctcc cgacatgggc aaggcttgga ccgtggcagt tcgtgttttg      900

```

gggtctcctat gagaagttaa gactgctggc aggaatctct tccttctaga cctgagaacc 960
tggaagaacga aatttgagat ttgtgttctt tagttcttac ttgttagttg ttacacattt 1020
tgtaagaacc ttgagaagta gcatcagttt ctgattaacg cgagaagagt t

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..305

(D) OTHER INFORMATION: / Ceres Seq. ID 1567184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

Met Glu Arg Ser Arg Val Thr Arg Glu Ala Pro Thr Gly Thr Arg Ile
1 5 10 15
Leu Leu Ala Ser Leu Ser Ala Met Val Ala Glu Ser Val Thr Phe Pro
20 25 30
Ile Asp Leu Thr Lys Thr Arg Met Gln Leu His Gly Ser Gly Ser Ala
35 40 45
Ser Gly Ala His Arg Ile Gly Ala Phe Gly Val Val Ser Glu Ile Ala
50 55 60
Arg Lys Glu Gly Val Ile Gly Leu Tyr Lys Gly Leu Ser Pro Ala Ile
65 70 75 80
Ile Arg His Leu Phe Tyr Thr Pro Ile Arg Ile Ile Gly Tyr Glu Asn
85 90 95
Leu Lys Gly Leu Ile Val Arg Ser Glu Thr Asn Asn Ser Glu Ser Leu
100 105 110
Pro Leu Ala Thr Lys Ala Leu Val Gly Gly Phe Ser Gly Val Ile Ala
115 120 125
Gln Val Val Ala Ser Pro Ala Asp Leu Val Lys Val Arg Met Gln Ala
130 135 140
Asp Gly Arg Leu Val Ser Gln Gly Leu Lys Pro Arg Tyr Ser Gly Pro
145 150 155 160
Ile Glu Ala Phe Thr Lys Ile Leu Gln Ser Glu Gly Val Lys Gly Leu
165 170 175
Trp Lys Gly Val Leu Pro Asn Ile Gln Arg Ala Phe Leu Val Asn Met
180 185 190
Gly Glu Leu Ala Cys Tyr Asp His Ala Lys His Phe Val Ile Asp Lys
195 200 205
Lys Ile Ala Glu Asp Asn Ile Phe Ala His Thr Leu Ala Ser Ile Met
210 215 220
Ser Gly Leu Ala Ser Thr Ser Leu Ser Cys Pro Ala Asp Val Val Lys
225 230 235 240
Thr Arg Met Met Asn Gln Gly Glu Asn Ala Val Tyr Arg Asn Ser Tyr
245 250 255
Asp Cys Leu Val Lys Thr Val Lys Phe Glu Gly Ile Arg Ala Leu Trp
260 265 270
Lys Gly Phe Phe Pro Thr Trp Ala Arg Leu Gly Pro Trp Gln Phe Val
275 280 285
Phe Trp Val Ser Tyr Glu Lys Phe Arg Leu Leu Ala Gly Ile Ser Ser
290 295 300
Phe
305

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..282

(D) OTHER INFORMATION: / Ceres Seq. ID 1567185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

Met	Val	Ala	Glu	Ser	Val	Thr	Phe	Pro	Ile	Asp	Leu	Thr	Lys	Thr	Arg
1			5						10					15	
Met	Gln	Leu	His	Gly	Ser	Gly	Ser	Ala	Ser	Gly	Ala	His	Arg	Ile	Gly
			20					25					30		
Ala	Phe	Gly	Val	Val	Ser	Glu	Ile	Ala	Arg	Lys	Glu	Gly	Val	Ile	Gly
			35					40					45		
Leu	Tyr	Lys	Gly	Leu	Ser	Pro	Ala	Ile	Ile	Arg	His	Leu	Phe	Tyr	Thr
			50				55				60				
Pro	Ile	Arg	Ile	Ile	Gly	Tyr	Glu	Asn	Leu	Lys	Gly	Leu	Ile	Val	Arg
					70					75				80	
Ser	Glu	Thr	Asn	Asn	Ser	Glu	Ser	Leu	Pro	Leu	Ala	Thr	Lys	Ala	Leu
				85					90					95	
Val	Gly	Gly	Phe	Ser	Gly	Val	Ile	Ala	Gln	Val	Val	Ala	Ser	Pro	Ala
			100					105					110		
Asp	Leu	Val	Lys	Val	Arg	Met	Gln	Ala	Asp	Gly	Arg	Leu	Val	Ser	Gln
			115				120					125			
Gly	Leu	Lys	Pro	Arg	Tyr	Ser	Gly	Pro	Ile	Glu	Ala	Phe	Thr	Lys	Ile
			130				135				140				
Leu	Gln	Ser	Glu	Gly	Val	Lys	Gly	Leu	Trp	Lys	Gly	Val	Leu	Pro	Asn
			145				150				155			160	
Ile	Gln	Arg	Ala	Phe	Leu	Val	Asn	Met	Gly	Glu	Leu	Ala	Cys	Tyr	Asp
				165					170					175	
His	Ala	Lys	His	Phe	Val	Ile	Asp	Lys	Lys	Ile	Ala	Glu	Asp	Asn	Ile
			180					185					190		
Phe	Ala	His	Thr	Leu	Ala	Ser	Ile	Met	Ser	Gly	Leu	Ala	Ser	Thr	Ser
			195					200					205		
Leu	Ser	Cys	Pro	Ala	Asp	Val	Val	Lys	Thr	Arg	Met	Met	Asn	Gln	Gly
			210				215						220		
Glu	Asn	Ala	Val	Tyr	Arg	Asn	Ser	Tyr	Asp	Cys	Leu	Val	Lys	Thr	Val
			225				230				235			240	
Lys	Phe	Glu	Gly	Ile	Arg	Ala	Leu	Trp	Lys	Gly	Phe	Phe	Pro	Thr	Trp
				245					250					255	
Ala	Arg	Leu	Gly	Pro	Trp	Gln	Phe	Val	Phe	Trp	Val	Ser	Tyr	Glu	Lys
				260				265					270		
Phe	Arg	Leu	Leu	Ala	Gly	Ile	Ser	Ser	Phe						
			275				280								

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..266

(D) OTHER INFORMATION: / Ceres Seq. ID 1567186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

Met	Gln	Leu	His	Gly	Ser	Gly	Ser	Ala	Ser	Gly	Ala	His	Arg	Ile	Gly
1			5							10				15	
Ala	Phe	Gly	Val	Val	Ser	Glu	Ile	Ala	Arg	Lys	Glu	Gly	Val	Ile	Gly
			20					25					30		
Leu	Tyr	Lys	Gly	Leu	Ser	Pro	Ala	Ile	Ile	Arg	His	Leu	Phe	Tyr	Thr
			35				40					45			
Pro	Ile	Arg	Ile	Ile	Gly	Tyr	Glu	Asn	Leu	Lys	Gly	Leu	Ile	Val	Arg

50	55	60
Ser Glu Thr Asn Asn Ser Glu Ser Leu Pro Leu Ala Thr Lys Ala Leu		
65	70	75
Val Gly Gly Phe Ser Gly Val Ile Ala Gln Val Val Ala Ser Pro Ala		80
85	90	95
Asp Leu Val Lys Val Arg Met Gln Ala Asp Gly Arg Leu Val Ser Gln		
100	105	110
Gly Leu Lys Pro Arg Tyr Ser Gly Pro Ile Glu Ala Phe Thr Lys Ile		
115	120	125
Leu Gln Ser Glu Gly Val Lys Gly Leu Trp Lys Gly Val Leu Pro Asn		
130	135	140
Ile Gln Arg Ala Phe Leu Val Asn Met Gly Glu Leu Ala Cys Tyr Asp		
145	150	155
His Ala Lys His Phe Val Ile Asp Lys Lys Ile Ala Glu Asp Asn Ile		
165	170	175
Phe Ala His Thr Leu Ala Ser Ile Met Ser Gly Leu Ala Ser Thr Ser		
180	185	190
Leu Ser Cys Pro Ala Asp Val Val Lys Thr Arg Met Met Asn Gln Gly		
195	200	205
Glu Asn Ala Val Tyr Arg Asn Ser Tyr Asp Cys Leu Val Lys Thr Val		
210	215	220
Lys Phe Glu Gly Ile Arg Ala Leu Trp Lys Gly Phe Phe Pro Thr Trp		
225	230	235
Ala Arg Leu Gly Pro Trp Gln Phe Val Phe Trp Val Ser Tyr Glu Lys		
245	250	255
Phe Arg Leu Leu Ala Gly Ile Ser Ser Phe		
260	265	

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

gcgtgtgcat	cggttttctca	gattcctgaa	taatcattcc	cttcggatcc	caaaatcccc	60
aaacctcacc	cactcctcca	tctcccggtat	tcggattccc	agaatcatgc	ccatggagaaa	120
cgacaatggc	ccacacgttg	gcaacgtcgt	cgctcaccgt	gagcaagcga	ccaagattaa	180
cgagactgat	ggaaggttgc	cgagagaatcg	cgagaccggg	gttgctctcg	acaccggaaag	240
tggtagcgag	agagagagagc	aagggggttg	agagtcggca	gttgctgtgg	cggtgccggg	300
ggaggagagc	ggatcgattt	cggtggggaga	gctacctgct	ccccgatctt	ctctgtctag	360
agttccgttt	actaatctaa	gccaaattga	tgccgatctt	gctcttgctc	gcacactcca	420
agaacaggag	cgggcgctata	tgatgttgac	catgaatagt	gaaatcagtg	actatggagc	480
ctgggaaact	ggaagctatg	tatacagatga	ggatgagttt	gatgaccccg	agaatgagga	540
tgaggatgat	gatgaagatg	aatatgaaac	agatgatgat	cctcaggaag	atgggcttga	600
tgccaattgt	cacgcgaatg	aagatgatca	aggaagatgac	gggAactctg	acattgaaga	660
agttgtctat	acagatgatg	aggcctatgc	tagagctctt	caagaagctg	aagaaaagga	720
tatggctgct	agattgtctg	ccttatctgg	gttagoaaac	cggtgtggtg	aaagctcaga	780
ggatgagagt	catacttctc	aggatgccag	ggatgagatg	gatcctgatg	agctttcata	840
tgaggagttg	cttgcaacttg	gcgacattgt	gggaaccgaa	agtagaggtat	tgctgtctga	900
tacaattgct	tctttgcctt	caaaaagata	taaagaagga	gacaatcaga	acggaaccaa	960
tgagtcatgt	gttatatgtc	gtttagacta	tgaggatgac	gaagacctga	tactgtctcc	1020
atgcaaacat	tcttaaccat	cggagtgcac	aaacaactgg	ttgaagataa	ataaggtttg	1080
ccccgtatgc	agtgcagaag	tttcaacctc	gaacctctga	caaaagctga	gaggcagaag	1140
aagaaagatt	cagaaagaat	cataagctaa	gaacctcaaa	accttagctg	ccgtgtttga	1200
cactctttat	aaacaaaata	acatcatcag	atttccttgg	atcctttaaa	aaatctcaaa	1260
gattgg						

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 375 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..375

(D) OTHER INFORMATION: / Ceres Seq. ID 1567210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

Ser Cys His Arg Phe Leu Arg Phe Leu Asn Asn His Ser Leu Pro Ile
1 5 10 15
Pro Lys Ser Pro Asn Leu Ile His Ser Ser Ile Ser Arg Ile Arg Ile
20 25 30
Pro Arg Ile Met Pro Met Glu Asn Asp Asn Gly Pro His Val Gly Asn
35 40 45
Val Val Val Thr Ala Glu Gln Ala Thr Lys Ile Asn Glu Thr Asp Gly
50 55 60
Arg Leu Pro Glu Asn Arg Gln Thr Gly Val Val Ser Asp Thr Gly Ser
65 70 75 80
Gly Ser Glu Arg Gly Glu Gln Gly Val Gly Ser Ala Val Ala Val
85 90 95
Ala Val Pro Val Glu Glu Ser Gly Ser Ile Ser Val Gly Glu Leu Pro
100 105 110
Ala Pro Arg Ser Ser Ser Ala Arg Val Pro Phe Thr Asn Leu Ser Gln
115 120 125
Ile Asp Ala Asp Leu Ala Leu Ala Arg Thr Leu Gln Glu Gln Glu Arg
130 135 140
Ala Tyr Met Met Leu Thr Met Asn Ser Glu Ile Ser Asp Tyr Gly Ser
145 150 155 160
Trp Glu Thr Gly Ser Tyr Val Tyr Asp Glu Asp Glu Phe Asp Asp Pro
165 170 175
Glu Asn Glu Asp Glu Asp Asp Asp Glu Asp Glu Tyr Glu Thr Asp Asp
180 185 190
Asp Pro Gln Glu Asp Gly Leu Asp Val Asn Val His Ala Asn Glu Asp
195 200 205
Asp Gln Glu Asp Asp Gly Asn Ser Asp Ile Glu Glu Val Ala Tyr Thr
210 215 220
Asp Asp Glu Ala Tyr Ala Arg Ala Leu Gln Glu Ala Glu Glu Arg Asp
225 230 235 240
Met Ala Ala Arg Leu Ser Ala Leu Ser Gly Leu Ala Asn Arg Val Val
245 250 255
Glu Asp Leu Glu Asp Glu Ser His Thr Ser Gln Asp Ala Arg Asp Glu
260 265 270
Met Asp Pro Asp Glu Leu Ser Tyr Glu Glu Leu Leu Ala Leu Gly Asp
275 280 285
Ile Val Gly Thr Glu Ser Arg Gly Leu Ser Ala Asp Thr Ile Ala Ser
290 295 300
Leu Pro Ser Lys Arg Tyr Lys Glu Gly Asp Asn Gln Asn Gly Thr Asn
305 310 315 320
Glu Ser Cys Val Ile Cys Arg Leu Asp Tyr Glu Asp Asp Glu Asp Leu
325 330 335
Ile Leu Leu Pro Cys Lys His Ser Tyr His Ser Glu Cys Ile Asn Asn
340 345 350
Trp Leu Lys Ile Asn Lys Val Cys Pro Val Cys Ser Ala Glu Val Ser
355 360 365
Thr Ser Thr Ser Gly Gln Ser
370 375

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..340

(D) OTHER INFORMATION: / Ceres Seq. ID 1567211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

Met Pro Met Glu Asn Asp Asn Gly Pro His Val Gly Asn Val Val Val
1 5 10 15
Thr Ala Glu Gln Ala Thr Lys Ile Asn Glu Thr Asp Gly Arg Leu Pro
20 25 30
Glu Asn Arg Gln Thr Gly Val Val Ser Asp Thr Gly Ser Gly Ser Glu
35 40 45
Arg Gly Glu Gln Gly Val Gly Glu Ser Ala Val Ala Val Ala Val Pro
50 55 60
Val Glu Glu Ser Gly Ser Ile Ser Val Gly Glu Leu Pro Ala Pro Arg
65 70 75 80
Ser Ser Ser Ala Arg Val Pro Phe Thr Asn Leu Ser Gln Ile Asp Ala
85 90 95
Asp Leu Ala Leu Ala Arg Thr Leu Gln Glu Gln Glu Arg Ala Tyr Met
100 105 110
Met Leu Thr Met Asn Ser Glu Ile Ser Asp Tyr Gly Ser Trp Glu Thr
115 120 125
Gly Ser Tyr Val Tyr Asp Glu Asp Glu Phe Asp Asp Pro Glu Asn Glu
130 135 140
Asp Glu Asp Asp Asp Glu Asp Glu Tyr Glu Thr Asp Asp Pro Gln
145 150 155 160
Glu Asp Gly Leu Asp Val Asn Val His Ala Asn Glu Asp Asp Gln Glu
165 170 175
Asp Asp Gly Asn Ser Asp Ile Glu Glu Val Ala Tyr Thr Asp Asp Glu
180 185 190
Ala Tyr Ala Arg Ala Leu Gln Glu Ala Glu Glu Arg Asp Met Ala Ala
195 200 205
Arg Leu Ser Ala Leu Ser Gly Leu Ala Asn Arg Val Val Glu Asp Leu
210 215 220
Glu Asp Glu Ser His Thr Ser Gln Asp Ala Arg Asp Glu Met Asp Pro
225 230 235 240
Asp Glu Leu Ser Tyr Glu Glu Leu Leu Ala Leu Gly Asp Ile Val Gly
245 250 255
Thr Glu Ser Arg Gly Leu Ser Ala Asp Thr Ile Ala Ser Leu Pro Ser
260 265 270
Lys Arg Tyr Lys Glu Gly Asp Asn Gln Asn Gly Thr Asn Glu Ser Cys
275 280 285
Val Ile Cys Arg Leu Asp Tyr Glu Asp Asp Glu Asp Leu Ile Leu Leu
290 295 300
Pro Cys Lys His Ser Tyr His Ser Glu Cys Ile Asn Asn Trp Leu Lys
305 310 315 320
Ile Asn Lys Val Cys Pro Val Cys Ser Ala Glu Val Ser Thr Ser Thr
325 330 335
Ser Gly Gln Ser
340

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 338 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..338

(D) OTHER INFORMATION: / Ceres Seq. ID 1567212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

Met Glu Asn Asp Asn Gly Pro His Val Gly Asn Val Val Val Thr Ala
1 5 10 15
Glu Gln Ala Thr Lys Ile Asn Glu Thr Asp Gly Arg Leu Pro Glu Asn
20 25 30
Arg Gln Thr Gly Val Val Ser Asp Thr Gly Ser Gly Ser Glu Arg Gly
35 40 45
Glu Gln Gly Val Gly Glu Ser Ala Val Ala Val Ala Val Pro Val Glu
50 55 60
Glu Ser Gly Ser Ile Ser Val Gly Glu Leu Pro Ala Pro Arg Ser Ser
65 70 75 80
Ser Ala Arg Val Pro Phe Thr Asn Leu Ser Gln Ile Asp Ala Asp Leu
85 90 95
Ala Leu Ala Arg Thr Leu Gln Glu Gln Glu Arg Ala Tyr Met Met Leu
100 105 110
Thr Met Asn Ser Glu Ile Ser Asp Tyr Gly Ser Trp Glu Thr Gly Ser
115 120 125
Tyr Val Tyr Asp Glu Asp Glu Phe Asp Asp Pro Glu Asn Glu Asp Glu
130 135 140
Asp Asp Asp Glu Asp Glu Tyr Glu Thr Asp Asp Asp Pro Gln Glu Asp
145 150 155 160
Gly Leu Asp Val Asn Val His Ala Asn Glu Asp Asp Gln Glu Asp Asp
165 170 175
Gly Asn Ser Asp Ile Glu Glu Val Ala Tyr Thr Asp Asp Glu Ala Tyr
180 185 190
Ala Arg Ala Leu Gln Glu Ala Glu Glu Arg Asp Met Ala Ala Arg Leu
195 200 205
Ser Ala Leu Ser Gly Leu Ala Asn Arg Val Val Glu Asp Leu Glu Asp
210 215 220
Glu Ser His Thr Ser Gln Asp Ala Arg Asp Glu Met Asp Pro Asp Glu
225 230 235 240
Leu Ser Tyr Glu Glu Leu Leu Ala Leu Gly Asp Ile Val Gly Thr Glu
245 250 255
Ser Arg Gly Leu Ser Ala Asp Thr Ile Ala Ser Leu Pro Ser Lys Arg
260 265 270
Tyr Lys Glu Gly Asp Asn Gln Asn Gly Thr Asn Glu Ser Cys Val Ile
275 280 285
Cys Arg Leu Asp Tyr Glu Asp Asp Glu Asp Leu Ile Leu Leu Pro Cys
290 295 300
Lys His Ser Tyr His Ser Glu Cys Ile Asn Asn Trp Leu Lys Ile Asn
305 310 315 320
Lys Val Cys Pro Val Cys Ser Ala Glu Val Ser Thr Ser Thr Ser Gly
325 330 335
Gln Ser

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1665 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1665

(D) OTHER INFORMATION: / Ceres Seq. ID 1567213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

gttaagagat	cettctccct	cttcgaagat	gagcggtagc	gtgaaggata	tcgtttcaaa	60
ggcggaGctt	gataacttgc	gccagagcgg	cgcaccagtc	gtgcttcaat	ctcgggcttc	120
ttggtgtgat	gcttcgaagc	agatggatca	agttttctct	catctcgtca	ctgatttccc	180
tcgtgctcac	ttctttaggg	ttgaagctga	ggaacatcct	gagatatctg	aggcttactc	240
tggtgctgct	gtgccttatt	togtctctct	caaggatggt	aaaactgtgg	atacacttga	300
gggtgcagat	ccatcaagtt	tagctaataa	ggttggcaaa	gttgctggtt	ctagtacttc	360
tcgggaGcct	gctgctcctg	caagcttagg	gttggtgctg	gggccaacga	ttcttgaaac	420
tgtaagagag	aatgcgaaag	cttctttaca	agaccgagct	cagcctgtat	ctaccgcgca	480
tgctctcaag	agccgttttg	aaaagctcac	taattctcac	cctgtcatgt	tattcatgaa	540
aggtatttct	gaagagccta	gggtgtgggtt	tagcaggaaa	gtagtgtaca	ttttgaaaga	600
ggttaacgct	gattttggaa	gttttgacat	actatcggat	aacgaaagtc	gagagggttt	660
gaagaatttc	tctaactggc	caacgtttcc	tcagctgtac	tgcaacggag	agcgtcttgg	720
tggaagtcat	atcgcataag	cgtgcacga	gagcggtgaa	ctaaaagatg	ctttcaaaaga	780
tcctggggatc	acgacagttg	gttcaaaaga	aagtcaggat	gaagctggaa	aaggaggagg	840
ggtagttcca	ggaaacacag	gccttaagtga	gacctccgga	gctcggctcg	aaggtctggt	900
caattccaaa	ccagttatgc	tggtcatgaa	aggaagacca	gaagaaccaa	agtgtggggtt	960
cagtgggaaa	gtgggttgaaa	tcttcaacca	agaaaaaatc	gagtttgga	gtttcgatat	1020
ccctcttagat	gacgaagttc	gccaaaggctt	taaaagtgat	tcaaaactgtg	caagctatcc	1080
tcagctttac	gtgaaaggcg	agcttatggg	tggatcagac	attgtcttgg	agatgcacaa	1140
gagcgttgag	gtcaaaaaag	tctaccgaga	aagggatcac	tggagaacag	agtcttgaag	1200
atagatgtga	ggcactgatt	aattcctcgg	aagtaatgct	attcatgaaa	ggttcaccag	1260
atgaaccgaa	atgcggattt	agctccaaa	ttgtgaaaag	attgagagga	gaaaacgtga	1320
gtttcggtac	gtttgatatc	ttgactgatg	aagaagtaag	gcaagggatt	aagaatttct	1380
caaatcggcc	aacttttctc	cagctatact	acaaaggtga	gttaatttga	ggatgtgata	1440
tcattatgga	gctaaagtga	agtggtgatc	tcaaagcaac	tctatccgat	taagtaatat	1500
atacaagctc	ctgctcgtct	gtttgccttg	gtgagagaga	acatttcagt	tatggttaata	1560
atagtcttta	gggtgttaca	acattgatat	tggtgcttct	caagcttttg	cttgttattt	1620
ctattgctga	gtctattaga	ttcataacta	ttttctctct	tttgt		

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..398

(D) OTHER INFORMATION: / Ceres Seq. ID 1567214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

Leu	Arg	Asp	Pro	Ser	Pro	Ser	Ser	Lys	Met	Ser	Gly	Thr	Val	Lys	Asp
1			5					10						15	
Ile	Val	Ser	Lys	Ala	Glu	Leu	Asp	Asn	Leu	Arg	Gln	Ser	Gly	Ala	Pro
			20					25						30	
Val	Val	Leu	His	Phe	Trp	Ala	Ser	Trp	Cys	Asp	Ala	Ser	Lys	Gln	Met
			35				40					45			
Asp	Gln	Val	Phe	Ser	His	Leu	Ala	Thr	Asp	Phe	Pro	Arg	Ala	His	Phe
			50				55				60				
Phe	Arg	Val	Glu	Ala	Glu	Glu	His	Pro	Glu	Ile	Ser	Glu	Ala	Tyr	Ser
			65				70				75			80	
Val	Ala	Ala	Val	Pro	Tyr	Phe	Val	Phe	Phe	Lys	Asp	Gly	Lys	Thr	Val
			85				90						95		
Asp	Thr	Leu	Glu	Gly	Ala	Asp	Pro	Ser	Ser	Leu	Ala	Asn	Lys	Val	Gly
			100				105						110		
Lys	Val	Ala	Gly	Ser	Ser	Thr	Ser	Ala	Glu	Pro	Ala	Ala	Pro	Ala	Ser
			115				120						125		
Leu	Gly	Leu	Ala	Ala	Gly	Pro	Thr	Ile	Leu	Glu	Thr	Val	Lys	Glu	Asn
			130				135						140		
Ala	Lys	Ala	Ser	Leu	Gln	Asp	Arg	Ala	Gln	Pro	Val	Ser	Thr	Ala	Asp
			145				150				155				160

Ala Leu Lys Ser Arg Leu Glu Lys Leu Thr Asn Ser His Pro Val Met
165 170 175
Leu Phe Met Lys Gly Ile Pro Glu Glu Pro Arg Cys Gly Phe Ser Arg
180 185 190
Lys Val Val Asp Ile Leu Lys Glu Val Asn Val Asp Phe Gly Ser Phe
195 200 205
Asp Ile Leu Ser Asp Asn Glu Val Arg Glu Gly Leu Lys Lys Phe Ser
210 215 220
Asn Trp Pro Thr Phe Pro Gln Leu Tyr Cys Asn Gly Glu Leu Leu Gly
225 230 235 240
Gly Ala Asp Ile Ala Ile Ala Met His Glu Ser Gly Glu Leu Lys Asp
245 250 255
Ala Phe Lys Asp Leu Gly Ile Thr Thr Val Gly Ser Lys Glu Ser Gln
260 265 270
Asp Glu Ala Gly Lys Gly Gly Gly Val Ser Ser Gly Asn Thr Gly Leu
275 280 285
Ser Glu Thr Leu Arg Ala Arg Leu Glu Gly Leu Val Asn Ser Lys Pro
290 295 300
Val Met Leu Phe Met Lys Gly Arg Pro Glu Glu Pro Lys Cys Gly Phe
305 310 315 320
Ser Gly Lys Val Val Glu Ile Leu Asn Gln Glu Lys Ile Glu Phe Gly
325 330 335
Ser Phe Asp Ile Leu Leu Asp Asp Glu Val Arg Gln Gly Leu Lys Val
340 345 350
Tyr Ser Asn Trp Ser Ser Tyr Pro Gln Leu Tyr Val Lys Gly Glu Leu
355 360 365
Met Gly Gly Ser Asp Ile Val Leu Glu Met Gln Lys Ser Gly Glu Leu
370 375 380
Lys Lys Val Tyr Arg Glu Arg Asp His Trp Arg Thr Glu Ser
385 390 395

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 389 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..389

(D) OTHER INFORMATION: / Ceres Seq. ID 1567215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

Met Ser Gly Thr Val Lys Asp Ile Val Ser Lys Ala Glu Leu Asp Asn
1 5 10 15
Leu Arg Gln Ser Gly Ala Pro Val Val Leu His Phe Trp Ala Ser Trp
20 25 30
Cys Asp Ala Ser Lys Gln Met Asp Gln Val Phe Ser His Leu Ala Thr
35 40 45
Asp Phe Pro Arg Ala His Phe Phe Arg Val Glu Ala Glu Glu His Pro
50 55 60
Glu Ile Ser Glu Ala Tyr Ser Val Ala Val Pro Tyr Phe Val Phe
65 70 75 80
Phe Lys Asp Gly Lys Thr Val Asp Thr Leu Glu Gly Ala Asp Pro Ser
85 90 95
Ser Leu Ala Asn Lys Val Gly Lys Val Ala Gly Ser Ser Thr Ser Ala
100 105 110
Glu Pro Ala Ala Pro Ala Ser Leu Gly Leu Ala Ala Gly Pro Thr Ile
115 120 125
Leu Glu Thr Val Lys Glu Asn Ala Lys Ala Ser Leu Gln Asp Arg Ala
130 135 140
Gln Pro Val Ser Thr Ala Asp Ala Leu Lys Ser Arg Leu Glu Lys Leu

145 150 155 160
Thr Asn Ser His Pro Val Met Leu Phe Met Lys Gly Ile Pro Glu Glu
165 170 175
Pro Arg Cys Gly Phe Ser Arg Lys Val Val Asp Ile Leu Lys Glu Val
180 185 190
Asn Val Asp Phe Gly Ser Phe Asp Ile Leu Ser Asp Asn Glu Val Arg
195 200 205
Glu Gly Leu Lys Lys Phe Ser Asn Trp Pro Thr Phe Pro Gln Leu Tyr
210 215 220
Cys Asn Gly Glu Leu Leu Gly Gly Ala Asp Ile Ala Ile Ala Met His
225 230 235 240
Glu Ser Gly Glu Leu Lys Asp Ala Phe Lys Asp Leu Gly Ile Thr Thr
245 250 255
Val Gly Ser Lys Glu Ser Gln Asp Glu Ala Gly Lys Gly Gly Val
260 265 270
Ser Ser Gly Asn Thr Gly Leu Ser Glu Thr Leu Arg Ala Arg Leu Glu
275 280 285
Gly Leu Val Asn Ser Lys Pro Val Met Leu Phe Met Lys Gly Arg Pro
290 295 300
Glu Glu Pro Lys Cys Gly Phe Ser Gly Lys Val Val Glu Ile Leu Asn
305 310 315 320
Gln Glu Lys Ile Glu Phe Gly Ser Phe Asp Ile Leu Leu Asp Asp Glu
325 330 335
Val Arg Gln Gly Leu Lys Val Tyr Ser Asn Trp Ser Ser Tyr Pro Gln
340 345 350
Leu Tyr Val Lys Gly Glu Leu Met Gly Gly Ser Asp Ile Val Leu Glu
355 360 365
Met Gln Lys Ser Gly Glu Leu Lys Lys Val Tyr Arg Glu Arg Asp His
370 375 380
Trp Arg Thr Glu Ser
385

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..351

(D) OTHER INFORMATION: / Ceres Seq. ID 1567216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

Met Asp Gln Val Phe Ser His Leu Ala Thr Asp Phe Pro Arg Ala His
1 5 10 15
Phe Phe Arg Val Glu Ala Glu Glu His Pro Glu Ile Ser Glu Ala Tyr
20 25 30
Ser Val Ala Ala Val Pro Tyr Phe Val Phe Phe Lys Asp Gly Lys Thr
35 40 45
Val Asp Thr Leu Glu Gly Ala Asp Pro Ser Ser Leu Ala Asn Lys Val
50 55 60
Gly Lys Val Ala Gly Ser Ser Thr Ser Ala Glu Pro Ala Ala Pro Ala
65 70 75 80
Ser Leu Gly Leu Ala Ala Gly Pro Thr Ile Leu Glu Thr Val Lys Glu
85 90 95
Asn Ala Lys Ala Ser Leu Gln Asp Arg Ala Gln Pro Val Ser Thr Ala
100 105 110
Asp Ala Leu Lys Ser Arg Leu Glu Lys Leu Thr Asn Ser His Pro Val
115 120 125
Met Thr Phe Met Lys Gly Ile Pro Glu Glu Pro Arg Cys Gly Phe Ser
130 135 140

Arg Lys Val Val Asp Ile Leu Lys Glu Val Asn Val Asp Phe Gly Ser
145 150 155 160
Phe Asp Ile Leu Ser Asp Asn Glu Val Arg Glu Gly Leu Lys Lys Phe
165 170 175
Ser Asn Trp Pro Thr Phe Pro Gln Leu Tyr Cys Asn Gly Glu Leu Leu
180 185 190
Gly Gly Ala Asp Ile Ala Ile Ala Met His Glu Ser Gly Glu Leu Lys
195 200 205
Asp Ala Phe Lys Asp Leu Gly Ile Thr Thr Val Gly Ser Lys Glu Ser
210 215 220
Gln Asp Glu Ala Gly Lys Gly Gly Gly Val Ser Ser Gly Asn Thr Gly
225 230 235 240
Leu Ser Glu Thr Leu Arg Ala Arg Leu Glu Gly Leu Val Asn Ser Lys
245 250 255
Pro Val Met Leu Phe Met Lys Gly Arg Pro Glu Glu Pro Lys Cys Gly
260 265 270
Phe Ser Gly Lys Val Val Glu Ile Leu Asn Gln Glu Lys Ile Glu Phe
275 280 285
Gly Ser Phe Asp Ile Leu Leu Asp Asp Glu Val Arg Gln Gly Leu Lys
290 295 300
Val Tyr Ser Asn Trp Ser Ser Tyr Pro Gln Leu Tyr Val Lys Gly Glu
305 310 315 320
Leu Met Gly Gly Ser Asp Ile Val Leu Glu Met Gln Lys Ser Gly Glu
325 330 335
Leu Lys Lys Val Tyr Arg Glu Arg Asp His Trp Arg Thr Glu Ser
340 345 350

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 788 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..788

(D) OTHER INFORMATION: / Ceres Seq. ID 1567240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

aaaaacggtag	aaaccttggt	ttaaacgctc	acggtcccta	tataaaccta	tgagctagcg	60
acgacaagta	ttcagtataa	tcaatcagaa	aacaagtaga	aactttaaaa	cgagagagag	120
agaaagaaat	ggcgacatcg	ggaacgtacg	tgacggaggt	tcgcgtgaaa	ggatcggcgg	180
agaaacacata	caagagctgg	aagagcgaga	accatgtctt	cgctgacgcc	attggccacc	240
acatccaaaa	tgtcgttggt	cacgaaggcg	aacatgaact	tcacgggtct	atcaggagtt	300
gggactacac	atatgatgga	aagaaggaga	tgttcaaaga	gaagagagag	atagatgatg	360
agaaataaac	attgacgaaa	agaggactgg	atggtcacgt	gatggagcat	tcocaaagat	420
ttgatatacat	ctacgaattt	attcccaaat	ctgaggatag	ctgcgtctgc	aaaatcacta	480
tgatatggga	gaagcgcaac	gatgactttc	ccgaaccaag	cggtcacatg	aaattcgtea	540
agcaaatggg	tggtgcattt	gaagcgacag	tcaacaaaag	ttaacccaaa	ccatcacogt	600
catcactatc	tcgatcgata	ttgtattatt	atggtgtctt	ttcgataaat	aatataataa	660
agggggtctt	gtggagtttc	tattctctgt	aactgtttgg	ttttggaata	tgctgtgata	720
tgttgtCtat	gctcatcata	tatcggtttc	gatataatga	gtattaataa	aagtagcttc	780
agtatatcc						

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1567241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

Met Ala Thr Ser Gly Thr Tyr Val Thr Glu Val Pro Leu Lys Gly Ser
1 5 10 15
Ala Glu Lys His Tyr Lys Ser Trp Lys Ser Glu Asn His Val Phe Ala
20 25 30
Asp Ala Ile Gly His His Ile Gln Asn Val Val Val His Glu Gly Glu
35 40 45
His Asp Ser His Gly Ser Ile Arg Ser Trp Asp Tyr Thr Tyr Asp Gly
50 55 60
Lys Lys Glu Met Phe Lys Lys Arg Glu Ile Asp Asp Glu Asn Lys
65 70 75 80
Thr Leu Thr Lys Arg Gly Leu Asp Gly His Val Met Glu His Leu Lys
85 90 95
Val Phe Asp Ile Ile Tyr Glu Phe Ile Pro Lys Ser Glu Asp Ser Cys
100 105 110
Val Cys Lys Ile Thr Met Ile Trp Glu Lys Arg Asn Asp Asp Phe Pro
115 120 125
Glu Pro Ser Gly Tyr Met Lys Phe Val Lys Gln Met Val Val Asp Ile
130 135 140
Glu Gly His Val Asn Lys Ala
145 150

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1567242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

Met Phe Lys Glu Lys Arg Glu Ile Asp Asp Glu Asn Lys Thr Leu Thr
1 5 10 15
Lys Arg Gly Leu Asp Gly His Val Met Glu His Leu Lys Val Phe Asp
20 25 30
Ile Ile Tyr Glu Phe Ile Pro Lys Ser Glu Asp Ser Cys Val Cys Lys
35 40 45
Ile Thr Met Ile Trp Glu Lys Arg Asn Asp Asp Phe Pro Glu Pro Ser
50 55 60
Gly Tyr Met Lys Phe Val Lys Gln Met Val Val Asp Ile Glu Gly His
65 70 75 80
Val Asn Lys Ala

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1311 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1311

(D) OTHER INFORMATION: / Ceres Seq. ID 1567251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

aagttttcttt atcttttagt ttcccggtaa aaaatctctc tgctcatgtct atgtttcttcc 60
acgtcggttc taattctcca agacagaatc tctaaacttc attttgctcc ttttccacac 120

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aaaaattttTc tctccctcca aagaccacaa aaaaattttt tcttctcttc aacttcaagt 180
atctctctttt attcacacag atagcatcca aaacccaaaa tccataaaccc ttctctctgtt 240
aaaagattttc tctttttcaa cttcccacga aaaaaaaaaa aaaaacattc tgttagaaaa 300
ccatgagaggg tctgcgggct tgttacagtg aacacgccat aaagtatcca gatacatatt 360
gttcaggcttc ttccaatcat tcttatatat ctccgacatt acctcttcca atccccgaca 420
cagtaaacac cacttataaa tcatatctcc cttcttcoga aaaaaccgctc tctgtttcac 480
tcacctgggtc ggataaatctc accgtctgtca tctcaaacgcc gccgaatacca tactctgttt 540
cactcagaaa accctaaaggc tcaagaaagt tgactttctc ctccggttca ctcaacggcg 600
agatccctatg ggaatttatcg gaagagagta cgaatacaac ggacctgaac caataaagaag 660
attcttctgtc gtcgtctgtg taaattccga gattaccctc ggagtcggcg acgttgacca 720
cgagcgagac acgtcatcat cgtcgtctgt gcgagtctca aaaaacggaga gattctctgtg 780
aacttggttgg ctacgacga aagctcaatt ctccgacgtc ggaaggaaac acgagataca 840
gattcaatgc ggcggaggag gwggwggagg aggaggagag gaaggggtatt tatggaaagt 900
gaaaagctctc gaaacgatg cggtttatgt tgataaaggg aaagtgtttt cggtagaaga 960
ggttaagtgg aacttttagag ggaatcaaac catgtttttc gatggaatgc ttatagacat 1020
gatgtgggat ttacacgact ggttctacaa agaaacggtg tctgtctgtt cgactagttc 1080
atcgtctaaa acggcgctgt cgtcatcgct ttcttcaact tcatcgctca ctctccgtg 1140
tgctgtgttt atgttttaga ggaggagtgt tttgatagt agattatgga ttgatgaaga 1200
tgaacaagag agtaagatga agaagaatat tggttctaga gatgagaaac atctgttttc 1260
atttattcatt tgtgcctcta aaaagtgacc aaataaacia ataaacattt t

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(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

```

Met Arg Gly Leu Ala Ala Cys Tyr Ser Glu His Ala Ile Lys Val Ser
1      5      10      15
Asp Thr Tyr Cys Ser Gly Pro Ser Asn His Ser Tyr Ile Ser Pro Thr
20     25     30
Leu Pro Pro Ser Ile Pro Asp Thr Val Thr Thr Thr Tyr Lys Ser Tyr
35     40     45
Leu Pro Ser Ser Asp Lys Pro Val Ser Val Ser Leu Thr Trp Ser Asp
50     55     60
Asn Leu Thr Val Val Ile Ser Thr Pro Pro Lys Ser Tyr Ser Val Ser
65     70     75     80
Leu Arg Lys Pro Lys Gly Ser Arg Lys Leu Thr Ser Ser Ser Gly Ser
85     90     95
Leu Asn Ala Glu Ile Leu Trp Asp Leu Ser Glu Glu Ser Thr Lys Thr
100    105    110
Thr Asp Leu Asn Glu
115

```

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..226
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

```

Met Gly Ser Ile Gly Arg Glu Tyr Glu Asn Asn Gly Pro Glu Pro Ile

```

1	5	10	15
Arg Arg Phe Phe Val Val Val Val Val Asn Ser Glu Ile Thr Leu Gly			
20	25	30	
Val Gly Asp Val Asp His Glu Arg Asp Thr Ser Ser Ser Ser Trp			
35	40	45	
Arg Val Ser Lys Thr Glu Arg Phe Ser Gly Thr Cys Trp Leu Thr Thr			
50	55	60	
Lys Ala Gln Phe Ser Asp Val Gly Arg Lys His Glu Ile Gln Ile Gln			
65	70	75	80
Cys Gly Gly Gly Xaa Xaa Gly Gly Gly Glu Gly Tyr Leu Trp			
85	90	95	
Lys Val Lys Ser Pro Glu Thr Met Ser Val Tyr Val Asp Lys Arg Lys			
100	105	110	
Val Phe Ser Val Lys Lys Leu Lys Trp Asn Phe Arg Gly Asn Gln Thr			
115	120	125	
Met Phe Phe Asp Gly Met Leu Ile Asp Met Met Trp Asp Leu His Asp			
130	135	140	
Trp Phe Tyr Lys Glu Thr Leu Ser Ser Val Ser Thr Ser Ser Ser Ser			
145	150	155	160
Lys Thr Ala Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Ser Thr Pro			
165	170	175	
Pro Cys Ala Val Phe Met Phe Arg Arg Arg Ser Gly Phe Asp Ser Arg			
180	185	190	
Leu Trp Ile Asp Glu Asp Glu Gln Glu Ser Lys Met Lys Lys Asn Ile			
195	200	205	
Gly Ser Arg Asp Glu Lys His Ser Phe Ser Leu Ile Cys Ala Ser			
210	215	220	
Lys Lys			
225			

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1567254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

Met Ser Val Tyr Val Asp Lys Arg Lys Val Phe Ser Val Lys Lys Leu	
1	5
Lys Trp Asn Phe Arg Gly Asn Gln Thr Met Phe Phe Asp Gly Met Leu	
20	25
Ile Asp Met Met Trp Asp Leu His Asp Trp Phe Tyr Lys Glu Thr Leu	
35	40
Ser Ser Val Ser Thr Ser Ser Ser Ser Lys Thr Ala Ser Ser Ser Ser	
50	55
Ser Ser Ser Thr Ser Ser Ser Thr Pro Pro Cys Ala Val Phe Met Phe	
65	70
Arg Arg Arg Ser Gly Phe Asp Ser Arg Leu Trp Ile Asp Glu Asp Glu	
85	90
Gln Glu Ser Lys Met Lys Lys Asn Ile Gly Ser Arg Asp Glu Lys His	
100	105
Ser Phe Ser Leu Ile Ile Cys Ala Ser Lys Lys	
115	120

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1590 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1590
(D) OTHER INFORMATION: / Ceres Seq. ID 1567261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

ctcgcttcga	tagctactga	tttgattcta	tggttcgttc	cagtcgccga	aggtgtcact	60
cgcaacgcgt	ggcaattact	cgcgatcttc	ctcgccacca	tcgtcgggat	cataactcag	120
ccgctctctc	tcggtgctgt	tgctctaatg	ggattaggag	cttcgcttct	caccaaaaac	180
ctaagctctc	cgccgcgctt	ctccgcttct	ggagatccaa	ccccgtgctt	catcgctctt	240
gcctctctct	tcgctcgcgg	tttcatcaaa	accggtctcg	gtaacccgtg	agcttaccag	300
ttcgtagac	ttctcgtag	ctctccctct	ggtctcggtt	acagtcctcg	cttcagtgaa	360
gctcttttag	ctccggcgat	tccttctgtc	tcggctcggt	cgggtggaa	ctttctcccg	420
ttgggtgaa	ctctctgtgt	tgcttctgtg	agtaacggtg	gggatggaa	agagcacgct	480
cttgctcgt	ggttgatgct	tacttcttct	cagactctcg	tgatctcttc	ttctatgttc	540
ttgacggcta	tggtcgcgaa	ctcttctgag	gctaattttg	cgtttaacac	gattaagcag	600
acgattggat	ggactgattg	ggctaaaagt	gcgattgtac	caggacttgt	gtctttgatt	660
gttggtccgt	ttcttttgta	tctcatctat	ctctctacgg	tgaagcagac	tcctgatgct	720
cttaagctgg	ctcaggaaaa	gcttgacaag	atgggacctc	tgcttaagaa	cgaattgatt	780
atggctgcga	ctttattcct	caacggttgg	ctctggatct	ttggagctaa	gttggtgtga	840
gatgctgtga	ctgcagccat	ttctggatta	tcagtccttc	ttgtgacagg	tggttctgaca	900
tggaagaggt	gcttagctga	gtcggctgca	tgggacacac	tcacctgggt	cgctgctctc	960
attcgatggt	ctgggttatc	taacaaaat	ggctctcatt	agtggttcag	ccagacgcga	1020
gtcaagtttg	tgggaggatt	gggtttgtca	tggcagctat	cttttgcatt	ctctgtcttc	1080
ttgtatttct	acaactcata	cttctttgtc	agtggagctg	cccaactatg	tgcGtatgtt	1140
cactgccttt	ttatcggttt	caacgcgtct	aggcaactca	cttacttttg	cagccttggt	1200
ctttcgcttc	ctttccaacc	tgatggggag	attgacccat	tatgggtatg	ggtctgcgcc	1260
tatctctcac	ggagctaaat	acgtgcccgt	ggctaaatgg	tggtgctgat	gattcctgat	1320
ctcaatagtc	aacattctca	cttggtcttg	tgtaggtgtg	gcctggtgga	agttcaatgg	1380
cttggtgtga	ggaccacgat	acaccaatct	tcccatttct	ttccttactt	atatatatga	1440
ctctttagaa	cggcttttag	attcagattt	gagaaggatt	gaaatcaggg	ttataaggat	1500
tgagcagagt	ttttctgcaa	tttttattct	cactcacaca	cattttgaag	tgtaagcaat	1560
cttaacttgc	gtcaattttg	tttgatttcc				

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 425 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..425
(D) OTHER INFORMATION: / Ceres Seq. ID 1567262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

Leu	Ala	Ser	Ile	Ala	Thr	Asp	Leu	Ile	Leu	Trp	Phe	Val	Pro	Val	Pro
1				5					10					15	
Glu	Gly	Val	Thr	Arg	Asn	Ala	Trp	Gln	Leu	Leu	Ala	Ile	Phe	Leu	Ala
				20				25				30			
Thr	Ile	Val	Gly	Ile	Ile	Thr	Gln	Pro	Leu	Pro	Leu	Gly	Ala	Val	Ala
				35			40					45			
Leu	Met	Gly	Leu	Gly	Ala	Ser	Val	Leu	Thr	Lys	Thr	Leu	Thr	Phe	Ala
				50			55					60			
Ala	Ala	Phe	Ser	Ala	Phe	Gly	Asp	Pro	Ile	Pro	Trp	Leu	Ile	Ala	Leu
				65			70				75			80	
Ala	Phe	Phe	Phe	Ala	Arg	Gly	Phe	Ile	Lys	Thr	Gly	Leu	Gly	Asn	Arg
				85			90					95			
Val	Ala	Tyr	Gln	Gln	Phe	Val	Arg	Leu	Phe	Gly	Ser	Ser	Ser	Leu	Leu
				100			105					110			

Gly Tyr Ser Leu Val Phe Ser Glu Ala Leu Leu Ala Pro Ala Ile Pro
115 120 125
Ser Val Ser Ala Arg Ala Gly Gly Ile Phe Leu Pro Leu Val Lys Ser
130 135 140
Leu Cys Val Ala Cys Gly Ser Asn Val Gly Asp Gly Thr Glu His Arg
145 150 155 160
Leu Gly Ser Trp Leu Met Leu Thr Cys Phe Gln Thr Ser Val Ile Ser
165 170 175
Ser Ser Met Phe Leu Thr Ala Met Ala Ala Asn Pro Leu Ser Ala Asn
180 185 190
Leu Ala Phe Asn Thr Ile Lys Gln Thr Ile Gly Trp Thr Asp Trp Ala
195 200 205
Lys Ala Ala Ile Val Pro Gly Leu Val Ser Leu Ile Val Val Pro Phe
210 215 220
Leu Leu Tyr Leu Ile Tyr Pro Pro Thr Val Lys Ser Ser Pro Asp Ala
225 230 235 240
Pro Lys Leu Ala Gln Glu Lys Leu Asp Lys Met Gly Pro Met Ser Lys
245 250 255
Asn Glu Leu Ile Met Ala Ala Thr Leu Phe Leu Thr Val Gly Leu Trp
260 265 270
Ile Phe Gly Ala Lys Leu Gly Val Asp Ala Val Thr Ala Ala Ile Leu
275 280 285
Gly Leu Ser Val Leu Leu Val Thr Gly Val Val Thr Trp Lys Glu Cys
290 295 300
Leu Ala Glu Ser Val Ala Trp Asp Thr Leu Thr Trp Phe Ala Ala Leu
305 310 315 320
Ile Ala Met Ala Gly Tyr Leu Asn Lys Tyr Gly Leu Ile Glu Trp Phe
325 330 335
Ser Gln Thr Val Val Lys Phe Val Gly Gly Leu Gly Leu Ser Trp Gln
340 345 350
Leu Ser Phe Gly Ile Leu Val Leu Leu Tyr Phe Tyr Thr His Tyr Phe
355 360 365
Phe Ala Ser Gly Ala Ala His Ile Gly Ala Tyr Val His Cys Leu Phe
370 375 380
Ile Gly Phe Asn Arg Ser Arg His Ser Thr Leu Leu Cys Ser Leu Gly
385 390 395 400
Ser Cys Val Pro Phe Gln Pro Asp Gly Arg Ile Asp Pro Leu Trp Tyr
405 410 415
Arg Val Cys Ala Tyr Leu Leu Arg Ser
420 425

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..376

(D) OTHER INFORMATION: / Ceres Seq. ID 1567263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

Met Gly Leu Gly Ala Ser Val Leu Thr Lys Thr Leu Thr Phe Ala Ala
1 5 10 15
Ala Phe Ser Ala Phe Gly Asp Pro Ile Pro Trp Leu Ile Ala Leu Ala
20 25 30
Phe Phe Phe Ala Arg Gly Phe Ile Lys Thr Gly Leu Gly Asn Arg Val
35 40 45
Ala Tyr Gln Phe Val Arg Leu Phe Gly Ser Ser Ser Leu Gly Leu Gly
50 55 60
Tyr Ser Leu Val Phe Ser Glu Ala Leu Leu Ala Pro Ala Ile Pro Ser

65	70	75	80
Val Ser Ala Arg	Ala Gly Gly Ile Phe Leu Pro Leu Val Lys Ser Leu		
	85	90	95
Cys Val Ala Cys	Gly Ser Asn Val Gly Asp Gly Thr Glu His Arg Leu		
	100	105	110
Gly Ser Trp Leu Met Leu Thr Cys Phe Gln Thr Ser Val Ile Ser Ser			
	115	120	125
Ser Met Phe Leu Thr Ala Met Ala Ala Asn Pro Leu Ser Ala Asn Leu			
	130	135	140
Ala Phe Asn Thr Ile Lys Gln Thr Ile Gly Trp Thr Asp Trp Ala Lys			
	145	150	155
Ala Ala Ile Val Pro Gly Leu Val Ser Leu Ile Val Val Pro Phe Leu			
	165	170	175
Leu Tyr Leu Ile Tyr Pro Pro Thr Val Lys Ser Ser Pro Asp Ala Pro			
	180	185	190
Lys Leu Ala Gln Glu Lys Leu Asp Lys Met Gly Pro Met Ser Lys Asn			
	195	200	205
Glu Leu Ile Met Ala Ala Thr Leu Phe Leu Thr Val Gly Leu Trp Ile			
	210	215	220
Phe Gly Ala Lys Leu Gly Val Asp Ala Val Thr Ala Ala Ile Leu Gly			
	225	230	235
Leu Ser Val Leu Leu Val Thr Gly Val Val Thr Trp Lys Glu Cys Leu			
	245	250	255
Ala Glu Ser Val Ala Trp Asp Thr Leu Thr Trp Phe Ala Ala Leu Ile			
	260	265	270
Ala Met Ala Gly Tyr Leu Asn Lys Tyr Gly Leu Ile Glu Trp Phe Ser			
	275	280	285
Gln Thr Val Val Lys Phe Val Gly Gly Leu Gly Leu Ser Trp Gln Leu			
	290	295	300
Ser Phe Gly Ile Leu Val Leu Leu Tyr Phe Tyr Thr His Tyr Phe Phe			
	305	310	315
Ala Ser Gly Ala Ala His Ile Gly Ala Tyr Val His Cys Leu Phe Ile			
	325	330	335
Gly Phe Asn Arg Ser Arg His Ser Thr Leu Leu Cys Ser Leu Gly Ser			
	340	345	350
Cys Val Pro Phe Gln Pro Asp Gly Arg Ile Asp Pro Leu Trp Tyr Arg			
	355	360	365
Val Cys Ala Tyr Leu Leu Arg Ser			
	370	375	

(2) INFORMATION FOR SEQ ID NO:536:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 260 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..260
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

Met Leu Thr Cys Phe Gln Thr Ser Val Ile Ser Ser Ser Met Phe Leu			
1	5	10	15
Thr Ala Met Ala Ala Asn Pro Leu Ser Ala Asn Leu Ala Phe Asn Thr			
	20	25	30
Ile Lys Gln Thr Ile Gly Trp Thr Asp Trp Ala Lys Ala Ala Ile Val			
	35	40	45
Pro Gly Leu Val Ser Leu Ile Val Val Pro Phe Leu Leu Tyr Leu Ile			
	50	55	60
Tyr Pro Pro Thr Val Lys Ser Ser Pro Asp Ala Pro Lys Leu Ala Gln			
65	70	75	80

Glu Lys Leu Asp Lys Met Gly Pro Met Ser Lys Asn Glu Leu Ile Met
85 90 95
Ala Ala Thr Leu Phe Leu Thr Val Gly Leu Trp Ile Phe Gly Ala Lys
100 105 110
Leu Gly Val Asp Ala Val Thr Ala Ala Ile Leu Gly Leu Ser Val Leu
115 120 125
Leu Val Thr Gly Val Val Thr Trp Lys Glu Cys Leu Ala Glu Ser Val
130 135 140
Ala Trp Asp Thr Leu Thr Trp Phe Ala Ala Leu Ile Ala Met Ala Gly
145 150 155 160
Tyr Leu Asn Lys Tyr Gly Leu Ile Glu Trp Phe Ser Gln Thr Val Val
165 170 175
Lys Phe Val Gly Gly Leu Gly Leu Ser Trp Gln Leu Ser Phe Gly Ile
180 185 190
Leu Val Leu Leu Tyr Phe Tyr Thr His Tyr Phe Phe Ala Ser Gly Ala
195 200 205
Ala His Ile Gly Ala Tyr Val His Cys Leu Phe Ile Gly Phe Asn Arg
210 215 220
Ser Arg His Ser Thr Leu Leu Cys Ser Leu Gly Ser Cys Val Pro Phe
225 230 235 240
Gln Pro Asp Gly Arg Ile Asp Pro Leu Trp Tyr Arg Val Cys Ala Tyr
245 250 255
Leu Leu Arg Ser
260

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

actgggtctt	cttcagcttc	tgagttctct	cctctctctc	tatctctcaa	gtgggctttg	60
ctttgtctgt	tttgtctctc	ctcgacgact	cacttttgca	gattctcata	aattcttcaa	120
agctttgagt	cttttttcag	attcgaagg	cggttttata	tatgcttcaa	atctcttacc	180
caaatcaggt	atggagactc	tgcatccatt	ctctcacta	cctatctctg	accaccggtt	240
cgttttcaa	gagatgggtg	gctttcacag	ctcgagtgcg	ggtagctgga	ctaaagaaga	300
gaacaagatg	ttcgacagag	ctcttgcgat	atacgtgcga	gactcgcctg	atcgtcggtt	360
taaaattgct	tccatgatcc	ctggaaagac	tggttttgat	gttatgaagc	aataatgtaa	420
gcttgaagaa	gacgttttgc	atattgaagc	aggacgtgtt	cccattcctg	gttatcctgc	480
agctttctct	cccttggggg	ttgacacgga	catgtgtcgt	aaacggccta	gtggagctag	540
aggatctgat	caagatcgaa	agaaaggagt	cccttgga	gaggaagaac	acaggagatt	600
cttgttaggc	ctactcaagt	acggtaaagg	agattggaga	aacatatacg	gaaacttcgt	660
gggtgcaaa	acggccaacg	aagtgccgag	ccacgcccaa	aagtattacc	agagacagct	720
ctccggagcc	aaggacaaac	cgaggccaag	tatccatgac	atcacaccgc	gcaatctctc	780
tcaatgccaa	tctcaacgtg	tctttttccg	atcatagaga	tattctccct	gatttagggt	840
ttatcgataa	ggatgatacg	gaggaggagg	taattattat	gggtcagaat	ctctcttcag	900
aaaactctgt	ttctccatca	ccaacttcat	tcgaagctgc	cattaaactc	gccggagaaa	960
atgtcttcag	tgccggagct	taaggcaaca	tagaatcccc	aaactcagcg	ttcttaagaa	1020
ctctgagttt	gaaactgtta	ttagagaaat	ataagcaaaa	ccaagtattat	tatatatgta	1080
tttgtgtggt	taaaaagtaag	aacttgtttt	tactctgtat	ttttgtgttt	ctgtctacta	1140
aatacctggt	atgttaaaaa	attctgtgct				

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..271
(D) OTHER INFORMATION: / Ceres Seq. ID 1567266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

Leu Gly Leu Leu Gln Leu Leu Ser Leu Leu Ser Leu Tyr Leu Ser
1 5 10 15
Ser Gly Leu Cys Phe Ala Val Phe Val Phe Leu Arg Arg Leu Thr Phe
20 25 30
Ala Asp Ser His Lys Phe Phe Lys Ala Leu Ser Leu Phe Ser Asp Ser
35 40 45
Lys Val Gly Phe Ile Tyr Ala Ser Asn Leu Leu Pro Lys Ser Gly Met
50 55 60
Glu Thr Leu His Pro Phe Ser His Leu Pro Ile Ser Asp His Arg Phe
65 70 75 80
Val Val Gln Glu Met Val Ser Phe His Ser Ser Ser Ser Gly Ser Trp
85 90 95
Thr Lys Glu Glu Asn Lys Met Phe Glu Arg Ala Leu Ala Ile Tyr Ala
100 105 110
Glu Asp Ser Pro Asp Arg Trp Phe Lys Val Ala Ser Met Ile Pro Gly
115 120 125
Lys Thr Val Phe Asp Val Met Lys Gln Tyr Ser Lys Leu Glu Glu Asp
130 135 140
Val Phe Asp Ile Glu Ala Gly Arg Val Pro Ile Pro Gly Tyr Pro Ala
145 150 155 160
Ala Ser Ser Pro Leu Gly Phe Asp Thr Asp Met Cys Arg Lys Arg Pro
165 170 175
Ser Gly Ala Arg Gly Ser Asp Gln Asp Arg Lys Lys Gly Val Pro Trp
180 185 190
Thr Glu Glu Glu His Arg Arg Phe Leu Leu Gly Leu Leu Lys Tyr Gly
195 200 205
Lys Gly Asp Trp Arg Asn Ile Ser Arg Asn Phe Val Val Ser Lys Thr
210 215 220
Pro Thr Gln Val Ala Ser His Ala Gln Lys Tyr Tyr Gln Arg Gln Leu
225 230 235 240
Ser Gly Ala Lys Asp Lys Arg Arg Pro Ser Ile His Asp Ile Thr Thr
245 250 255
Gly Lys Ser Ser Gln Cys Gln Ser Gln Pro Phe Leu Phe Arg Ser
260 265 270

(2) INFORMATION FOR SEQ ID NO:539:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..208
(D) OTHER INFORMATION: / Ceres Seq. ID 1567267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

Met Glu Thr Leu His Pro Phe Ser His Leu Pro Ile Ser Asp His Arg
1 5 10 15
Phe Val Val Gln Glu Met Val Ser Phe His Ser Ser Ser Ser Gly Ser
20 25 30
Trp Thr Lys Glu Glu Asn Lys Met Phe Glu Arg Ala Leu Ala Ile Tyr
35 40 45
Ala Glu Asp Ser Pro Asp Arg Trp Phe Lys Val Ala Ser Met Ile Pro
50 55 60

Gly	Lys	Thr	Val	Phe	Asp	Val	Met	Lys	Gln	Tyr	Ser	Lys	Leu	Glu	Glu	
65					70				75						80	
Asp	Val	Phe	Asp	Ile	Glu	Ala	Gly	Arg	Val	Pro	Ile	Pro	Gly	Tyr	Pro	
			85					90						95		
Ala	Ala	Ser	Ser	Pro	Leu	Gly	Phe	Asp	Thr	Asp	Met	Cys	Arg	Lys	Arg	
			100					105					110			
Pro	Ser	Gly	Ala	Arg	Gly	Ser	Asp	Gln	Asp	Arg	Lys	Lys	Gly	Val	Pro	
		115					120					125				
Trp	Thr	Glu	Glu	Glu	His	Arg	Arg	Phe	Leu	Leu	Gly	Leu	Leu	Lys	Tyr	
		130				135					140					
Gly	Lys	Gly	Asp	Trp	Arg	Asn	Ile	Ser	Arg	Asn	Phe	Val	Val	Ser	Lys	
145					150					155					160	
Thr	Pro	Thr	Gln	Val	Ala	Ser	His	Ala	Gln	Lys	Tyr	Tyr	Gln	Arg	Gln	
			165						170					175		
Leu	Ser	Gly	Ala	Lys	Asp	Lys	Arg	Arg	Pro	Ser	Ile	His	Asp	Ile	Thr	
			180					185					190			
Thr	Gly	Lys	Ser	Ser	Gln	Cys	Gln	Ser	Gln	Pro	Phe	Leu	Phe	Arg	Ser	
		195					200					205				

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1567268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

Met	Val	Ser	Phe	His	Ser	Ser	Ser	Ser	Gly	Ser	Trp	Thr	Lys	Glu	Glu	
1			5						10				15			
Asn	Lys	Met	Phe	Glu	Arg	Ala	Leu	Ala	Ile	Tyr	Ala	Glu	Asp	Ser	Pro	
		20						25					30			
Asp	Arg	Trp	Phe	Lys	Val	Ala	Ser	Met	Ile	Pro	Gly	Lys	Thr	Val	Phe	
		35					40					45				
Asp	Val	Met	Lys	Gln	Tyr	Ser	Lys	Leu	Glu	Glu	Asp	Val	Phe	Asp	Ile	
		50				55					60					
Glu	Ala	Gly	Arg	Val	Pro	Ile	Pro	Gly	Tyr	Pro	Ala	Ala	Ser	Ser	Pro	
65					70				75					80		
Leu	Gly	Phe	Asp	Thr	Asp	Met	Cys	Arg	Lys	Arg	Pro	Ser	Gly	Ala	Arg	
			85					90					95			
Gly	Ser	Asp	Gln	Asp	Arg	Lys	Lys	Gly	Val	Pro	Trp	Thr	Glu	Glu	Glu	
		100						105					110			
His	Arg	Arg	Phe	Leu	Leu	Gly	Leu	Leu	Lys	Tyr	Gly	Lys	Gly	Asp	Trp	
		115					120					125				
Arg	Asn	Ile	Ser	Arg	Asn	Phe	Val	Val	Ser	Lys	Thr	Pro	Thr	Gln	Val	
		130				135					140					
Ala	Ser	His	Ala	Gln	Lys	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Gly	Ala	Lys	
145					150					155					160	
Asp	Lys	Arg	Arg	Pro	Ser	Ile	His	Asp	Ile	Thr	Thr	Gly	Lys	Ser	Ser	
			165					170						175		
Gln	Cys	Gln	Ser	Gln	Pro	Phe	Leu	Phe	Arg	Ser						
			180					185								

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..480
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567273
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:
ctaaagattg caaatccgtg ttctatctct ctcaacaatt atttcccctg cttccaaagc 60
tttgacaaca ttctatttca aaaacttttag ttttgagttt tttttttctt gtatacttct 120
ccccaaaata tgagcgatcc caagtatgca tatccttacc cgccaccggg aaattaccoc 180
caaggtccgc Caccgcgcgt ggGagtaccg ccacagtatt atcctccacc accgccaccg 240
cctctctctc caccaccacc acgaaaagtt ggttttcttg aaggactatt agcagctctg 300
tgttgtgtgt gcttgggtgga tgaatgttgc tgtgaccoga ccattatatg ctttgattaa 360
gttttcagga aaaagtagt ctgttaattt cattatgctt atgagggtta tacaataatt 420
gtttgatat catgtgata ctactttctt ttctgtgcgc ttttaattagg ttttagtctt 480

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..76
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567274
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:
Met Ser Asp Pro Lys Tyr Ala Tyr Pro Tyr Pro Ala Pro Gly Asn Tyr
1 5 10 15
Pro Gln Gly Pro Pro Pro Pro Val Gly Val Pro Pro Gln Tyr Tyr Pro
20 25 30
Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Arg Lys Val Gly
35 40 45
Phe Leu Glu Gly Leu Leu Ala Ala Leu Cys Cys Cys Cys Leu Val Asp
50 55 60
Glu Cys Cys Cys Asp Pro Thr Ile Ile Cys Phe Asp
65 70 75

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..48
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567275
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:
Met His Ile Leu Thr Arg His Arg Glu Ile Thr Arg Lys Val Arg His
1 5 10 15
Arg Arg Trp Glu Tyr Arg His Ser Ile Ile Leu His His Arg His Arg
20 25 30
Leu Leu Leu His His His His Glu Lys Leu Val Phe Leu Lys Asp Tyr
35 40 45

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 949 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..949
(D) OTHER INFORMATION: / Ceres Seq. ID 1567284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

aatctctcgt	cgtcatttct	tcgtctcacc	gttgaatctg	aaaatgatcg	ccggagtatt	60
gcgcgcgatct	tcactcccg	cgaggcgac	tctctcgcgc	gcgttagcct	ccttcaattc	120
gtgtatttcg	cacaattctc	ctccagccac	caccggagct	tcctgcagct	ctcgattcac	180
tctcgcgtcg	tctctctaact	cgtttggcat	cagagcgagg	aacatccaca	ttagatctga	240
gcgcgtcgat	attgttcccg	caGgaatcgc	gtcacaaggt	tacgcacctg	tcacaaagga	300
tcgcaaaaac	gagatgaaga	aagctaagat	taaaaattct	ccagacaaat	tcagaccatt	360
gagtaggaag	gagatcgctc	tccagaaaga	gccagcagaa	gaaagcacat	caaaagataaa	420
aggaacaaa	atttgtatag	cgattcggto	tttgtttaac	ccggaaaaag	aagcttggtg	480
tcttctctct	cacactcgta	aagtgcgaat	gcccgatata	cgaactctgt	acacgggtgt	540
gcggtcgcct	cacgtcgata	agaagtctag	agaacagttt	gagatgaggt	tcaagaaaacg	600
ttttcttgtc	atcaaaagtc	agagtcgatga	gttgagcaag	aagctgtttt	ggttaaaaacg	660
ttatcgattt	cttgagctc	aatagaact	ccagttccat	tgcaagaccc	gtttggatat	720
gactcaagtg	ttaggcaaca	tcaatggctc	caccaccaat	gcttactgag	atggcctaaa	780
acatcatttt	gtagaagttt	caagacccaa	ccgggtacta	tgcaataatt	tcgaacctta	840
cggtcccatg	aaaccagctt	tgcttccat	cagatcaagt	agttattttt	ttgcttagta	900
taaacaatgtg	tttttgaacg	attttgaag	atacaattga	gtttcagtt		

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..255
(D) OTHER INFORMATION: / Ceres Seq. ID 1567285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

Ile	Ser	Arg	Arg	His	Phe	Phe	Val	Ser	Pro	Leu	Asn	Leu	Lys	Met	Ile
1			5						10					15	
Ala	Gly	Val	Leu	Arg	Arg	Ser	Ser	Leu	Pro	Ser	Arg	Gln	Thr	Leu	Ser
			20					25					30		
Ala	Ala	Leu	Ala	Ser	Phe	Asn	Ser	Cys	Ile	Ser	His	Asn	Leu	Thr	Pro
			35				40					45			
Ala	Thr	Thr	Gly	Ala	Ser	Val	Ser	Ser	Arg	Phe	Thr	Leu	Ala	Ser	Ser
			50			55					60				
Pro	Asn	Ser	Phe	Gly	Ile	Arg	Ala	Arg	Asn	Ile	His	Ile	Arg	Ser	Glu
						70				75				80	
Pro	Ser	Met	Ile	Val	Pro	Ala	Gly	Ile	Ala	Ser	Gln	Gly	Tyr	Ala	Thr
				85				90					95		
Val	Thr	Lys	Asp	Arg	Lys	Asn	Glu	Ile	Lys	Lys	Ala	Lys	Ile	Lys	Ile
				100			105						110		
Ser	Pro	Asp	Asn	Val	Arg	Pro	Leu	Ser	Arg	Lys	Glu	Ile	Ala	Leu	Gln
				115			120				125				
Lys	Glu	Pro	Ala	Glu	Glu	Ser	Thr	Ser	Lys	Ile	Lys	Gly	Thr	Lys	Ile
				130			135				140				
Cys	Ile	Ala	Ile	Arg	Ser	Phe	Val	Asn	Pro	Glu	Lys	Gln	Ala	Trp	Cys
				145			150				155				160
Leu	Pro	Pro	His	Thr	Arg	Lys	Val	Ala	Met	Pro	Asp	Thr	Arg	Thr	Leu
				165					170					175	
Tyr	Thr	Val	Leu	Arg	Ser	Pro	His	Val	Asp	Lys	Lys	Ser	Arg	Glu	Gln
				180				185						190	

(2) INFORMATION FOR SEO ID NO:546:

(A) LENGTH: 241 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..241

(D) OTHER INFORMATION: / Ceres Seq. ID 1567286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1567287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

```
Met Ile Val Pro Ala Gly Ile Ala Ser Gln Gly Tyr Ala Thr Val Thr
1      5      10      15
Lys Asp Arg Lys Asn Glu Ile Lys Lys Ala Lys Ile Lys Ile Ser Pro
20     25     30
Asp Asn Val Arg Pro Leu Ser Arg Lys Glu Ile Ala Leu Gln Lys Glu
35     40     45
Pro Ala Glu Glu Ser Thr Ser Lys Ile Lys Gly Thr Lys Ile Cys Ile
50     55     60
Ala Ile Arg Ser Phe Val Asn Pro Glu Lys Gln Ala Trp Cys Leu Pro
65     70     75     80
Pro His Thr Arg Lys Val Ala Met Pro Asp Thr Arg Thr Leu Tyr Thr
85     90     95
Val Leu Arg Ser Pro His Val Asp Lys Lys Ser Arg Glu Gln Phe Glu
100    105    110
Met Arg Phe Lys Lys Arg Phe Leu Val Ile Lys Ala Gln Ser His Glu
115    120    125
Leu Ser Lys Lys Leu Phe Trp Leu Lys Arg Tyr Arg Ile Leu Gly Ala
130    135    140
Gln Tyr Glu Leu Gln Phe His Cys Lys Thr Arg Leu Asp Met Thr Gln
145    150    155    160
Val Leu Gly Asn Ile Asn Gly Ser Thr Thr Asn Ala Tyr
165    170
```

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1698 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1698

(D) OTHER INFORMATION: / Ceres Seq. ID 1567288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

```
cywagamacat cctaatacaaa aaatacaatc gtcttcttcta tcatatttcto ttcttcttct 60
ccaagaaaac cctgaagaag aaatgggggt ccttaaggcca accatggcga ttctttttct 120
agcgatgtgt cgcggtttcat cagccgtgga catgtcaatc atctcctacg acgagaaaaca 180
tggcgctctc accaccggtg gcggtagcga agccgaggtt atgagtatct acgagcatg 240
gttggtgaaa caggcgaaag ctccagagcca gaactctctt gttgagaaag atccagcgtt 300
cgagatcttt aaagacaatc ttctgtttctg cgatgaacat aacgagaaga atcttaagta 360
tagattgggt ttgactcgtt ttgcggatct tactaacgat gagtatagat ccaagtatct 420
tggagctaaag atggagaaga aaggtgagag aaggactagc ctacggtaag aggtcgtgt 480
cggtgatgag ctaccggagt ctattgactg gaggaagaaa ggagccgtgg ctgaggtcaa 540
agatcagggt ggttgcgga gttgttgggc gttttcaaac attggagcag tggagggaat 600
aaaccagcat gtaaccggag acctaaataac ctgtgtcgaa caagagttgg tcgattgtga 660
cacttcaatc aacgaaggtt gtaacggagg tcttatggac tatgcttttg agttcattat 720
caagaatggt ggaatcgata cagacaaaaga ttatccttac aagggtgttg atggaacttg 780
tgaccagatc aggaaaaaac ctaaaagtgt cactatcgat tcatatgagg atgttccaac 840
ttaccgcgag gaatcggtga aAgaaagcag ttgctcatca accattaAg cactgccatt 900
gasgctggtg gtctgtcgct cccagctctat gattcgggta tattttatgg aagtgttgga 960
acacaacgag accaccgagt ttgctgggtt ggatacggaa ctgagaacgg caaagattac 1020
tggattgtga gaaactcatg gggtaaaaagc tggggagaga gtggatacct aaggatggcg 1080
cgtaaatcgt cgtcttccatc aggaaaaatgt ggaatcgcca ttgaaccttc ataccogata 1140
aagaattggc aaaaaccggc aaaccgggga ccttccacctc catctcccat caagctccca 1200
accctaagtg acagtttacta cacttgtcct gagagcaaca cttgtgtgtg tctgttttag 1260
tatgccaagt atgtctttgc ttggggatgt tgcccactag aagcagccac ttctgtgtat 1320
gacaaatata gtgtgtgccc tcacgagtac ccggtttgtg accttgatca aggaacctgt 1380
ttattgagca agaacagctc atttagtgtt aaggccttaa agcgtaaac ccgaacggcca 1440
```

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ttctgtgtcac aaggcagaaaa gaacattgcc taaacattgc ttcttcaaga ggactctggc	1500
tcattgagaga agagatctct ctgaagggat ttatcagatg ctttttaagt ttgtgtttta	1560
tgccataact agatacataa aaaatgcagc tgttggtttt cgtgtatata aaaaaaggac	1620
cctatgtttt attcagtttc atagtgggtt ttcattgata cagtacattt attgttaatt	1680
caagaaaatt gaattttt	

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..295
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567289

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

Xaa	Xaa	His	Pro	Asn	Gln	Lys	Ile	Gln	Ser	Ser	Ser	Ser	Ser	Phe	Ser
1			5					10						15	
Leu	Leu	Leu	Leu	Gln	Glu	Asn	Thr	Glu	Glu	Met	Gly	Phe	Leu	Lys	
			20					25				30			
Pro	Thr	Met	Ala	Ile	Leu	Phe	Leu	Ala	Met	Val	Ala	Val	Ser	Ser	Ala
		35					40				45				
Val	Asp	Met	Ser	Ile	Ile	Ser	Tyr	Asp	Glu	Lys	His	Gly	Val	Ser	Thr
	50					55					60				
Thr	Gly	Gly	Arg	Ser	Glu	Ala	Glu	Val	Met	Ser	Ile	Tyr	Glu	Ala	Trp
	65				70				75				80		
Leu	Val	Lys	His	Gly	Lys	Ala	Gln	Ser	Gln	Asn	Ser	Leu	Val	Glu	Lys
			85					90					95		
Asp	Arg	Arg	Phe	Glu	Ile	Phe	Lys	Asp	Asn	Leu	Arg	Phe	Val	Asp	Glu
			100				105					110			
His	Asn	Glu	Lys	Asn	Leu	Ser	Tyr	Arg	Leu	Gly	Leu	Thr	Arg	Phe	Ala
	115					120					125				
Asp	Leu	Thr	Asn	Asp	Glu	Tyr	Arg	Ser	Lys	Tyr	Leu	Gly	Ala	Lys	Met
	130				135						140				
Glu	Lys	Lys	Gly	Glu	Arg	Arg	Thr	Ser	Leu	Arg	Tyr	Glu	Ala	Arg	Val
	145				150				155					160	
Gly	Asp	Glu	Leu	Pro	Glu	Ser	Ile	Asp	Trp	Arg	Lys	Lys	Gly	Ala	Val
			165					170					175		
Ala	Glu	Val	Lys	Asp	Gln	Gly	Gly	Cys	Gly	Ser	Cys	Trp	Ala	Phe	Ser
			180					185					190		
Thr	Ile	Gly	Ala	Val	Glu	Gly	Ile	Asn	Gln	Ile	Val	Thr	Gly	Asp	Leu
	195						200					205			
Ile	Thr	Leu	Ser	Glu	Gln	Glu	Leu	Val	Asp	Cys	Asp	Thr	Ser	Tyr	Asn
	210				215						220				
Glu	Gly	Cys	Asn	Gly	Gly	Leu	Met	Asp	Tyr	Ala	Phe	Glu	Phe	Ile	Ile
	225				230					235				240	
Lys	Asn	Gly	Gly	Ile	Asp	Thr	Asp	Lys	Asp	Tyr	Pro	Tyr	Lys	Gly	Val
			245					250					255		
Asp	Gly	Thr	Cys	Asp	Gln	Ile	Arg	Lys	Asn	Ala	Lys	Val	Val	Thr	Ile
			260				265					270			
Asp	Ser	Tyr	Glu	Asp	Val	Pro	Thr	Tyr	Ser	Glu	Glu	Ser	Leu	Lys	Glu
	275						280					285			
Ser	Ser	Cys	Ser	Ser	Thr	His									
	290					295									

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..268

(D) OTHER INFORMATION: / Ceres Seq. ID 1567290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

```
Met Gly Phe Leu Lys Pro Thr Met Ala Ile Leu Phe Leu Ala Met Val
1      5      10      15
Ala Val Ser Ser Ala Val Asp Met Ser Ile Ile Ser Tyr Asp Glu Lys
20      25      30
His Gly Val Ser Thr Thr Gly Gly Arg Ser Glu Ala Glu Val Met Ser
35      40      45
Ile Tyr Glu Ala Trp Leu Val Lys His Gly Lys Ala Gln Ser Gln Asn
50      55      60
Ser Leu Val Glu Lys Asp Arg Arg Phe Glu Ile Phe Lys Asp Asn Leu
65      70      75      80
Arg Phe Val Asp Glu His Asn Glu Lys Asn Leu Ser Tyr Arg Leu Gly
85      90      95
Leu Thr Arg Phe Ala Asp Leu Thr Asn Asp Glu Tyr Arg Ser Lys Tyr
100      105      110
Leu Gly Ala Lys Met Glu Lys Lys Gly Glu Arg Arg Thr Ser Leu Arg
115      120      125
Tyr Glu Ala Arg Val Gly Asp Glu Leu Pro Glu Ser Ile Asp Trp Arg
130      135      140
Lys Lys Gly Ala Val Ala Glu Val Lys Asp Gln Gly Gly Cys Gly Ser
145      150      155      160
Cys Trp Ala Phe Ser Thr Ile Gly Ala Val Glu Gly Ile Asn Gln Ile
165      170      175
Val Thr Gly Asp Leu Ile Thr Leu Ser Glu Gln Glu Leu Val Asp Cys
180      185      190
Asp Thr Ser Tyr Asn Glu Gly Cys Asn Gly Gly Leu Met Asp Tyr Ala
195      200      205
Phe Glu Phe Ile Ile Lys Asn Gly Gly Ile Asp Thr Asp Lys Asp Tyr
210      215      220
Pro Tyr Lys Gly Val Asp Gly Thr Cys Asp Gln Ile Arg Lys Asn Ala
225      230      235      240
Lys Val Val Thr Ile Asp Ser Tyr Glu Asp Val Pro Thr Tyr Ser Glu
245      250      255
Glu Ser Leu Lys Glu Ser Ser Cys Ser Ser Thr His
260      265
```

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..261

(D) OTHER INFORMATION: / Ceres Seq. ID 1567291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

```
Met Ala Ile Leu Phe Leu Ala Met Val Ala Val Ser Ser Ala Val Asp
1      5      10      15
Met Ser Ile Ile Ser Tyr Asp Glu Lys His Gly Val Ser Thr Thr Gly
20      25      30
Gly Arg Ser Glu Ala Glu Val Met Ser Ile Tyr Glu Ala Trp Leu Val
35      40      45
Lys His Gly Lys Ala Gln Ser Gln Asn Ser Leu Val Glu Lys Asp Arg
50      55      60
Arg Phe Glu Ile Phe Lys Asp Asn Leu Arg Phe Val Asp Glu His Asn
```


65		70		75		80
Glu Lys Asn Leu Ser	Tyr Arg Leu Gly	Leu Thr Arg Phe Ala Asp Leu				
	85		90		95	
Thr Asn Asp Glu Tyr Arg Ser Lys Tyr	Leu Gly Ala Lys Met Glu Lys					
	100		105		110	
Lys Gly Glu Arg Arg Thr Ser Leu Arg Tyr Glu Ala Arg Val Gly Asp						
	115		120		125	
Glu Leu Pro Glu Ser Ile Asp Trp Arg Lys Lys Gly Ala Val Ala Glu						
	130		135		140	
Val Lys Asp Gln Gly Gly Cys Gly Ser Cys Trp Ala Phe Ser Thr Ile						
	145		150		155	
Gly Ala Val Glu Gly Ile Asn Gln Ile Val Thr Gly Asp Leu Ile Thr						
	165		170		175	
Leu Ser Glu Gln Glu Leu Val Asp Cys Asp Thr Ser Tyr Asn Glu Gly						
	180		185		190	
Cys Asn Gly Gly Leu Met Asp Tyr Ala Phe Glu Phe Ile Ile Lys Asn						
	195		200		205	
Gly Gly Ile Asp Thr Asp Lys Asp Tyr Pro Tyr Lys Gly Val Asp Gly						
	210		215		220	
Thr Cys Asp Gln Ile Arg Lys Asn Ala Lys Val Val Thr Ile Asp Ser						
	225		230		235	
Tyr Glu Asp Val Pro Thr Tyr Ser Glu Glu Ser Leu Lys Glu Ser Ser						
	245		250		255	
Cys Ser Ser Thr His						
	260					

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

aactctcatc	ttctttttct	ttctttttct	ctctttttct	attgcttgtt	gattgatgat	60
cttgaagcaa	ggatcatgag	gttccttcaac	agatttctgt	tggaggatat	gcccaaaagaa	120
acctttttcgt	actctctctgt	taaaaaataat	tgcattccaag	agttgaaaaac	tctaggatcac	180
tgctcatctc	attgtcttga	cgagtgctct	tccatctgcg	agatcgctcg	aattccaagtt	240
ctttccaccac	ctgcagagat	ccaccacgac	gacaacttaa	agaggatctt	gatcatctct	300
gcttcatctc	tcatcacaac	tctgttttct	cttactttac	ttgttctctg	cttcaagttt	360
tactatagga	ggagaagatc	aataacaaca	tcaagaagat	ggagtatgga	agaagctagg	420
aattgggatt	tgtatggacc	agcacctgtt	attgttgatc	atccgatttg	gcatacaga	480
accatagggt	tgaattccaac	ggttataagt	tccatcaaac	tttgtcagta	tagtaaaaaa	540
gatgggtgtt	tggaaaggaac	tgattgtctc	gtttgtttaa	gcgaatttca	agaagaagag	600
acgcttagat	tgttaccaaa	gtgtaaacat	gcttttcatc	ttatttgtat	tgatacttgg	660
cttagatcac	acaccaattg	tccgcttagt	cggtgtccta	tcgttgaggc	caacacaatg	720
attgatgatc	atagtgaagg	gctagaggag	ataagtgtga	tgattccaga	agaaaatgga	780
gatgataccg	atgaagaata	cgaggagaag	agagatggct	ttgttagtaa	tattagttaga	840
gatcatgggt	agtcacaaca	acagcagagt	agacgatcac	tgctgttggg	tcgtttatog	900
ggttttaagg	taagtgaagt	tggtgtgggt	agagaaaagg	agaagtgtga	gagaggcaat	960
aattatggtt	ctgggaggtc	aagttttatt	aagagatcta	tcctttacag	tgaaaagttag	1020
tactagttag	cttcagtgct	aataataaaa	acaagaagtc	cataaaagta	gtaagtttct	1080
tgaagaagaa	aatcaaatca	aacccaacaa	catatagggt	gtattcatat	gtatgaaggt	1140
gataataagt	tacgattatc	aaagctatgc	actcttgtaa	agtttaaaag	gagttttgac	1200
aactcttact	actctgtcta	gataactctg	atttgtggat	taagtataaa	tatacaccaa	1260
actTcgtttt	gtatgttaac	tattttattg	tcctcaagaa	ataccatctg	gatttttaatt	1320
attttt						

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..339
(D) OTHER INFORMATION: / Ceres Seq. ID 1567306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

Asn	Ser	His	Leu	Leu	Phe	Ser	Phe	Phe	Phe	Leu	Phe	Leu	His	Cys	Leu
1			5						10					15	
Leu	Ile	Asp	Asp	Leu	Glu	Ala	Arg	Ile	Met	Arg	Phe	Leu	His	Arg	Phe
			20					25					30		
Leu	Leu	Glu	Asp	Met	Pro	Lys	Glu	Thr	Phe	Ser	Asp	Ser	Leu	Cys	Lys
			35				40					45			
Asn	Asn	Cys	Ile	Gln	Glu	Leu	Lys	Thr	Leu	Gly	Tyr	Cys	Ser	Ser	Tyr
			50			55				60					
Cys	Leu	Asp	Glu	Cys	Pro	Ser	Ile	Cys	Glu	Ile	Val	Val	Ile	Ser	Gly
65				70					75					80	
Leu	Ser	Pro	Pro	Ala	Glu	Ile	His	His	Asp	Asp	Asn	Leu	Lys	Arg	Ile
				85					90				95		
Leu	Ile	Ile	Ser	Ala	Ser	Ser	Ile	Ile	Thr	Thr	Leu	Phe	Leu	Leu	Thr
			100					105					110		
Leu	Leu	Val	Leu	Cys	Phe	Lys	Phe	Tyr	Arg	Arg	Arg	Arg	Ser	Ile	
			115				120			125					
Thr	Thr	Ser	Ser	Arg	Arg	Trp	Ser	Met	Glu	Glu	Ala	Arg	Asn	Trp	Asp
			130			135				140					
Asp	Gly	Pro	Ala	Pro	Val	Ile	Val	Asp	His	Pro	Ile	Trp	His	Ile	Arg
145				150					155					160	
Thr	Ile	Gly	Leu	Asn	Pro	Thr	Val	Ile	Ser	Ser	Ile	Lys	Val	Cys	Gln
			165					170					175		
Tyr	Ser	Lys	Lys	Asp	Gly	Val	Val	Glu	Gly	Thr	Asp	Cys	Ser	Val	Cys
			180					185				190			
Leu	Ser	Glu	Phe	Glu	Glu	Glu	Thr	Leu	Arg	Leu	Leu	Pro	Lys	Cys	
			195			200				205					
Lys	His	Ala	Phe	His	Leu	Tyr	Cys	Ile	Asp	Thr	Trp	Leu	Arg	Ser	His
			210			215				220					
Thr	Asn	Cys	Pro	Leu	Ser	Arg	Ala	Pro	Ile	Val	Glu	Ala	Asn	Thr	Met
225				230					235					240	
Ile	Asp	Asp	His	Ser	Glu	Gly	Leu	Glu	Glu	Ile	Ser	Val	Met	Ile	Pro
			245					250					255		
Glu	Glu	Asn	Gly	Asp	Asp	Thr	Asp	Glu	Glu	Ile	Glu	Glu	Glu	Arg	Asp
			260			265						270			
Gly	Phe	Val	Ser	Asn	Ile	Ser	Arg	Asp	His	Gly	Glu	Ser	Gln	Gln	Gln
			275			280				285					
Arg	Val	Arg	Arg	Ser	Val	Ser	Leu	Asp	Ser	Leu	Ser	Gly	Leu	Arg	Val
			290			295				300					
Ser	Glu	Val	Val	Val	Gly	Arg	Glu	Lys	Glu	Lys	Leu	Lys	Arg	Gly	Asn
305				310					315				320		
Asn	Ile	Gly	Ser	Gly	Arg	Ser	Ser	Leu	Leu	Lys	Arg	Ser	Ile	Ser	Tyr
			325					330					335		

Ser Gly Lys

(2) INFORMATION FOR SEQ ID NO:554:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..314

(D) OTHER INFORMATION: / Ceres Seq. ID 1567307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

Met Arg Phe Leu His Arg Phe Leu Leu Glu Asp Met Pro Lys Glu Thr
1 5 10 15
Phe Ser Asp Ser Leu Cys Lys Asn Asn Cys Ile Gln Glu Leu Lys Thr
20 25 30
Leu Gly Tyr Cys Ser Ser Tyr Cys Leu Asp Glu Cys Pro Ser Ile Cys
35 40 45
Glu Ile Val Val Ile Ser Gly Leu Ser Pro Pro Ala Glu Ile His His
50 55 60
Asp Asp Asn Leu Lys Arg Ile Leu Ile Ile Ser Ala Ser Ser Ile Ile
65 70 75 80
Thr Thr Leu Phe Leu Leu Thr Leu Leu Val Leu Cys Phe Lys Phe Tyr
85 90 95
Tyr Arg Arg Arg Arg Ser Ile Thr Thr Ser Arg Arg Trp Ser Met Glu
100 105 110
Glu Ala Arg Asn Trp Asp Phe Asp Gly Pro Ala Pro Val Ile Val Asp
115 120 125
His Pro Ile Trp His Ile Arg Thr Ile Gly Leu Asn Pro Thr Val Ile
130 135 140
Ser Ser Ile Lys Val Cys Gln Tyr Ser Lys Lys Asp Gly Val Val Glu
145 150 155 160
Gly Thr Asp Cys Ser Val Cys Leu Ser Glu Phe Glu Glu Glu Glu Thr
165 170 175
Leu Arg Leu Leu Pro Lys Cys Lys His Ala Phe His Leu Tyr Cys Ile
180 185 190
Asp Thr Trp Leu Arg Ser His Thr Asn Cys Pro Leu Ser Arg Ala Pro
195 200 205
Ile Val Glu Ala Asn Thr Met Ile Asp Asp His Ser Glu Gly Leu Glu
210 215 220
Glu Ile Ser Val Met Ile Pro Glu Glu Asn Gly Asp Asp Thr Asp Glu
225 230 235 240
Glu Ile Glu Glu Glu Arg Asp Gly Phe Val Ser Asn Ile Ser Arg Asp
245 250 255
His Gly Glu Ser Gln Gln Arg Val Arg Arg Ser Val Ser Leu Asp
260 265 270
Ser Leu Ser Gly Leu Arg Val Ser Glu Val Val Val Gly Arg Glu Lys
275 280 285
Glu Lys Leu Lys Arg Gly Asn Asn Ile Gly Ser Gly Arg Ser Ser Leu
290 295 300
Leu Lys Arg Ser Ile Ser Tyr Ser Gly Lys
305 310

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..303

(D) OTHER INFORMATION: / Ceres Seq. ID 1567308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

Met Pro Lys Glu Thr Phe Ser Asp Ser Leu Cys Lys Asn Asn Cys Ile
1 5 10 15
Gln Glu Leu Lys Thr Leu Gly Tyr Cys Ser Ser Tyr Cys Leu Asp Glu

aaaagaagatc	aaacatacga	tagcttggac	tctttttggc	gtcatgatgc	tctctcaatc	60
tctcatcttta	gctttctctc	tctctctctt	tgctggatca	ttgtttttatc	tcacataatgg	120
atttcaaattt	tcattactcg	atagacttta	acgaagatca	aaacccatcac	gaccaacacct	180
tttttctatc	tcttgagctc	tcttctctgc	ttcatcatca	tcatcattcat	catcatcatc	240
aagtcctctc	taattcttca	tcttcttctt	cgctccattc	atcgctctctc	tcttaacctc	300
ctttcttgtat	caactctcaa	gaagatcaac	atgttgctca	gacacacatc	gatcactcgtg	360
atcatctctc	ttttctctca	ccctcaaggc	ccaagatggt	tgtggctaac	tgtgggatcat	420
catcatgcga	tcacatggtg	ccaaggatgc	agacaagatc	gaactaacgc	ataaagaaaa	480
aagatcacga	agaccaacc	catctctctc	atcaaaaacc	gacaaaacc	gttcagactc	540
gcacagaagc	gttgatgtcc	ccaaagatgc	ggttgatcaa	gaaaaaacatc	accacaata	600
aacagctcac	tgatcagact	aataataata	atcataaaga	aagtgtcatc	tacctcttga	660
atcataagac	taatttcgac	gaggatcaca	atgaagatct	taatttcbaa	gagctcttga	720
ccaggaaagac	cacggccgcg	atcccgcaga	atctgcacaa	tacatacaac	gagacagcgtt	780
atagtaatac	caatgcgtgc	attagcctgc	tgtcggatgt	taaacacac	aagactcctc	840

tttggcgaag	tggacctcga	ggtcccaagt	ctctttgtaa	cgcgatgtgt	atacggcaaa	900
gaaaggcgaag	gogagccgct	atggccgcgg	ccgctgcagc	cgcgacgcaa	gaggtggcgg	960
tagcgcgcccg	agtgcaacaa	ttaccgcgtg	aaaagaagtt	gcaaaataaa	aaaaaagaga	1020
tcaaacggag	gggaaaaata	caatcactct	cctccaatgt	tggcccaagg	caaaaagtgc	1080
aagatcaaaag	aggaagagga	gaaggMaatg	gaagcggaaa	cggttgcggg	agattcagag	1140
atcagcaaat	ctacaacttc	ttctaattct	tcgatttcgt	caaaacaatt	ttgcttcgat	1200
gatttgacaa	taatgtgtgag	caaaaagctca	gcttatcaac	aagtgttccc	acaagatgag	1260
aaggaggctg	ctgttttgcg	catggctctg	tcgtatggaa	tggttcacgg	ttgatcagat	1320
catcacaaata	tcttcattac	aaaaagggtt	attttaatag	taatatatag	attatagtaa	1380
tcataataat	gattgattgt	taaatcttgg	agtgattagt	ttagtttttg	cagttggctc	1440
aaatatcagga	gtcaaaaacat	tttataataa	gagtggttga	gagtttaata	tgataaattaa	1500
tagctctata	taagttttgg	gagattttgg	ttttgagttt	gtgtgttttt	tgttttccga	1560
tggaaacgaac	attagtcacc	cgataatgtg	ggtaattctt	gttcatttac	aagttttata	1620
tgactgtatt	gtgtaacgag	gttgagagaa	taataataac	aattaagggt		

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..349
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

Met	Asp	Ser	Asn	Phe	His	Tyr	Ser	Ile	Asp	Leu	Asn	Glu	Asp	Gln	Asn
1			5						10					15	
His	His	Glu	Gln	Pro	Phe	Phe	Tyr	Pro	Leu	Gly	Ser	Ser	Ser	Ser	Leu
			20					25						30	
His	His	His	His	His	His	His	His	Gln	Val	Pro	Ser	Asn	Ser	Ser	
			35				40				45				
Ser	Ser	Ser	Ser	Ser	Ile	Ser	Ser	Leu	Ser	Ser	Tyr	Leu	Pro	Phe	Leu
			50			55					60				
Ile	Asn	Ser	Gln	Glu	Asp	Gln	His	Val	Ala	Tyr	Asn	Asn	Thr	Tyr	His
			65			70			75					80	
Ala	Asp	His	Leu	His	Leu	Ser	Gln	Pro	Leu	Lys	Ala	Lys	Met	Phe	Val
			85					90					95		
Ala	Asn	Gly	Gly	Ser	Ser	Ser	Cys	Asp	His	Met	Val	Pro	Lys	Lys	Glu
			100				105						110		
Thr	Arg	Leu	Lys	Leu	Thr	Ile	Arg	Lys	Lys	Asp	His	Glu	Asp	Gln	Pro
			115				120					125			
His	Pro	Leu	His	Gln	Asn	Pro	Thr	Lys	Pro	Asp	Ser	Asp	Ser	Asp	Lys
			130				135				140				
Trp	Leu	Met	Ser	Pro	Lys	Met	Arg	Leu	Ile	Lys	Lys	Thr	Ile	Thr	Asn
			145			150				155					160
Asn	Lys	Gln	Leu	Thr	Asp	Gln	Thr	Asn	Asn	Asn	Asn	His	Lys	Glu	Ser
			165					170					175		
Asp	His	Tyr	Pro	Leu	Asn	His	Lys	Thr	Asn	Phe	Asp	Glu	Asp	His	His
			180				185					190			
Glu	Asp	Leu	Asn	Phe	Lys	Asn	Val	Leu	Thr	Arg	Lys	Thr	Thr	Ala	Ala
			195				200					205			
Thr	Thr	Glu	Asn	Arg	Tyr	Asn	Thr	Ile	Asn	Glu	Asn	Gly	Tyr	Ser	Asn
			210				215					220			
Asn	Asn	Gly	Val	Ile	Arg	Val	Cys	Ser	Asp	Cys	Asn	Thr	Thr	Lys	Thr
			225				230			235					240
Pro	Leu	Trp	Arg	Ser	Gly	Pro	Arg	Gly	Pro	Lys	Ser	Leu	Cys	Asn	Ala
			245					250					255		
Cys	Gly	Ile	Arg	Gln	Arg	Lys	Ala	Arg	Arg	Ala	Ala	Met	Ala	Ala	Ala
			260				265					270			
Ala	Ala	Ala	Gly	Asp	Gln	Glu	Val	Ala	Val	Ala	Pro	Arg	Val	Gln	Gln

(2) INFORMATION FOR SEQ ID NO:558:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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(A) NAME/KEY: peptide

(B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1567311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..243
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567312
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

Met	Val	Pro	Lys	Lys	Glu	Thr	Arg	Leu	Lys	Leu	Thr	Ile	Arg	Lys	Lys
1			5					10					15		
Asp	His	Glu	Asp	Gln	Pro	His	Pro	Leu	His	Gln	Asn	Pro	Thr	Lys	Pro
			20					25				30			
Asp	Ser	Asp	Ser	Asp	Lys	Trp	Leu	Met	Ser	Pro	Lys	Met	Arg	Leu	Ile
		35					40				45				
Lys	Lys	Thr	Ile	Thr	Asn	Asn	Lys	Gln	Leu	Thr	Asp	Gln	Thr	Asn	Asn
	50					55					60				
Asn	Asn	His	Lys	Glu	Ser	Asp	His	Tyr	Pro	Leu	Asn	His	Lys	Thr	Asn
	65			70				75					80		
Phe	Asp	Glu	Asp	His	His	Glu	Asp	Leu	Asn	Phe	Lys	Asn	Val	Leu	Thr
			85					90					95		
Arg	Lys	Thr	Thr	Ala	Ala	Thr	Thr	Glu	Asn	Arg	Tyr	Asn	Thr	Ile	Asn
			100					105					110		
Glu	Asn	Gly	Tyr	Ser	Asn	Asn	Asn	Gly	Val	Ile	Arg	Val	Cys	Ser	Asp
		115				120					125				
Cys	Asn	Thr	Thr	Lys	Thr	Pro	Leu	Trp	Arg	Ser	Gly	Pro	Arg	Gly	Pro
	130					135					140				
Lys	Ser	Leu	Cys	Asn	Ala	Cys	Gly	Ile	Arg	Gln	Arg	Lys	Ala	Arg	Arg
	145			150				155						160	
Ala	Ala	Met	Ala	Ala	Ala	Ala	Ala	Gly	Asp	Gln	Glu	Val	Ala	Val	
			165					170					175		
Ala	Pro	Arg	Val	Gln	Gln	Leu	Pro	Leu	Lys	Lys	Lys	Leu	Gln	Asn	Lys
			180					185					190		
Lys	Lys	Glu	Ile	Lys	Arg	Arg	Gly	Lys	Ile	Gln	Ser	Leu	Ser	Ser	Asn
		195					200					205			
Gly	Gly	Gln	Gly	Gln	Lys	Val	Gln	Asp	Gln	Arg	Gly	Arg	Gly	Glu	Xaa
	210					215					220				
Asn	Gly	Ser	Gly	Asn	Gly	Cys	Arg	Arg	Phe	Arg	Asp	Gln	Gln	Ile	Tyr
	225				230					235				240	
Asn	Phe	Phe													

(2) INFORMATION FOR SEQ ID NO:560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1018 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1018
(D) OTHER INFORMATION: / Ceres Seq. ID 1567317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

accttttacaa	ctaactcata	agtaaaacac	agacagtttt	tagatggcata	agatatattc	60
cccttctttt	cccggtactc	tctgtctttg	cattttttact	ctcttgacgc	taatgttcat	120
tcgggttttcc	gtcgcagccc	cgacattcgt	cgaggatttc	aaagccgcct	ggctcggaatc	180
tcacatccgt	caaatggaag	acggaaaagc	tatccagctc	gtccttgatc	agagcaactgg	240
atgtggattt	gcttccaaaa	gaaaatatct	attcggaaga	gtgagcatga	ggatcaaaat	300
cattcccgga	gactctgcgc	gtacgGtcac	cgcttttctac	atgaactccg	atacggccac	360
ggtgagagac	gagctagatt	ttgagttctt	gggaaaacaga	agtggtcaac	cttactcaagt	420
gcaaacacaac	atatttgcct	atggcacaag	agatagagaa	caaagagtta	atcttttggtt	480
cgacccatct	atggattacc	acactttacac	tatcttatgg	tcacacaaac	acattgtttt	540
ttacgtagac	gatgtgccaa	taagagaata	caaaaacacac	gaagccaaga	acatagctta	600
cccaacatca	caacctatgg	gagtatactc	aacattatgg	gaagcagatg	actggggcaac	660

acgtgggtgga ttagagaaaa ttgattggag caaagctcca ttttatgctt attacaagaa 720
tttcgacatc gaaggtgtgc ctgttctctg accaaccttt tTgtccatcg aacctcata 780
atttggtggga aggttatgcc tatcagtctc ttaacgccgt tgaagctoga cgttaccggg 840
gggtagtagt aaaccatatt gtttatgatt attgtactga ccggtctagg ttctctgtcc 900
caccaccgga gtgtcgtgct tgaataat tgcatacgtc cgttgcaatg atcatgttcc 960
gtctgtacg agatattata tataaattgt gggaaaatgt ggattgtatt gtcctctt

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..245

(D) OTHER INFORMATION: / Ceres Seq. ID 1567318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

Met Ala Lys Ile Tyr Ser Pro Ser Phe Pro Gly Thr Leu Cys Leu Cys
1 5 10 15
Ile Phe Thr Leu Leu Thr Leu Met Phe Ile Arg Val Ser Ala Arg Pro
20 25 30
Ala Thr Phe Val Glu Asp Phe Lys Ala Ala Trp Ser Glu Ser His Ile
35 40 45
Arg Gln Met Glu Asp Gly Lys Ala Ile Gln Leu Val Leu Asp Gln Ser
50 55 60
Thr Gly Cys Gly Phe Ala Ser Lys Arg Lys Tyr Leu Phe Gly Arg Val
65 70 75 80
Ser Met Arg Ile Lys Leu Ile Pro Gly Asp Ser Ala Gly Thr Val Thr
85 90 95
Ala Phe Tyr Met Asn Ser Asp Thr Ala Thr Val Arg Asp Glu Leu Asp
100 105 110
Phe Glu Phe Leu Gly Asn Arg Ser Gly Gln Pro Tyr Ser Val Gln Thr
115 120 125
Asn Ile Phe Ala His Gly Lys Gly Asp Arg Glu Gln Arg Val Asn Leu
130 135 140
Trp Phe Asp Pro Ser Met Asp Tyr His Thr Tyr Thr Ile Leu Trp Ser
145 150 155 160
His Lys His Ile Val Phe Tyr Val Asp Asp Val Pro Ile Arg Glu Tyr
165 170 175
Lys Asn Asn Glu Ala Lys Asn Ile Ala Tyr Pro Thr Ser Gln Pro Met
180 185 190
Gly Val Tyr Ser Thr Leu Trp Glu Ala Asp Asp Trp Ala Thr Arg Gly
195 200 205
Gly Leu Glu Lys Ile Asp Trp Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr
210 215 220
Lys Asp Phe Asp Ile Glu Gly Cys Pro Val Pro Gly Pro Thr Phe Leu
225 230 235 240
Ser Ile Glu Pro Ser
245

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..222

(D) OTHER INFORMATION: / Ceres Seq. ID 1567319

Met	Phe	Ile	Arg	Val	Ser	Ala	Arg	Pro	Ala	Thr	Phe	Val	Glu	Asp	Phe
1			5						10					15	
Lys	Ala	Ala	Trp	Ser	Glu	Ser	His	Ile	Arg	Gln	Met	Glu	Asp	Gly	Lys
			20					25					30		
Ala	Ile	Gln	Leu	Val	Leu	Asp	Gln	Ser	Thr	Gly	Cys	Gly	Phe	Ala	Ser
		35					40					45			
Lys	Arg	Lys	Tyr	Leu	Phe	Gly	Arg	Val	Ser	Met	Arg	Ile	Lys	Leu	Ile
		50				55					60				
Pro	Gly	Asp	Ser	Ala	Gly	Thr	Val	Thr	Ala	Phe	Tyr	Met	Asn	Ser	Asp
65					70					75					80
Thr	Ala	Thr	Val	Arg	Asp	Glu	Leu	Asp	Phe	Glu	Phe	Leu	Gly	Asn	Arg
				85					90					95	
Ser	Gly	Gln	Pro	Tyr	Ser	Val	Gln	Thr	Asn	Ile	Phe	Ala	His	Gly	Lys
			100					105					110		
Gly	Asp	Arg	Glu	Gln	Arg	Val	Asn	Leu	Trp	Phe	Asp	Pro	Ser	Met	Asp
			115				120					125			
Tyr	His	Thr	Tyr	Thr	Ile	Leu	Trp	Ser	His	Lys	His	Ile	Val	Phe	Tyr
					135						140				
Val	Asp	Asp	Val	Pro	Ile	Arg	Glu	Tyr	Lys	Asn	Asn	Glu	Ala	Lys	Asn
145					150					155					160
Ile	Ala	Tyr	Pro	Thr	Ser	Gln	Pro	Met	Gly	Val	Tyr	Ser	Thr	Leu	Trp
				165					170					175	
Glu	Ala	Asp	Asp	Trp	Ala	Thr	Arg	Gly	Gly	Leu	Glu	Lys	Ile	Asp	Trp
				180				185					190		
Ser	Lys	Ala	Pro	Phe	Tyr	Ala	Tyr	Tyr	Lys	Asp	Phe	Asp	Ile	Glu	Gly
		195					200					205			
Cys	Pro	Val	Pro	Gly	Pro	Thr	Phe	Leu	Ser	Ile	Glu	Pro	Ser		
	210					215					220				

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..195

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:563:

Glu Asp Gly Lys Ala Ile Gln Leu Val Leu A

5					10					15					
Cys	Gly	Phe	Ala	Ser	Lys	Arg	Lys	Tyr	Leu	Phe	Gly	Arg	Val	Ser	Met
20							25					30			
Arg	Ile	Lys	Leu	Ile	Pro	Gly	Asp	Ser	Ala	Gly	Thr	Val	Thr	Ala	Phe
35						40					45				
Tyr	Met	Asn	Ser	Asp	Thr	Ala	Thr	Val	Arg	Asp	Glu	Leu	Asp	Phe	Glu
50						55					60				
Phe	Leu	Gly	Asn	Arg	Ser	Gly	Gln	Pro	Tyr	Ser	Val	Gln	Thr	Asn	Ile
65					70					75					80
Phe	Ala	His	Gly	Lys	Gly	Asp	Arg	Glu	Gln	Arg	Val	Asn	Leu	Trp	Phe
85								90				95			
Asp	Pro	Ser	Met	Asp	Tyr	His	Thr	Tyr	Thr	Ile	Leu	Trp	Ser	His	Lys
100							105					110			
His	Ile	Val	Phe	Tyr	Val	Asp	Asp	Val	Pro	Ile	Arg	Glu	Tyr	Lys	Asn
115						120					125				
Asn	Glu	Ala	Lys	Asn	Ile	Ala	Tyr	Pro	Thr	Ser	Gln	Pro	Met	Gly	Val
130					135						140				
Tyr	Ser	Thr	Leu	Trp	Glu	Ala	Asp	Asp	Trp	Ala	Thr	Arg	Gly	Gly	Leu
145					150					155				160	

Glu Lys Ile Asp Trp Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr Lys Asp
165 170 175
Phe Asp Ile Glu Gly Cys Pro Val Pro Gly Pro Thr Phe Leu Ser Ile
180 185 190
Glu Pro Ser
195

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..280
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

agaaagcgag agcgaNtgat tcagaagatt ctgagaatga agaggatgag gatgaagaag	60
tagtagtaga agaagaagag gaggaagaag acgaggagag tagtgaagat gccggagagag	120
gaagtcaaaa cgaaggagaa ctaaaaactg aggatggtgg tgaaggagaa agcgaataat	180
tgtaagatcg ttggtgtgtt gtaatgtagc ctagtctcac tatgtactgt ttagagagtgg	240
tgatatatttg taccttttta atgtgtcaat catatttatg	

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

Lys Ala Arg Ala Xaa Asp Ser Glu Asp Ser Glu Asn Glu Glu Asp Glu	
1 5 10 15	
Asp Glu Glu Val Val Val Glu Glu Glu Glu Glu Glu Asp Glu Gly	
20 25 30	
Gly Ser Glu Asp Gly Gly Glu Gly Ser Gln Asn Glu Gly Glu Leu Lys	
35 40 45	
Thr Glu Asp Gly Gly Glu Glu Ser Glu	
50 55	

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

ctgccaaaca tatacatcaa agcttgactc tctttttctc tcccatggaa tcgacaaaaga	60
agcaagtctc gctggagcta ctcccatggt tagttgtcca caccgatgga accgtagaga	120
gactagcggg aaccgaggtt tgtctctccg gtttgatccc aataaccggg gttttctcta	180
aagatatcat tatcgaaaccg aaaaaccggtt tatctgcccg aatctatoga cctttctcga	240
ttcaaccogg tcagaagatt cctctcatgc tctattttca tggcggtgca tttctcatct	300
cctccacttc ctctccctct taccacacca gtcttaacaa aattgtcaat caggctaacg	360

tcatagccgt	ctctgtcaat	tacagactag	caccagaaca	tccacttctc	acagcgtaag	420
aagactcatg	gactgcgcta	aatactatcc	aagccataaa	cgagccgtgg	atcaacgact	480
acgcgcactt	ggacagtata	ttctagtgg	gagatagcgc	cggagctaata	atctcgacc	540
acctgcatt	togagccaaa	caatctgacc	Aaaaccgtga	aaataaaagg	cattggaatg	600
atccaccact	atttttggg	aaacacaact	atcggagcag	agatcaaaga	cgaagcgatg	660
aaacaaatgg	tggaaggatg	gtgggaattt	gtgtgccctt	ccaagaaagg	atctgatgac	720
ccgtggatta	atccgttttg	ggacgggtca	ccggatcttg	gagggttagg	gtgtgagaga	780
gtgatgatta	ctgtggcgga	gaaagatata	ttgaatgaga	gagggaaagt	gtattttgaa	840
agatttggtg	agagtgagtg	gaaaggaaaag	gttgagatta	tggagacgaa	agagaaagat	900
catgtttttc	atatattttg	gcccgattgt	gatgaagcta	tggagatggt	acgatgcttg	960
gctctcttta	taaaccaagt	tgaagcttga	tattatttgt	tttgccataa	tttgatggct	1020
tttttaagt	ttgtataaatt	tttcatgttt	tgtaaattgt	gtgttatttg	tcttttcttt	1080
taaatttggt	tattacattt	atatgtgggt	aaatttgtgt	ttttttcc		

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..237
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

Ala	Lys	His	Ile	His	Gln	Ser	Leu	Thr	Leu	Phe	Phe	Ser	Pro	Met	Glu
1		5						10						15	
Ser	Thr	Lys	Lys	Gln	Val	Ser	Leu	Glu	Leu	Leu	Pro	Trp	Leu	Val	Val
		20						25					30		
His	Thr	Asp	Gly	Thr	Val	Glu	Arg	Leu	Ala	Gly	Thr	Glu	Val	Cys	Pro
		35					40				45				
Pro	Gly	Leu	Asp	Pro	Ile	Thr	Gly	Val	Phe	Ser	Lys	Asp	Ile	Ile	Ile
		50					55				60				
Glu	Pro	Lys	Thr	Gly	Leu	Ser	Ala	Arg	Ile	Tyr	Arg	Pro	Phe	Ser	Ile
		65					70			75				80	
Gln	Pro	Gly	Gln	Lys	Ile	Pro	Leu	Met	Leu	Tyr	Phe	His	Gly	Gly	Ala
			85					90						95	
Phe	Leu	Ile	Ser	Ser	Thr	Ser	Phe	Pro	Ser	Tyr	His	Thr	Ser	Leu	Asn
			100					105					110		
Lys	Ile	Val	Asn	Gln	Ala	Asn	Val	Ile	Ala	Val	Ser	Val	Asn	Tyr	Arg
			115				120						125		
Leu	Ala	Pro	Glu	His	Pro	Leu	Pro	Thr	Ala	Tyr	Glu	Asp	Ser	Trp	Thr
			130				135					140			
Ala	Leu	Asn	Thr	Ile	Gln	Ala	Ile	Asn	Glu	Pro	Trp	Ile	Asn	Asp	Tyr
			145				150				155				160
Ala	Asp	Leu	Asp	Ser	Ile	Phe	Leu	Val	Gly	Asp	Ser	Ala	Gly	Ala	Asn
			165					170						175	
Ile	Ser	His	His	Leu	Ala	Phe	Arg	Ala	Lys	Gln	Ser	Asp	Gln	Asn	Arg
			180					185					190		
Glu	Asn	Lys	Arg	His	Trp	Asn	Asp	Pro	Pro	Ile	Phe	Leu	Gly	Asn	Thr
			195				200					205			
Thr	Tyr	Arg	Ser	Arg	Asp	Gln	Arg	Arg	Ser	Asp	Glu	Thr	Asn	Gly	Gly
			210				215					220			
Arg	Met	Val	Gly	Ile	Cys	Val	Pro	Leu	Gln	Glu	Arg	Ile			
			225				230				235				

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1567333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

```
Met Glu Ser Thr Lys Lys Gln Val Ser Leu Glu Leu Leu Pro Trp Leu
1      5      10      15
Val Val His Thr Asp Gly Thr Val Glu Arg Leu Ala Gly Thr Glu Val
      20      25      30
Cys Pro Pro Gly Leu Asp Pro Ile Thr Gly Val Phe Ser Lys Asp Ile
      35      40      45
Ile Ile Glu Pro Lys Thr Gly Leu Ser Ala Arg Ile Tyr Arg Pro Phe
50      55      60
Ser Ile Gln Pro Gly Gln Lys Ile Pro Leu Met Leu Tyr Phe His Gly
65      70      75      80
Gly Ala Phe Leu Ile Ser Ser Thr Ser Phe Pro Ser Tyr His Thr Ser
      85      90      95
Leu Asn Lys Ile Val Asn Gln Ala Asn Val Ile Ala Val Ser Val Asn
      100      105      110
Tyr Arg Leu Ala Pro Glu His Pro Leu Pro Thr Ala Tyr Glu Asp Ser
      115      120      125
Trp Thr Ala Leu Asn Thr Ile Gln Ala Ile Asn Glu Pro Trp Ile Asn
130      135      140
Asp Tyr Ala Asp Leu Asp Ser Ile Phe Leu Val Gly Asp Ser Ala Gly
145      150      155      160
Ala Asn Ile Ser His His Leu Ala Phe Arg Ala Lys Gln Ser Asp Gln
      165      170      175
Asn Arg Glu Asn Lys Arg His Trp Asn Asp Pro Pro Ile Phe Leu Gly
      180      185      190
Asn Thr Thr Tyr Arg Ser Arg Asp Gln Arg Arg Ser Asp Glu Thr Asn
195      200      205
Gly Gly Arg Met Val Gly Ile Cys Val Pro Leu Gln Glu Arg Ile
210      215      220
```

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1567334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

```
Met Leu Tyr Phe His Gly Gly Ala Phe Leu Ile Ser Ser Thr Ser Phe
1      5      10      15
Pro Ser Tyr His Thr Ser Leu Asn Lys Ile Val Asn Gln Ala Asn Val
      20      25      30
Ile Ala Val Ser Val Asn Tyr Arg Leu Ala Pro Glu His Pro Leu Pro
      35      40      45
Thr Ala Tyr Glu Asp Ser Trp Thr Ala Leu Asn Thr Ile Gln Ala Ile
50      55      60
Asn Glu Pro Trp Ile Asn Asp Tyr Ala Asp Leu Asp Ser Ile Phe Leu
65      70      75      80
Val Gly Asp Ser Ala Gly Ala Asn Ile Ser His His Leu Ala Phe Arg
      85      90      95
Ala Lys Gln Ser Asp Gln Asn Arg Glu Asn Lys Arg His Trp Asn Asp
      100      105      110
Pro Pro Ile Phe Leu Gly Asn Thr Thr Tyr Arg Ser Arg Asp Gln Arg
```

115 120 125
Arg Ser Asp Glu Thr Asn Gly Gly Arg Met Val Gly Ile Cys Val Pro
130 135 140
Leu Gln Glu Arg Ile
145

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1877 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1877

(D) OTHER INFORMATION: / Ceres Seq. ID 1567335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

aaacacaaac	aMcaattaag	ctaaaaaaa	aaccaaagga	tgtctcagaa	actcatgttc	60
ttgttcaccc	ttgcctgcct	ctcctcggtta	ccatctcctt	ttatctccgc	ccaaataccg	120
gccattggaa	atgccacttc	accgtcaaat	atatgtagat	tgccgccgga	tcacatcttat	180
gtgatgcgg	ttcttccaaa	ccagcccgga	gatataatt	ctcaccgacg	tttgtctcta	240
cgaagatccc	tctccagccc	gccggttcat	ttcgtatgat	gacgctgaac	ttgaccggaa	300
aggcaaaagt	ctcgtctaaat	ccacagtagg	ggctctcgaa	gactgcaaat	tcctagccag	360
cctgactatg	gactacctcc	ttagtactgc	acagacggct	gattccaaca	aaacactgtc	420
gttatctagg	gccgaggatg	ttcatcatt	ttctgagtgt	gccatcaaca	atgagcaaac	480
ttgtcttgaa	ggactttaaat	cgaaacggct	ctttccgggt	atcttttcaa	540	
cgatacaaaa	ctctatgggg	ttgtctctgc	ctttttctcc	aaaaggttgg	tgccaaagaa	600
gcacaaagtc	agaccgattt	ggcaaccaca	agccagggtc	aaaaagtgtt	tttgtttccg	660
taacggtaaa	ttaccgttaa	agatgacgga	aagggcacgt	gccgtttaca	acaccgctgac	720
tagaagaaag	ttcttccaat	cggatgcaga	cgccgttcag	gtgagcgaca	ttgtgacggt	780
gatccagaac	gggacgggaa	acttccagac	cataaaagcc	gccattgcag	ctgcacacaaa	840
taaaaactgac	ggtagtagcg	gttacttctt	gattctacga	acggccggct	gtgacgagaa	900
atacgtggaa	gttcccaaga	acaagagata	ttgtgatgat	atcgggtgac	gcatcaacaa	960
gaccgttatc	accggaaaca	ggagtgtcgt	tgatggatgg	acaactttca	attcagccac	1020
attttattcta	tcagggtccca	actttattgg	ttgtaaacata	acaatccgca	atacggcgac	1080
accaacacaaa	ggccaaagctt	tgccattgag	gagtggtggg	gaactgtctg	ttttctacag	1140
ttgtagtgtt	gaagcctatc	aagacacggt	atacacacat	ttcttcagac	agttttatcg	1200
tgaaatgtgat	gtctatggta	ctgtttgatt	tatatattgt	aacgctgcag	ttgtattaca	1260
aaactgtaat	ttgtatccac	gtcaaccctcg	caaaagttcaa	tcgaacggag	ttacgggtcca	1320
aggtcgtact	gatccgaacc	aaaacactgg	gacggcaatt	catggttgta	ctataagacc	1380
ggcagatgat	ttggctacga	gcaactatac	agtgaagact	tatcttggct	gacctgagaa	1440
ggaattattct	agaacccgtg	tcattgcaaa	ttacatagac	gggtttctag	aacccgagtg	1500
ttggaatgca	tggtctggtg	attttgcatt	gagcacactt	tactacggcg	aatataataa	1560
taaccggaact	ggtttctgaa	cgacaaaccg	agtcacttgg	cctggtttac	acgtcatcaa	1620
cgcaactgat	gcttccaatt	tcacgggtc	caatttctct	gttggtgaa	gttggtatgg	1680
acaaaccggga	gtgccttttg	gtgggtgact	gatcgcataa	tcaaccaacc	ttatactata	1740
tatgatattgt	taattagtta	aattatttaa	tcattcatgt	gttggttttt	taatacaaaa	1800
attatttaagt	gggtcctgat	tcgaatacgt	ttgaataaac	tttaacttac	tattgtacaa	1860
ccgaatggtt	ttctctcg					

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..529

(D) OTHER INFORMATION: / Ceres Seq. ID 1567336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

Met Pro Leu His Arg Gln Ile Tyr Val Asp Ser Arg Arg Ile His Leu
1 5 10 15
Ile Val Asp Arg Phe Phe Gln Thr Ser Pro Glu Ile Tyr Ile Pro Thr
20 25 30
Asp Val Cys Leu Tyr Glu Asp Pro Ser Pro Ala Arg Arg Phe Ile Ser
35 40 45
Met Ile Asp Ala Glu Leu Asp Arg Lys Gly Lys Val Ala Ala Lys Ser
50 55 60
Thr Val Gly Ala Leu Glu Asp Cys Lys Phe Leu Ala Ser Leu Thr Met
65 70 75 80
Asp Tyr Leu Leu Ser Ser Ser Gln Thr Ala Asp Ser Thr Lys Thr Leu
85 90 95
Ser Leu Ser Arg Ala Glu Asp Val His Thr Phe Leu Ser Ala Ala Ile
100 105 110
Thr Asn Glu Gln Thr Cys Leu Glu Gly Leu Lys Ser Thr Ala Ser Glu
115 120 125
Asn Gly Leu Ser Gly Asp Leu Phe Asn Asp Thr Lys Leu Tyr Gly Val
130 135 140
Ser Leu Ala Leu Phe Ser Lys Gly Trp Val Pro Arg Arg Gln Arg Ser
145 150 155 160
Arg Pro Ile Trp Gln Pro Gln Ala Arg Phe Lys Lys Phe Phe Gly Phe
165 170 175
Arg Asn Gly Lys Leu Pro Leu Lys Met Thr Glu Arg Ala Arg Ala Val
180 185 190
Tyr Asn Thr Val Thr Arg Arg Lys Leu Leu Gln Ser Asp Ala Asp Ala
195 200 205
Val Gln Val Ser Asp Ile Val Thr Val Ile Gln Asn Gly Thr Gly Asn
210 215 220
Phe Thr Thr Ile Asn Ala Ala Ile Ala Ala Ala Pro Asn Lys Thr Asp
225 230 235 240
Gly Ser Asn Gly Tyr Phe Leu Ile Tyr Val Thr Ala Gly Leu Tyr Glu
245 250 255
Glu Tyr Val Glu Val Pro Lys Asn Lys Arg Tyr Val Met Met Ile Gly
260 265 270
Asp Gly Ile Asn Gln Thr Val Ile Thr Gly Asn Arg Ser Val Val Asp
275 280 285
Gly Trp Thr Thr Phe Asn Ser Ala Thr Phe Ile Leu Ser Gly Pro Asn
290 295 300
Phe Ile Gly Val Asn Ile Thr Ile Arg Asn Thr Ala Gly Pro Thr Lys
305 310 315 320
Gly Gln Ala Val Ala Leu Arg Ser Gly Gly Asp Leu Ser Val Phe Tyr
325 330 335
Ser Cys Ser Phe Glu Ala Tyr Gln Asp Thr Leu Tyr Thr His Ser Leu
340 345 350
Arg Gln Phe Tyr Arg Glu Cys Asp Val Tyr Gly Thr Val Asp Phe Ile
355 360 365
Phe Gly Asn Ala Ala Val Val Leu Gln Asn Cys Asn Leu Tyr Pro Arg
370 375 380
Gln Pro Arg Lys Gly Gln Ser Asn Glu Val Thr Ala Gln Gly Arg Thr
385 390 395 400
Asp Pro Asn Gln Asn Thr Gly Thr Ala Ile His Gly Cys Thr Ile Arg
405 410 415
Pro Ala Asp Asp Leu Ala Thr Ser Asn Tyr Thr Val Lys Thr Tyr Leu
420 425 430
Gly Arg Pro Trp Lys Glu Tyr Ser Arg Thr Val Val Met Gln Thr Tyr
435 440 445
Ile Asp Gly Phe Leu Glu Pro Ser Gly Trp Asn Ala Trp Ser Gly Asp
450 455 460
Phe Ala Leu Ser Thr Leu Tyr Tyr Ala Glu Tyr Asn Asn Thr Gly Pro
465 470 475 480
Gly Ser Asp Thr Thr Asn Arg Val Thr Trp Pro Gly Tyr His Val Ile

(2) INFORMATION FOR SEO ID NO:572:

(A) LENGTH: 481 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..481
(D) OTHER INFORMATION: / Ceres Seq. ID 1567337

Met	Ile	Asp	Ala	Glu	Leu	Asp	Arg	Lys	Gly	Lys	Val	Ala	Ala	Lys	Ser
1			5					10						15	
Thr	Val	Gly	Ala	Leu	Glu	Asp	Cys	Lys	Phe	Leu	Ala	Ser	Leu	Thr	Met
		20						25					30		
Asp	Tyr	Leu	Leu	Ser	Ser	Ser	Gln	Thr	Ala	Asp	Ser	Thr	Lys	Thr	Leu
		35					40					45			
Ser	Leu	Ser	Arg	Ala	Glu	Asp	Val	His	Thr	Phe	Leu	Ser	Ala	Ala	Ile
	50					55					60				
Thr	Asn	Glu	Gln	Thr	Cys	Leu	Glu	Gly	Leu	Lys	Ser	Thr	Ala	Ser	Glu
65					70					75					80
Asn	Gly	Leu	Ser	Gly	Asp	Leu	Phe	Asn	Asp	Thr	Lys	Leu	Tyr	Gly	Val
				85					90					95	
Ser	Leu	Ala	Leu	Phe	Ser	Lys	Gly	Trp	Val	Pro	Arg	Arg	Gln	Arg	Ser
		100					105						110		
Arg	Pro	Ile	Trp	Gln	Pro	Gln	Ala	Arg	Phe	Lys	Lys	Phe	Phe	Gly	Phe
		115				120						125			
Arg	Asn	Gly	Lys	Leu	Pro	Leu	Lys	Met	Thr	Glu	Arg	Ala	Arg	Ala	Val
	130					135					140				
Tyr	Asn	Thr	Val	Thr	Arg	Arg	Lys	Leu	Leu	Gln	Ser	Asp	Ala	Asp	Ala
145					150					155					160
Val	Gln	Val	Ser	Asp	Ile	Val	Thr	Val	Ile	Gln	Asn	Gly	Thr	Gly	Asn
				165					170					175	
Phe	Thr	Thr	Ile	Asn	Ala	Ala	Ile	Ala	Ala	Ala	Pro	Asn	Lys	Thr	Asp
			180					185					190		
Gly	Ser	Asn	Gly	Tyr	Phe	Leu	Ile	Tyr	Val	Thr	Ala	Gly	Leu	Tyr	Glu
		195					200					205			
Glu	Tyr	Val	Glu	Val	Pro	Lys	Asn	Lys	Arg	Tyr	Val	Met	Met	Ile	Gly
	210					215					220				
Asp	Gly	Ile	Asn	Gln	Thr	Val	Ile	Thr	Gly	Asn	Arg	Ser	Val	Val	Asp
225				230						235					240
Gly	Trp	Thr	Thr	Phe	Asn	Ser	Ala	Thr	Phe	Ile	Leu	Ser	Gly	Pro	Asn
				245					250					255	
Phe	Ile	Gly	Val	Asn	Ile	Thr	Ile	Arg	Asn	Thr	Ala	Gly	Pro	Thr	Lys
		260						265					270		
Gly	Gln	Ala	Val	Ala	Leu	Arg	Ser	Gly	Gly	Asp	Leu	Ser	Val	Phe	Tyr
		275					280					285			
Ser	Cys	Ser	Phe	Glu	Ala	Tyr	Gln	Asp	Thr	Leu	Tyr	Thr	His	Ser	Leu
	290					295					300				
Arg	Gln	Phe	Tyr	Arg	Glu	Cys	Asp	Val	Tyr	Gly	Thr	Val	Asp	Phe	Ile
305					310					315					320
Phe	Gly	Asn	Ala	Ala	Val	Val	Leu	Gln	Asn	Cys	Asn	Leu	Tyr	Pro	Arg
				325					330					335	

Gln Pro Arg Lys Gly Gln Ser Asn Glu Val Thr Ala Gln Gly Arg Thr
340 345 350
Asp Pro Asn Gln Asn Thr Gly Thr Ala Ile His Gly Cys Thr Ile Arg
355 360 365
Pro Ala Asp Asp Leu Ala Thr Ser Asn Tyr Thr Val Lys Thr Tyr Leu
370 375 380
Gly Arg Pro Trp Lys Glu Tyr Ser Arg Thr Val Val Met Gln Thr Tyr
385 390 395
Ile Asp Gly Phe Leu Glu Pro Ser Gly Trp Asn Ala Trp Ser Gly Asp
405 410 415
Phe Ala Leu Ser Thr Leu Tyr Tyr Ala Glu Tyr Asn Asn Thr Gly Pro
420 425 430
Gly Ser Asp Thr Thr Asn Arg Val Thr Trp Pro Gly Tyr His Val Ile
435 440 445
Asn Ala Thr Asp Ala Ser Asn Phe Thr Val Thr Asn Phe Leu Val Gly
450 455 460
Glu Gly Trp Ile Gly Gln Thr Gly Val Pro Phe Val Gly Gly Leu Ile
465 470 475 480
Ala

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 450 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..450

(D) OTHER INFORMATION: / Ceres Seq. ID 1567338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

Met Asp Tyr Leu Leu Ser Ser Ser Gln Thr Ala Asp Ser Thr Lys Thr
1 5 10 15
Leu Ser Leu Ser Arg Ala Glu Asp Val His Thr Phe Leu Ser Ala Ala
20 25 30
Ile Thr Asn Glu Gln Thr Cys Leu Glu Gly Leu Lys Ser Thr Ala Ser
35 40 45
Glu Asn Gly Leu Ser Gly Asp Leu Phe Asn Asp Thr Lys Leu Tyr Gly
50 55 60
Val Ser Leu Ala Leu Phe Ser Lys Gly Trp Val Pro Arg Arg Gln Arg
65 70 75 80
Ser Arg Pro Ile Trp Gln Pro Gln Ala Arg Phe Lys Lys Phe Phe Gly
85 90 95
Phe Arg Asn Gly Lys Leu Pro Leu Lys Met Thr Glu Arg Ala Arg Ala
100 105 110
Val Tyr Asn Thr Val Thr Arg Arg Lys Leu Leu Gln Ser Asp Ala Asp
115 120 125
Ala Val Gln Val Ser Asp Ile Val Thr Val Ile Gln Asn Gly Thr Gly
130 135 140
Asn Phe Thr Thr Ile Asn Ala Ala Ile Ala Ala Pro Asn Lys Thr
145 150 155 160
Asp Gly Ser Asn Gly Tyr Phe Leu Ile Tyr Val Thr Ala Gly Leu Tyr
165 170 175
Glu Glu Tyr Val Glu Val Pro Lys Asn Lys Arg Tyr Val Met Met Ile
180 185 190
Gly Asp Gly Ile Asn Gln Thr Val Ile Thr Gly Asn Arg Ser Val Val
195 200 205
Asp Gly Trp Thr Thr Phe Asn Ser Ala Thr Phe Ile Leu Ser Gly Pro
210 215 220
Asn Phe Ile Gly Val Asn Ile Thr Ile Arg Asn Thr Ala Gly Pro Thr

225 230 235 240
Lys Gly Gln Ala Val Ala Leu Arg Ser Gly Gly Asp Leu Ser Val Phe
245 250 255
Tyr Ser Cys Ser Phe Glu Ala Tyr Gln Asp Thr Leu Tyr Thr His Ser
260 265 270
Leu Arg Gln Phe Tyr Arg Glu Cys Asp Val Tyr Gly Thr Val Asp Phe
275 280 285
Ile Phe Gly Asn Ala Ala Val Val Leu Gln Asn Cys Asn Leu Tyr Pro
290 295 300
Arg Gln Pro Arg Lys Gly Gln Ser Asn Glu Val Thr Ala Gln Gly Arg
305 310 315 320
Thr Asp Pro Asn Gln Asn Thr Gly Thr Ala Ile His Gly Cys Thr Ile
325 330 335
Arg Pro Ala Asp Asp Leu Ala Thr Ser Asn Tyr Thr Val Lys Thr Tyr
340 345 350
Leu Gly Arg Pro Trp Lys Glu Tyr Ser Arg Thr Val Met Gln Thr
355 360 365
Tyr Ile Asp Gly Phe Leu Glu Pro Ser Gly Trp Asn Ala Trp Ser Gly
370 375 380
Asp Phe Ala Leu Ser Thr Leu Tyr Tyr Ala Glu Tyr Asn Asn Thr Gly
385 390 395 400
Pro Gly Ser Asp Thr Thr Asn Arg Val Thr Trp Pro Gly Tyr His Val
405 410 415
Ile Asn Ala Thr Asp Ala Ser Asn Phe Thr Val Thr Asn Phe Leu Val
420 425 430
Gly Glu Gly Trp Ile Gly Gln Thr Gly Val Pro Phe Val Gly Gly Leu
435 440 445
Ile Ala
450

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1212
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

aaaatctctc	ttttcaagcc	aaatgaaagt	ttaaaacctt	tgaattgttt	attgaaagt	60
tacatttttc	tggtgaatcc	aactatgttt	agattgagaa	gtctctttgc	gctgaagagt	120
tcttgattg	tagaattgtc	atcacaaaac	gtcacagaag	caattcgctt	cgctccattt	180
cattgcacaa	gtgtttctgc	tgaaaaatcg	aggagtagat	ttggttctgc	tagagattcc	240
gaaGgcgaac	gatcttcaac	gaactcctcc	ataagattta	catgtaccgt	aaaggagaa	300
ggctgtaccca	gtgctaagaa	gactgtggat	aaactccttt	tccacagggg	aattaatgat	360
ccgcttcagca	atgagtgcca	tttcggggcca	agtcgcgtta	tccgggatag	gcataatgaag	420
aaaaaatctc	cgctctgcag	gggaaagaag	cctcgagata	agaaaaacaa	acgatggcac	480
agagaaggta	atccggacga	tgatttttgc	actgatgcta	ataatacat	cgagaacaaa	540
tggagagaac	gctggacagc	tcaatctcag	aaggcttcat	attcgaaga	ctcgacagcg	600
ggattgaaat	ggagagaagg	ctggagctgg	accaactaat	ctcagaggag	caaaaagttgg	660
ataaagaagt	ctttttagat	acctttgaac	gttgagttaa	ggctctgag	gaTgtttcta	720
ggattgcctc	ttgaaggtcc	catcaagggt	gatgatgtta	agaatgcctt	ccgatctctt	780
gcgttgaagt	ggcatccaga	taagcaccag	gggcctttct	aggtggcagc	gcaagagaaa	840
ttcaaacctc	gtgtttgatc	atacaagctc	ctctgtttct	cactcgcttg	acgtttacaca	900
taggcattga	tgcaccattt	gcatttagt	tgataaggct	gctttctgaa	cgttttccag	960
agatacaccc	gttttttagt	gatgggtttg	atttggttca	tgagaatcca	ccagctacaa	1020
gattgcacac	ggcacaccaa	tgtgtctctc	gtttttttcc	aacatttgat	acaaaaaaaca	1080
tgatgtgaa	agatttatgc	tagtgcacaa	cttttagctg	actgctttct	ttttttaaacc	1140
acactgatgt	gaaagacaat	aacttgagaa	tacatcggtg	atacaaaaac	ctattaaagc	1200

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aattttatttt gt

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..296

(D) OTHER INFORMATION: / Ceres Seq. ID 1567344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

Lys	Ile	Ser	Leu	Phe	Thr	Pro	Asn	Glu	Ser	Leu	Lys	Pro	Leu	Asn	Cys
1			5					10						15	
Leu	Leu	Lys	Val	Tyr	Ile	Phe	Leu	Leu	Asn	Pro	Thr	Met	Phe	Arg	Leu
			20					25					30		
Arg	Ser	Leu	Leu	Ser	Leu	Lys	Ser	Ser	Ser	Ile	Val	Glu	Leu	Ser	Ser
		35					40					45			
Gln	Asn	Val	Thr	Glu	Ala	Ile	Arg	Phe	Ala	Pro	Phe	His	Ser	Thr	Ser
	50					55				60					
Val	Leu	Ser	Glu	Lys	Ser	Arg	Ser	Arg	Phe	Gly	Ser	Ala	Arg	Asp	Ser
65				70					75					80	
Glu	Gly	Glu	Arg	Ser	Ser	Lys	Asn	Ser	Ser	Ile	Arg	Phe	Thr	Cys	Thr
			85						90				95		
Val	Lys	Glu	Lys	Gly	Arg	Thr	Ser	Ala	Lys	Lys	Thr	Val	Asp	Lys	Leu
			100					105					110		
Leu	Phe	His	Arg	Gly	Ile	Asn	Asp	Pro	Leu	Gln	Asn	Glu	Trp	His	Phe
			115				120					125			
Gly	Pro	Ser	Pro	Leu	Ile	Arg	Asp	Arg	His	Met	Lys	Lys	Lys	Ser	Pro
	130					135				140					
Pro	Gly	Arg	Gly	Lys	Lys	Pro	Arg	Asp	Lys	Lys	Thr	Lys	Arg	Trp	His
145				150					155					160	
Arg	Glu	Gly	Asn	Pro	Asp	Asp	Asp	Phe	Gly	Thr	Asp	Ala	Asn	Asn	Thr
			165					170					175		
Phe	Glu	Asn	Lys	Trp	Arg	Glu	Arg	Trp	Thr	Ala	Gln	Ser	Gln	Lys	Ala
			180				185						190		
Ser	Tyr	Ser	Lys	Asp	Ser	Thr	Ala	Gly	Phe	Glu	Trp	Arg	Glu	Gly	Trp
	195					200						205			
Ser	Trp	Thr	Thr	Gln	Ser	Gln	Arg	Ser	Lys	Ser	Trp	Asn	Lys	Glu	Ser
	210					215						220			
Phe	Asp	Glu	Pro	Leu	Asn	Val	Glu	Phe	Arg	Ser	Glu	Arg	Ile	Val	Leu
225					230					235				240	
Gly	Leu	Pro	Leu	Glu	Gly	Pro	Ile	Lys	Val	Asp	Asp	Val	Lys	Asn	Ala
			245						250				255		
Phe	Arg	Ser	Ser	Ala	Leu	Lys	Trp	His	Pro	Asp	Lys	His	Gln	Gly	Pro
			260				265						270		
Ser	Gln	Val	Ala	Ala	Gln	Glu	Lys	Phe	Lys	Leu	Cys	Val	Asp	Ala	Tyr
			275				280					285			
Lys	Ser	Leu	Cys	Ser	Ala	Leu	Ala								
	290					295									

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..268

(D) OTHER INFORMATION: / Ceres Seq. ID 1567345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

Met Phe Arg Leu Arg Ser Leu Leu Ser Leu Lys Ser Ser Ser Ile Val
1 5 10 15
Glu Leu Ser Ser Gln Asn Val Thr Glu Ala Ile Arg Phe Ala Pro Phe
20 25 30
His Ser Thr Ser Val Leu Ser Glu Lys Ser Arg Ser Arg Phe Gly Ser
35 40 45
Ala Arg Asp Ser Glu Gly Glu Arg Ser Ser Lys Asn Ser Ser Ile Arg
50 55 60
Phe Thr Cys Thr Val Lys Glu Lys Gly Arg Thr Ser Ala Lys Lys Thr
65 70 75 80
Val Asp Lys Leu Leu Phe His Arg Gly Ile Asn Asp Pro Leu Gln Asn
85 90 95
Glu Trp His Phe Gly Pro Ser Pro Leu Ile Arg Asp Arg His Met Lys
100 105 110
Lys Lys Ser Pro Pro Gly Arg Gly Lys Lys Pro Arg Asp Lys Lys Thr
115 120 125
Lys Arg Trp His Arg Glu Gly Asn Pro Asp Asp Asp Phe Gly Thr Asp
130 135 140
Ala Asn Asn Thr Phe Glu Asn Lys Trp Arg Glu Arg Trp Thr Ala Gln
145 150 155 160
Ser Gln Lys Ala Ser Tyr Ser Lys Asp Ser Thr Ala Gly Phe Glu Trp
165 170 175
Arg Glu Gly Trp Ser Trp Thr Thr Gln Ser Gln Arg Ser Lys Ser Trp
180 185 190
Asn Lys Glu Ser Phe Asp Glu Pro Leu Asn Val Glu Phe Arg Ser Glu
195 200 205
Arg Ile Val Leu Gly Leu Pro Leu Glu Gly Pro Ile Lys Val Asp Asp
210 215 220
Val Lys Asn Ala Phe Arg Ser Ser Ala Leu Lys Trp His Pro Asp Lys
225 230 235 240
His Gln Gly Pro Ser Gln Val Ala Ala Gln Glu Lys Phe Lys Leu Cys
245 250 255
Val Asp Ala Tyr Lys Ser Leu Cys Ser Ala Leu Ala
260 265

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1567346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

Met Lys Lys Lys Ser Pro Pro Gly Arg Gly Lys Lys Pro Arg Asp Lys
1 5 10 15
Lys Thr Lys Arg Trp His Arg Glu Gly Asn Pro Asp Asp Asp Phe Gly
20 25 30
Thr Asp Ala Asn Asn Thr Phe Glu Asn Lys Trp Arg Glu Arg Trp Thr
35 40 45
Ala Gln Ser Gln Lys Ala Ser Tyr Ser Lys Asp Ser Thr Ala Gly Phe
50 55 60
Glu Trp Arg Glu Gly Trp Ser Trp Thr Thr Gln Ser Gln Arg Ser Lys
65 70 75 80
Ser Trp Asn Lys Glu Ser Phe Asp Glu Pro Leu Asn Val Glu Phe Arg
85 90 95
Ser Glu Arg Ile Val Leu Gly Leu Pro Leu Glu Gly Pro Ile Lys Val

100 105 110
Asp Asp Val Lys Asn Ala Phe Arg Ser Ser Ala Leu Lys Trp His Pro
115 120 125
Asp Lys His Gln Gly Pro Ser Gln Val Ala Ala Gln Glu Lys Phe Lys
130 135 140
Leu Cys Val Asp Ala Tyr Lys Ser Leu Cys Ser Ala Leu Ala
145 150 155

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1077 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1077
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

actcacacat	ccacaaaag	agagttagag	attccaagga	ggagagtgcg	tgagCgtgac	60
aatggaaaac	gacaaaagat	ggtctctcgc	cgggaaaaca	gctctggtaa	ccggcgggac	120
tcgtggaatc	gggagagcag	ttgtagagga	actagcaaaa	tttttgcaaa	agttcataact	180
tgttcaagga	accagggaaga	gctaaatgca	tgcttgaatg	attggaaaagc	gaatgggttta	240
gtcgtgtctg	gttcggtttg	tgatgcttcg	gttagggatc	agagggagaa	gttgattcac	300
gaagctctct	ctgccttcag	tggaagctgc	aacatcctta	taaaccaatgt	tggaactaat	360
gtcaggaaac	caacagttga	atactcaagc	gaggaatatg	ccaaaatcat	gtcgaccaac	420
ttagaatccg	ctttccattt	atctcaaaat	gctcctcctc	ttctaaaagc	atctgtggtgc	480
ggaagcattg	tggtcatctc	ctctgtagct	ggcctgggtc	atcttagcac	tggtactatc	540
tatgtgtcaa	ctaaaggagc	acttaatcag	cttaacaagaa	atctagcttg	cgagtgggca	600
agcgacaaca	tcagaaccaa	ttgcgtggcg	ccatgggtaca	caagacctc	acttgtggaa	660
acgctacttg	agaagaagaa	atttgtggag	gctgtagttt	caaggaccoc	acttggggcg	720
gttgagaaac	caagaggaag	ctcatcgttg	gttgcccttc	tctgccttcc	cgcactcatc	780
tatattaccg	gacaggtcat	atccgtcgat	ggaggattca	ctgtcaacgg	tttagtcat	840
gctatgaagc	cttaaatctc	aatcgcaaca	ttactaataa	agcaagaatc	ctcgtgatgt	900
gttggtcttg	tttgtctttg	tttagttttt	gtgacttctt	taaacatata	gtaatatcaa	960
aacgtttgaa	tttctaattg	agccgttaaa	taaatcaagg	cacagtgttg	caccagttta	1020
gttagaccta	caacattttg	catgtattta	ggtatatgga	tgagagtatt	ttgatcg	

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..258
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

Met Val Ser Arg Arg Glu Asn Ser Ser Gly Asn Arg Arg Asp Ser Trp	
1 5 10 15	
Asn Arg Glu Ser Ser Cys Arg Gly Thr Ser Lys Ile Phe Ala Lys Val	
20 25 30	
His Thr Cys Ser Arg Asn Gln Glu Glu Leu Asn Ala Cys Leu Asn Asp	
35 40 45	
Trp Lys Ala Asn Gly Leu Val Val Ser Gly Ser Val Cys Asp Ala Ser	
50 55 60	
Val Arg Asp Gln Arg Glu Lys Leu Ile Gln Glu Ala Ser Ser Ala Phe	
65 70 75 80	
Ser Gly Lys Leu Asn Ile Leu Ile Asn Asn Val Gly Thr Asn Val Arg	
85 90 95	

Lys Pro Thr Val Glu Tyr Ser Ser Glu Glu Tyr Ala Lys Ile Met Ser
100 105 110
Thr Asn Leu Glu Ser Ala Phe His Leu Ser Gln Ile Ala His Pro Leu
115 120 125
Leu Lys Ala Ser Gly Val Gly Ser Ile Val Phe Ile Ser Ser Val Ala
130 135 140
Gly Leu Val His Leu Ser Ser Gly Ser Ile Tyr Gly Ala Thr Lys Gly
145 150 155 160
Ala Leu Asn Gln Leu Thr Arg Asn Leu Ala Cys Glu Trp Ala Ser Asp
165 170 175
Asn Ile Arg Thr Asn Cys Val Ala Pro Trp Tyr Ile Lys Thr Ser Leu
180 185 190
Val Glu Thr Leu Leu Glu Lys Lys Glu Phe Val Glu Ala Val Val Ser
195 200 205
Arg Thr Pro Leu Gly Arg Val Gly Glu Pro Glu Glu Val Ser Ser Leu
210 215 220
Val Ala Phe Leu Cys Leu Pro Ala Ser Ser Tyr Ile Thr Gly Gln Val
225 230 235 240
Ile Ser Val Asp Gly Gly Phe Thr Val Asn Gly Phe Ser Tyr Ala Met
245 250 255
Lys Pro

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

Met Ser Thr Asn Leu Glu Ser Ala Phe His Leu Ser Gln Ile Ala His
1 5 10 15
Pro Leu Leu Lys Ala Ser Gly Val Gly Ser Ile Val Phe Ile Ser Ser
20 25 30
Val Ala Gly Leu Val His Leu Ser Ser Gly Ser Ile Tyr Gly Ala Thr
35 40 45
Lys Gly Ala Leu Asn Gln Leu Thr Arg Asn Leu Ala Cys Glu Trp Ala
50 55 60
Ser Asp Asn Ile Arg Thr Asn Cys Val Ala Pro Trp Tyr Ile Lys Thr
65 70 75 80
Ser Leu Val Glu Thr Leu Leu Glu Lys Lys Glu Phe Val Glu Ala Val
85 90 95
Val Ser Arg Thr Pro Leu Gly Arg Val Gly Glu Pro Glu Glu Val Ser
100 105 110
Ser Leu Val Ala Phe Leu Cys Leu Pro Ala Ser Ser Tyr Ile Thr Gly
115 120 125
Gln Val Ile Ser Val Asp Gly Gly Phe Thr Val Asn Gly Phe Ser Tyr
130 135 140
Ala Met Lys Pro
145

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1438

(D) OTHER INFORMATION: / Ceres Seq. ID 1567371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

atcaaatata	aaccctccag	cctccaacaa	caaaatttac	caacactctc	tctttctctt	60
tctctctgaa	aacttaaaac	gatggctata	acgcgcactc	aaaacgacgg	cggtttcacta	120
aacgcgaata	agattttcgt	tgatcttggtg	gaactgatg	ttgagatcat	cacctccggt	180
cgctgtagta	tcccggcaca	ctccggcacc	ctcgcttcgg	tctcaccggc	actgacgaac	240
atcatcgaga	agccgaggaa	gattcacggc	ggatcatcga	agaaagtlat	taagattctc	300
gggtgtccat	gcgacgcggt	ttcagttctc	gtcagattcc	tctattctcc	gagtgtaagg	360
gagaatgaga	tggaaaaata	cgaatcccat	ctactggctt	tatcacagct	gtatattggtg	420
actcagttaa	agcaacgggtg	cactaaaggc	gtcggtgaga	gagtaaacgc	cgaaaaacgtt	480
gtcgatattc	tccagctggc	tgtctctcgc	gaacgacgtg	acctctgtct	caagtgtatg	540
cgattcattc	actacaagtt	caagaccggt	gaacagacag	aaggatggaa	gtttcttcaa	600
gaacacggtc	cttttcttga	acttgacatt	ctccaattca	tcgacgatgc	agaatcgagg	660
aagaaaaaga	gaaggagaca	cagacgagaa	cagaatctgt	atttgacgct	gagtgaaagg	720
atggaatgta	tagaacacat	atgcaccgaa	ggttgacac	tggtcggaac	atcgtctaac	780
ttagacaaca	agtaaacatg	tcaagcaaaa	cccggtccat	gcagtgcggt	tcgactgtgt	840
taaggacttc	aactctttat	acgtcacttt	gcagtatgca	agaaaagagt	cgatggcaca	900
gggtgtgtcc	gatgcaagag	aattgattcaa	ctctttagac	tccattcttc	gatttgtgac	960
caatctgaat	cttgccggtg	ccctcttttc	aggaatata	agaatagagg	tgaaggagac	1020
aagMaaaatg	gttgaggaca	cgaagtggaa	ggttctgggt	agaagagtga	cgcttgctaa	1080
agccatgtct	tgtgtgtctc	aatcaaaaga	WGaWaaaaagt	gaagtgttat	ttaagaaga	1140
agcagaatgt	ttgatcagaa	tccggaacaa	gttaattgta	atatacaata	tatgtgtttt	1200
tattagatta	tatagtgaag	gattgtttag	agccattaat	tacttgagct	ggaaggttta	1260
tttgtttgtt	atttgtctct	cggactgggt	tattgggtta	actttgctaa	tgagtacacc	1320
tttgaaatctg	tgtttttgtt	tggtcggtcg	aattatatag	aaatgtatta	ttggtataaa	1380
aaagtgtatta	gggttttttg	agacttttgt	gcaaaaagta	tacagattga	tccggttt	

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..253

(D) OTHER INFORMATION: / Ceres Seq. ID 1567372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

Met	Ala	Ile	Thr	Ala	Thr	Gln	Asn	Asp	Gly	Val	Ser	Leu	Asn	Ala	Asn
1				5					10				15		
Lys	Ile	Ser	Tyr	Asp	Leu	Val	Glu	Thr	Asp	Val	Glu	Ile	Ile	Thr	Ser
				20					25				30		
Gly	Arg	Arg	Gly	Ser	Ile	Pro	Ala	His	Ser	Gly	Ile	Leu	Ala	Ser	Val
				35					40				45		
Pro	Val	Leu	Thr	Asn	Ile	Ile	Glu	Lys	Pro	Arg	Lys	Ile	His	Gly	Gly
				50					55				60		
Ser	Ser	Lys	Lys	Val	Ile	Lys	Ile	Leu	Gly	Val	Pro	Cys	Asp	Ala	Val
65				70					75				80		
Ser	Val	Phe	Val	Arg	Phe	Leu	Tyr	Ser	Pro	Ser	Val	Thr	Glu	Asn	Glu
				85					90				95		
Met	Glu	Lys	Tyr	Gly	Ile	His	Leu	Leu	Ala	Leu	Ser	His	Val	Tyr	Met
				100					105				110		
Val	Thr	Gln	Leu	Lys	Gln	Arg	Cys	Thr	Lys	Gly	Val	Gly	Glu	Arg	Val
				115					120				125		
Thr	Ala	Glu	Asn	Val	Val	Asp	Ile	Leu	Gln	Leu	Ala	Arg	Leu	Cys	Asp
				130					135				140		
Ala	Pro	Asp	Leu	Cys	Leu	Lys	Cys	Met	Arg	Phe	Ile	His	Tyr	Lys	Phe
145				150					155				160		

Lys Thr Val Glu Gln Thr Glu Gly Trp Lys Phe Leu Gln Glu His Asp
165 170 175
Pro Phe Leu Glu Leu Asp Ile Leu Gln Phe Ile Asp Asp Ala Glu Ser
180 185 190
Arg Lys Lys Arg Arg Arg Arg His Arg Arg Glu Gln Asn Leu Tyr Leu
195 200 205
Gln Leu Ser Glu Ala Met Glu Cys Ile Glu His Ile Cys Thr Glu Gly
210 215 220
Cys Thr Leu Val Gly Pro Ser Ser Asn Leu Asp Asn Lys Ser Thr Cys
225 230 235 240
Gln Ala Lys Pro Gly Pro Cys Ser Ala Phe Ser Thr Cys
245 250

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1567373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

Met Glu Lys Tyr Gly Ile His Leu Leu Ala Leu Ser His Val Tyr Met
1 5 10 15
Val Thr Gln Leu Lys Gln Arg Cys Thr Lys Gly Val Gly Glu Arg Val
20 25 30
Thr Ala Glu Asn Val Val Asp Ile Leu Gln Leu Ala Arg Leu Cys Asp
35 40 45
Ala Pro Asp Leu Cys Leu Lys Cys Met Arg Phe Ile His Tyr Lys Phe
50 55 60
Lys Thr Val Glu Gln Thr Glu Gly Trp Lys Phe Leu Gln Glu His Asp
65 70 75 80
Pro Phe Leu Glu Leu Asp Ile Leu Gln Phe Ile Asp Asp Ala Glu Ser
85 90 95
Arg Lys Lys Arg Arg Arg Arg His Arg Arg Glu Gln Asn Leu Tyr Leu
100 105 110
Gln Leu Ser Glu Ala Met Glu Cys Ile Glu His Ile Cys Thr Glu Gly
115 120 125
Cys Thr Leu Val Gly Pro Ser Ser Asn Leu Asp Asn Lys Ser Thr Cys
130 135 140
Gln Ala Lys Pro Gly Pro Cys Ser Ala Phe Ser Thr Cys
145 150 155

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1567374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

Met Val Thr Gln Leu Lys Gln Arg Cys Thr Lys Gly Val Gly Glu Arg
1 5 10 15
Val Thr Ala Glu Asn Val Val Asp Ile Leu Gln Leu Ala Arg Leu Cys
20 25 30
Asp Ala Pro Asp Leu Cys Leu Lys Cys Met Arg Phe Ile His Tyr Lys

(D) OTHER INFORMATION: / Ceres Seq. ID 1567384

1	et	Ala	Arg	Lys	Lys	His	Arg	Lys	Leu	Phe	Pro	Thr	Leu	Ala	Ser	Glu
1	Thr	Asn	Lys	Thr	20	Leu	Asp	Cys	Ser	Asn	Gly	Val	Cys	Asp	Pro	Ile
Pro	Tyr	Asn	Cys	20	Tyr	Pro	Glu	Pro	Asp	Tyr	Tyr	Thr	Ile	Ser	Pro	Gln
Leu	Pro	Pro	Trp	35	Ser	Ser	Ser	Pro	Gln	Pro	Ser	Pro	Cys	Pro	Ser	Pro
Ser	Ile	Ser	Ala	50	Val	Tyr	70	Leu	Pro	Ser	Gln	Asp	75	Ser	Ser	Leu
65	Asp	Ala	Ile	Ser	Ile	Ile	Thr	Ile	Thr	Gly	90	Ala	Val	Leu	Ala	Ile
Leu	Thr	Gly	Phe	100	Phe	Leu	Val	Ala	Lys	Phe	Phe	Ser	Asp	Ser	Val	Asn
Arg	Val	Asn	Gln	115	Gly	Thr	Tyr	Gln	Ser	Asp	Asn	Glu	Asp	Asn	Asp	Thr
Val	Met	Glu	Glu	Glu	Phe	Gln	130	Asp	Arg	Glu	Gln	Val	Asp	His	Pro	Ile
130	Trp	Leu	Ile	Arg	Thr	Thr	Gly	Leu	Gln	Gln	Ser	Ile	Ile	Asn	Ser	Ile
145	Thr	Ile	Cys	Asn	Tyr	Xaa	Arg	Gly	Asp	Gly	Leu	Ile	Glu	Arg	Thr	Asp
Cys	Pro	Val	Cys	Leu	Asn	Glu	Phe	Glu	Glu	Asp	Glu	Ser	Leu	Arg	Leu	
Leu	Pro	Lys	Cys	Asn	His	Ala	Phe	His	Ile	Ser	Cys	Ile	Asp	Thr	Trp	
Leu	Ser	Ser	His	Thr	Asn	Cys	Pro	Leu	Cys	Arg	Ala	Gly	Ile	Ala	Met	
210	Ile	Ser	Val	Thr	Thr	Pro	Arg	Tyr	Ser	Gly	Pro	Val	Glu	Val	Thr	
225	Gly	Gly	Ser	Gly	Ser	His	Leu	Glu	Asn	Asp	Gly	Val	Asp	Glu	Glu	Asp
His	Gly	Glu	Ile	Glu	Asn	Arg	Val	Asp	Ser	Asp	Phe	Lys	Glu	Ser	Asp	
Asp	Ser	Asp	Ile	Arg	Ile	Glu	Ile	Tyr	Arg	Phe	Asp	Ser	Asp	Gly	Asp	
Gly	Ser	Glu	Thr	Glu	Thr	Lys	Glu	Arg	Val	Arg	Val	Leu	Lys	Glu	Cys	
305	Met	Asp	Pro	Asn	Gly	Gly	Asp	Ser	Val	Asn	Ser	Leu	Ser	His	Thr	Lys
Thr	His	Val	Glu	Ser	Val	Asp	Phe	Pro	Gly	Lys	Ser	Cys	Glu	Asn	Gln	
Ser	Glu	Glu	Phe	Thr	Arg	His	Asn	Gly	Glu	Asp	Glu	Ala	Ser	Cys	Ser	
Glu	Glu	Asn	Gly	Gly	Gly	Ser	Asn	Gln	Leu	Arg	Arg	Ser	Cys	Asp	Ser	
Gly	Glu	Leu	Asn	Gly	Glu	Thr	Thr	Gly	Asp	Glu	Gly	Lys	Ser	Gln	Ser	
385	Asp	Ile	Ser	Ser	Ser	Thr	Leu	Lys	Thr	Asn	Gly	Ser	Ser	Ser	Ser	Val
Ser	Cys	Phe	Asn	Lys	Asn	Lys	Ser	Ser	Val	Phe	Pro	Leu				400

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..284
(D) OTHER INFORMATION: / Ceres Seq. ID 1567385
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

Met	Glu	Glu	Glu	Phe	Gln	Asp	Arg	Glu	Gln	Val	Asp	His	Pro	Ile	Trp
1				5					10					15	
Leu	Ile	Arg	Thr	Thr	Gly	Leu	Gln	Gln	Ser	Ile	Ile	Asn	Ser	Ile	Thr
				20				25					30		
Ile	Cys	Asn	Tyr	Xaa	Arg	Gly	Asp	Gly	Leu	Ile	Glu	Arg	Thr	Asp	Cys
		35					40					45			
Pro	Val	Cys	Leu	Asn	Glu	Phe	Glu	Glu	Asp	Glu	Ser	Leu	Arg	Leu	Leu
		50				55					60				
Pro	Lys	Cys	Asn	His	Ala	Phe	His	Ile	Ser	Cys	Ile	Asp	Thr	Trp	Leu
		65				70				75				80	
Ser	Ser	His	Thr	Asn	Cys	Pro	Leu	Cys	Arg	Ala	Gly	Ile	Ala	Met	Ile
			85						90					95	
Ser	Val	Thr	Thr	Pro	Arg	Tyr	Ser	Gly	Pro	Val	Glu	Val	Thr	Pro	Gly
			100					105					110		
Gly	Ser	Gly	Ser	His	Leu	Glu	Asn	Asp	Gly	Val	Asp	Glu	Glu	Asp	His
		115					120					125			
Gly	Glu	Ile	Glu	Asn	Arg	Val	Asp	Ser	Asp	Phe	Lys	Glu	Ser	Asp	Asp
		130				135					140				
Ser	Asp	Ile	Arg	Ile	Glu	Ile	Tyr	Arg	Phe	Asp	Ser	Asp	Gly	Asp	Gly
				150					155					160	
Ser	Glu	Thr	Glu	Thr	Lys	Glu	Arg	Val	Arg	Val	Leu	Lys	Glu	Cys	Met
			165					170						175	
Asp	Pro	Asn	Gly	Gly	Asp	Ser	Val	Asn	Ser	Leu	Ser	His	Thr	Lys	Thr
			180					185					190		
His	Val	Glu	Ser	Val	Asp	Phe	Pro	Gly	Lys	Ser	Cys	Glu	Asn	Gln	Ser
			195				200					205			
Glu	Glu	Phe	Thr	Arg	His	Asn	Gly	Glu	Asp	Glu	Ala	Ser	Cys	Ser	Glu
			210			215					220				
Glu	Asn	Gly	Gly	Gly	Ser	Asn	Gln	Leu	Arg	Arg	Ser	Cys	Asp	Ser	Gly
			225			230					235			240	
Glu	Leu	Asn	Gly	Glu	Thr	Thr	Gly	Asp	Glu	Gly	Lys	Ser	Gln	Ser	Asp
			245						250					255	
Ile	Ser	Ser	Ser	Thr	Leu	Lys	Thr	Asn	Gly	Ser	Ser	Ser	Ser	Val	Ser
			260					265						270	
Cys	Phe	Asn	Lys	Asn	Lys	Ser	Ser	Val	Phe	Pro	Leu				
		275					280								

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2184 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2184

(D) OTHER INFORMATION: / Ceres Seq. ID 1567390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

accagccccc	taaataaac	accgggctct	gtttcaataa	aaaaaatccc	ctccctctca	60
tatttacctc	ccgaataaaa	ccggaggagg	agaaaaaaca	taaaaagcaa	aaaaaaaggt	120
aaaatcaaaa	agggaaaaaa	tatatataca	caaaaaaaa	aagtttagaa	aaatggcagt	180
aggaaagggt	gtggatctct	tgggcatcact	cctctagtgt	gtgggtgtgt	ccataggagt	240
tatcacgttc	gttaataaag	gaggcggcgc	caatggcgac	agtaaatggt	ccataaacct	300
tcatcagaaa	gcgggtccga	caatttgcca	gtcaaccaca	gaccaagggt	cgtagcgcaa	360
aacactcgac	ccagtcacaa	gtgatgatcc	aagcaagctt	gtcaaaagct	tcctgatggc	420
tactaaagac	gcgatccaaa	aatcctcaaa	cttcacggct	tcgacccgag	Gaggtatggg	480
tactaacatg	aacgcgacca	gcaagccgt	tcttgattac	tgcaagagag	tattgatgta	540

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cgctcttgag gatcttgaga ccattgttga agagatgggt gaggatcttc agcagagtgg    600
aactaagctt gaccagctca aacaatgggt aactggagtt ttcaactacc aaaccgagtt    660
tctttgacgc atcgaggagc ttgagctaaa gaagatcatg ggtgaaggaa tctctaatc    720
caaggtttttg accagtaacg ctatcgatac ctccatttcc gttgtttaccg cgatggccca    780
aatgggtgtc aaaagtgcagc aatagaaaga cataaccatg ggagccggag ccggtggagc    840
tgcaogtcgc cttcttgaag acaacgactc taagggactc cccaaatggt tttctggtaa    900
agacaggaag cttatggcta aggcgggacg tggcgctcca gctggcggtg atgatggat    960
cggtgaagcg ggtggtggtg gcggtgaagt caaggcgact catgtagtgg ctaagtagtg    1020
aagtgagacg ttttaagacca tttctgagcg ggttatggct tgcccggata aaaacctgtg    1080
aaggtgcatt atccatatac aggtcggtat ctacaatgaa caagtcaagaa tccctaagaa    1140
gaagaacaac attttcatgt tcggtgatgg tgctacacaa accatcattt cctttgacag    1200
aagtgtaaaa cttagccacg gaaccactac ttcaactcagt ggcacogctc aggtcgaaic    1260
tgaggggatt atggcgaagt ggattgggtt taagaacact gctggtccat tgggacacca    1320
agcggtcgca ctccggtgta acggagacgg tcggttcata ttcaactgta gattcgacgg    1380
ttaccaagac acactctacg tcaacaacgg acgtcaattc tacaggaaca ttgtttatc    1440
cggtacagtg gatttcatct tcggaaaaatc cgcaactgtg atccaaaact ctctcatct    1500
cgctcgaaag ggaagcccg gacaatccaa ctacgttacg gctgacgcta atgaaaaggg    1560
tgacgagatg aagatcggtt tctgtctcca taactgccg atcataccgg acaaggagct    1620
cgaagctgac aagctaacca tcaaatcgta cctagggaag ccgtggaaga agtttgccac    1680
gactgtgatt attggaactg agattgggtg tttgattaaa ccagaaggat ggaccgaagt    1740
gcaaggagaa caaaaccaca agactgtcaa atacattgag ttcaataacc gtggaccggg    1800
agctgcactc actcagagcg ctcttggttg taaggtggct aagctctgcg ctgaggttga    1860
aacttaccac gtggctaact gggttggtcc agctaactgg atccaagaag ccaacogtgc    1920
cgtccaacta ggtattgaag aggacaacac aaaaagttta agaataaaac agtatgtgat    1980
aatgtaagg taacgatacg acgtcgtctc tggggatcag aactcttttt tggatactat    2040
atcaaaagat aggttctag acgtgttgag atgatgttg tataagattg ctttctgtca    2100
cgtgcaaaag agggaaaaaa attgttttgt tatttttttt gtagtacaaa taattaatt    2160
ttttttatca catgttgat cctt

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(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..588

(D) OTHER INFORMATION: / Ceres Seq. ID 1567391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

```

Met Ala Val Gly Lys Val Val Val Ser Val Ala Ser Leu Leu Leu Val
1      5      10      15
Val Gly Val Ala Ile Gly Val Ile Thr Phe Val Asn Lys Gly Gly Gly
20      25      30
Ala Asn Gly Asp Ser Asn Gly Pro Ile Asn Ser His Gln Lys Ala Val
35      40      45
Gln Thr Ile Cys Gln Ser Thr Thr Asp Gln Gly Ser Cys Ala Lys Thr
50      55      60
Leu Asp Pro Val Lys Ser Asp Asp Pro Ser Lys Leu Val Lys Ala Phe
65      70      75      80
Leu Met Ala Thr Lys Asp Ala Ile Thr Lys Ser Ser Asn Phe Thr Ala
85      90      95
Ser Thr Glu Gly Gly Met Gly Thr Asn Met Asn Ala Thr Ser Lys Ala
100     105     110
Val Leu Asp Tyr Cys Lys Arg Val Leu Met Tyr Ala Leu Glu Asp Leu
115     120     125
Glu Thr Ile Val Glu Glu Met Gly Glu Asp Leu Gln Gln Ser Gly Thr
130     135     140
Lys Leu Asp Gln Leu Lys Gln Trp Leu Thr Gly Val Phe Asn Tyr Gln
145     150     155     160
Thr Asp Cys Leu Asp Asp Ile Glu Glu Val Glu Leu Lys Lys Ile Met

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(2) INFORMATION FOR SEQ ID NO:590:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 507 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

Met	Ala	Thr	Lys	Asp	Ala	Ile	Thr	Lys	Ser	Ser	Asn	Phe	Thr	Ala	Ser
1				5					10					15	
Thr	Glu	Gly	Gly	Met	Gly	Thr	Asn	Met	Asn	Ala	Thr	Ser	Lys	Ala	Val
			20					25					30		
Leu	Asp	Tyr	Cys	Lys	Arg	Val	Leu	Met	Tyr	Ala	Leu	Glu	Asp	Leu	Glu
		35					40					45			
Thr	Ile	Val	Glu	Glu	Met	Gly	Glu	Asp	Leu	Gln	Gln	Ser	Gly	Thr	Lys
		50				55					60				
Leu	Asp	Gln	Leu	Lys	Gln	Trp	Leu	Thr	Gly	Val	Phe	Asn	Tyr	Gln	Thr
65					70					75					80
Asp	Cys	Leu	Asp	Asp	Ile	Glu	Glu	Val	Glu	Leu	Lys	Lys	Ile	Met	Gly
				85					90					95	
Glu	Gly	Ile	Ser	Ser	Ser	Lys	Val	Leu	Thr	Ser	Asn	Ala	Ile	Asp	Ile
			100					105					110		
Phe	His	Ser	Val	Val	Thr	Ala	Met	Ala	Gln	Met	Gly	Val	Lys	Val	Asp
		115					120					125			
Asp	Met	Lys	Asn	Ile	Thr	Met	Gly	Ala	Gly	Ala	Gly	Gly	Ala	Ala	Arg
						135					140				
Arg	Leu	Leu	Glu	Asp	Asn	Asp	Ser	Lys	Gly	Leu	Pro	Lys	Trp	Phe	Ser
145					150					155				160	
Gly	Lys	Asp	Arg	Lys	Leu	Met	Ala	Lys	Ala	Gly	Arg	Gly	Ala	Pro	Ala
				165					170					175	
Gly	Gly	Asp	Asp	Gly	Ile	Gly	Glu	Gly	Gly	Gly	Gly	Gly	Gly	Lys	Ile
			180					185					190		
Lys	Ala	Thr	His	Val	Val	Ala	Lys	Asp	Gly	Ser	Gly	Gln	Phe	Lys	Thr
		195					200					205			
Ile	Ser	Glu	Ala	Val	Met	Ala	Cys	Pro	Asp	Lys	Asn	Pro	Gly	Arg	Cys
		210				215					220				
Ile	Ile	His	Ile	Lys	Ala	Gly	Ile	Tyr	Asn	Glu	Gln	Val	Arg	Ile	Pro
225				230					235					240	
Lys	Lys	Lys	Asn	Asn	Ile	Phe	Met	Phe	Gly	Asp	Gly	Ala	Thr	Gln	Thr
				245					250					255	
Ile	Ile	Thr	Phe	Asp	Arg	Ser	Val	Lys	Leu	Ser	Pro	Gly	Thr	Thr	Thr
		260						265					270		
Ser	Leu	Ser	Gly	Thr	Val	Gln	Val	Glu	Ser	Glu	Gly	Phe	Met	Ala	Lys
		275					280					285			
Trp	Ile	Gly	Phe	Lys	Asn	Thr	Ala	Gly	Pro	Leu	Gly	His	Gln	Ala	Val
		290				295					300				
Ala	Leu	Arg	Val	Asn	Gly	Asp	Arg	Ala	Val	Ile	Phe	Asn	Cys	Arg	Phe
305				310					315					320	
Asp	Gly	Tyr	Gln	Asp	Thr	Leu	Tyr	Val	Asn	Asn	Gly	Arg	Gln	Phe	Tyr
				325				330						335	
Arg	Asn	Ile	Val	Val	Ser	Gly	Thr	Val	Asp	Phe	Ile	Phe	Gly	Lys	Ser
			340					345				350			
Ala	Thr	Val	Ile	Gln	Asn	Ser									

450	455	460	
Thr Thr Gln Arg Pro Pro Trp Val Lys Val Ala Lys Ser Ala Ala Glu			
465	470	475	480
Val Glu Thr Tyr Thr Val Ala Asn Trp Val Gly Pro Ala Asn Trp Ile			
	485	490	495
Gln Glu Ala Asn Val Pro Val Gln Leu Gly Leu			
	500	505	

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..487
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

Met Gly Thr Asn Met Asn Ala Thr Ser Lys Ala Val Leu Asp Tyr Cys	
1	5 10 15
Lys Arg Val Leu Met Tyr Ala Leu Glu Asp Leu Glu Thr Ile Val Glu	
	20 25 30
Glu Met Gly Glu Asp Leu Gln Gln Ser Gly Thr Lys Leu Asp Gln Leu	
	35 40 45
Lys Gln Trp Leu Thr Gly Val Phe Asn Tyr Gln Thr Asp Cys Leu Asp	
	50 55 60
Asp Ile Glu Glu Val Glu Leu Lys Lys Ile Met Gly Glu Gly Ile Ser	
65	70 75 80
Asn Ser Lys Val Leu Thr Ser Asn Ala Ile Asp Ile Phe His Ser Val	
	85 90 95
Val Thr Ala Met Ala Gln Met Gly Val Lys Val Asp Asp Met Lys Asn	
	100 105 110
Ile Thr Met Gly Ala Gly Ala Gly Gly Ala Ala Arg Arg Leu Leu Glu	
	115 120 125
Asp Asn Asp Ser Lys Gly Leu Pro Lys Trp Phe Ser Gly Lys Asp Arg	
	130 135 140
Lys Leu Met Ala Lys Ala Gly Arg Gly Ala Pro Ala Gly Gly Asp Asp	
145	150 155 160
Gly Ile Gly Glu Gly Gly Gly Gly Gly Lys Ile Lys Ala Thr His	
	165 170 175
Val Val Ala Lys Asp Gly Ser Gly Gln Phe Lys Thr Ile Ser Glu Ala	
	180 185 190
Val Met Ala Cys Pro Asp Lys Asn Pro Gly Arg Cys Ile Ile His Ile	
	195 200 205
Lys Ala Gly Ile Tyr Asn Glu Gln Val Arg Ile Pro Lys Lys Lys Asn	
	210 215 220
Asn Ile Phe Met Phe Gly Asp Gly Ala Thr Gln Thr Ile Ile Thr Phe	
225	230 235 240
Asp Arg Ser Val Lys Leu Ser Pro Gly Thr Thr Thr Ser Leu Ser Gly	
	245 250 255
Thr Val Gln Val Glu Ser Glu Gly Phe Met Ala Lys Trp Ile Gly Phe	
	260 265 270
Lys Asn Thr Ala Gly Pro Leu Gly His Gln Ala Val Ala Leu Arg Val	
	275 280 285
Asn Gly Asp Arg Ala Val Ile Phe Asn Cys Arg Phe Asp Gly Tyr Gln	
290	295 300
Asp Thr Leu Tyr Val Asn Asn Gly Arg Gln Phe Tyr Arg Asn Ile Val	
305	310 315 320
Val Ser Gly Thr Val Asp Phe Ile Phe Gly Lys Ser Ala Thr Val Ile	
	325 330 335

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(B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1567395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

Tyr	Asn	Lys	Pro	Ser	Gly	Ala	Leu	His	Phe	Thr	Ala	Ser	Asn	Asn	Asp	
1		5							10					15		
Cys	Gly	Val	Arg	Asp	Phe	Asp	Met	Glu	Arg	Tyr	Gln	Leu	Val	Lys	His	
		20						25					30			
Phe	Arg	Phe	Pro	Trp	Pro	Val	Asn	His	Ala	Ser	Leu	Ser	Pro	Asp	Gly	
		35					40					45				
Lys	Leu	Leu	Ala	Ile	Val	Gly	Asp	Asn	Pro	Glu	Gly	Leu	Ile	Val	Asp	
	50					55				60						
Pro	Asn	Thr	Gly	Lys	Thr	Leu	Glu	Thr	Leu	Ser	Gly	His	Leu	Asp	Phe	
65				70					75					80		
Ser	Phe	Ala	Ser	Ala	Trp	His	Pro	Asp	Gly	Val	Thr	Phe	Ser	Thr	Gly	
			85					90					95			
Asn	Gln	Asp	Lys	Thr	Cys	Arg	Val	Trp	Asp	Ile	Arg	Asn	Leu	Ser	Gln	
		100						105					110			
Ser	Val	Thr	Val	Leu	Lys	Gly	Asn	Leu	Gly	Ala	Ile	Arg	Ser	Ile	Arg	
	115						120					125				
Tyr	Thr	Ser	Asp	Gly	Lys	Tyr	Met	Ala	Glu	Pro	Ala	Asp	Phe			
	130					135			140							
Val	His	Val	Tyr	Asp	Val	Ser	Asn	Gly	Tyr	Glu	Thr	Glu	Gln	Glu	Ile	
	145			150					155					160		
Asp	Phe	Phe	Gly	Glu	Ile	Ser	Gly	Ile	Ser	Phe	Ser	Pro	Asp	Thr	Glu	
			165					170						175		
Ala	Leu	Phe	Ile	Gly	Val	Trp	Asp	Arg	Thr	Tyr	Gly	Ser	Leu	Leu	Glu	
		180					185						190			
Phe	Gly	Arg	Arg	Arg	Asn	Tyr	Ser	Tyr	Leu	Asp	Ser	Tyr	Leu			
	195					200						205				

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..183

(D) OTHER INFORMATION: / Ceres Seq. ID 1567396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

Met	Glu	Arg	Tyr	Gln	Leu	Val	Lys	His	Phe	Arg	Phe	Pro	Trp	Pro	Val	
1		5							10					15		
Asn	His	Ala	Ser	Leu	Ser	Pro	Asp	Gly	Lys	Leu	Leu	Ala	Ile	Val	Gly	
		20						25					30			
Asp	Asn	Pro	Glu	Gly	Leu	Ile	Val	Asp	Pro	Asn	Thr	Gly	Lys	Thr	Leu	
		35					40					45				
Glu	Thr	Leu	Ser	Gly	His	Leu	Asp	Phe	Ser	Phe	Ala	Ser	Ala	Trp	His	
	50					55				60						
Pro	Asp	Gly	Val	Thr	Phe	Ser	Thr	Gly	Asn	Gln	Asp	Lys	Thr	Cys	Arg	
65				70					75					80		
Val	Trp	Asp	Ile	Arg	Asn	Leu	Ser	Gln	Ser	Val	Thr	Val	Leu	Lys	Gly	
			85					90					95			
Asn	Leu	Gly	Ala	Ile	Arg	Ser	Ile	Arg	Tyr	Thr	Ser	Asp	Gly	Lys	Tyr	
		100						105					110			
Met	Ala	Met	Ala	Glu	Pro	Ala	Asp	Phe	Val	His	Val	Tyr	Asp	Val	Ser	
	115						120						125			
Asn	Gly	Tyr	Glu	Thr	Glu	Gln	Glu	Ile	Asp	Phe	Phe	Gly	Glu	Ile	Ser	
	130					135						140				
Gly	Ile	Ser	Phe	Ser	Pro	Asp	Thr	Glu	Ala	Leu	Phe	Ile	Gly	Val	Trp	
	145				150				155				160			
Asp	Arg	Thr	Tyr	Gly	Ser	Leu	Leu	Glu	Phe	Gly	Arg	Arg	Arg	Asn	Tyr	

{2} INFORMATION FOR SEQ ID NO:596:

(A) LENGTH: 1449 base pairs

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..1449

(D) OTHER INFORMATION: / Ceres Seq. ID 1567405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

aaccactcat	ctcaattttt	cccacggctc	agattctctc	cgctctctat	tctttcccca	60
gaaaattgag	gcagcggatt	cgcgcgcctc	tatcttttat	ctgtctcttc	tcttcgaac	120
cttaattgcg	gattctctgt	ctgctttaac	agttcgtcga	tgagattttg	gaagaaacct	180
caacacggct	ttactgcacg	cgccgcggct	ctcaaaagtc	aaccacgcag	gaaatagagt	240
tgctgcgga	gactttatct	ggggaggaga	acagttctcg	ggaatgtgtg	ttcttgggat	300
tcgcgagaga	atcaaatctc	aagctcttcc	ggaaactgag	aaatcttaag	attcatcaag	360
agtcagtgaa	tcgatgtctc	gattgtgtgat	gcaaatcttg	caagtcctga	actaagaacg	420
aagatgggaa	tcttcacgtc	gtgtccaaag	attctacttc	tcgagaaaca	gagtactctg	480
ttcgaagacc	gtccgagaat	gtaataattc	tacacggggt	tgtggggtca	tcacattttt	540
gcagacaaac	tgtatttgaa	cacattccaa	aagatgatta	taggctcttc	gcgactgcgt	600
ttttgggatt	cggggagagt	ctcaagccaa	gggatagtct	ctataacttg	aaagatcatg	660
tggaatcacg	agagagatct	gtcattaagc	cataccaatt	agattctttt	catgtgggtg	720
caacattcaat	tggttggtta	atttgcgtct	ctttgggtcg	taaacattct	aacattgtta	780
aatccgttac	ctttttgtca	ccgccttatt	ttctctcttc	ggtagatgga	tcggtcttga	840
accgaattcg	tagaaagcgg	tgtgtggcac	cgcttcgctt	tgggacagcg	tgatgtcttt	900
gggtatgaaca	tttttgtgaa	tcgctatgat	ctataactct	caagcatcat	aagatatggg	960
agtgctcaat	caagctatct	ataggttaaa	gggagatcca	tttgaagact	aagcagacaa	1020
caaggcagca	acatcacatg	ctagggcata	gtatgcacaa	tgtatgatgt	gtgggtctca	1080

aagtcgctga tgaacatctt gaaaccctaa taaagtcctgg cgttaagatt cacttgatgc	1140
aaggcgactg tgaccacaatc gttccttcac attgctctgg caacatgaag aggacttttc	1200
cgccggtgga agttgatatac attactgggtg ctgatcatga tagtatgata agcggaagag	1260
gagaagagtt tgctgagagaa ttggagagca tttgggtttc atttaaagag tctggttagt	1320
tttttcaaac tttataggtg ggaggcactg tagtcgatgt cgactgacta caagtttgag	1380
tccgattgta agatcaagtc tattgttaat gagccatcta atggagcgcct atatggagtc	1440
caattatcg	

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..423

(D) OTHER INFORMATION: / Ceres Seq. ID 1567406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

Met	Ser	Phe	Pro	Arg	Lys	Phe	Gly	Thr	Ala	Ile	His	Ala	Ala	Leu	Ser
1			5					10						15	
Phe	Ile	Val	Phe	Phe	Phe	Asp	Leu	Ile	Asp	Ala	Ile	Leu	Cys	Val	
			20				25					30			
Val	Tyr	Glu	Phe	Val	Asp	Glu	Ile	Leu	Glu	Glu	Asn	Ser	Thr	Gly	Cys
			35				40					45			
Tyr	Cys	Thr	Ala	Ala	Ala	Pro	Gln	Ser	Leu	Thr	Thr	Asp	Glu	Asn	Glu
			50				55				60				
Leu	Ser	Ser	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Asn	Ser	Phe	Arg	Glu	Met
			65				70				75			80	
Trp	Phe	Leu	Gly	Phe	Ala	Arg	Glu	Phe	Lys	Ser	Lys	Leu	Ser	Arg	Lys
			85						90				95		
Leu	Arg	Lys	Ser	Lys	Ile	His	Gln	Glu	Ser	Val	Asn	Arg	Trp	Ser	Asp
			100					105				110			
Cys	Gly	Cys	Lys	Ser	Cys	Lys	Ser	Trp	Thr	Lys	Asn	Glu	Asp	Gly	Asn
			115				120					125			
Leu	His	Val	Val	Val	Lys	Asp	Ser	Thr	Ser	Arg	Glu	Thr	Glu	Tyr	Ser
			130				135					140			
Val	Gln	Glu	Pro	Ser	Glu	Asn	Val	Ile	Phe	Ile	His	Gly	Phe	Met	Gly
			145				150					155			160
Ser	Ser	His	Phe	Trp	Thr	Glu	Thr	Val	Phe	Glu	His	Ile	Gln	Lys	Asp
			165						170					175	
Asp	Tyr	Arg	Leu	Leu	Ala	Ile	Asp	Leu	Leu	Gly	Phe	Gly	Glu	Ser	Pro
			180						185				190		
Lys	Pro	Arg	Asp	Ser	Leu	Tyr	Thr	Leu	Lys	Asp	His	Val	Asp	Thr	Ile
			195				200					205			
Glu	Arg	Ser	Val	Ile	Lys	Pro	Tyr	Gln	Leu	Asp	Ser	Phe	His	Val	Val
			210				215					220			
Ala	His	Ser	Met	Gly	Cys	Leu	Ile	Ala	Leu	Ala	Leu	Ala	Ala	Lys	His
			225				230				235			240	
Ser	Asn	Ile	Val	Lys	Ser	Val	Thr	Leu	Val	Ala	Pro	Pro	Tyr	Phe	Pro
			245						250				255		
Ser	Ser	Val	Asp	Gly	Ser	Val	Leu	Asn	Arg	Ile	Ala	Arg	Lys	Arg	Leu
			260					265					270		
Trp	Pro	Pro	Leu	Ala	Phe	Gly	Thr	Ala	Val	Met	Ser	Trp	Tyr	Glu	His
			275				280					285			
Ile	Gly	Arg	Cys	Val	Cys	Phe	Ile	Ile	Cys	Lys	His	His	Lys	Ile	Trp
			290				295					300			
Glu	Trp	Leu	Ile	Lys	Leu	Cys	Ile	Gly	Lys	Arg	Glu	Ile	His	Trp	Lys
			305				310				315			320	
Ile	Lys	Asp	Ile	Thr	Arg	His	Thr	His	His	Ser	Ala	Trp	His	Ser	Met
			325					330						335	

His Asn Val Ile Cys Gly Gly Ser Lys Val Ala Asp Glu His Leu Glu
340 345 350
Thr Leu Ile Lys Ser Gly Val Lys Ile His Leu Met Gln Gly Asp Cys
355 360 365
Asp Gln Ile Val Pro Ser His Cys Ser Gly Asn Met Lys Arg Thr Phe
370 375 380
Pro Ala Val Glu Val Asp Ile Ile Thr Gly Ala Asp His Asp Ser Met
385 390 395 400
Ile Ser Gly Arg Gly Glu Glu Phe Ala Glu Lys Leu Glu Ser Ile Trp
405 410 415
Cys Ser Phe Lys Glu Ser Gly
420

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..344
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

Met Trp Phe Leu Gly Phe Ala Arg Glu Phe Lys Ser Lys Leu Ser Arg
1 5 10 15
Lys Leu Arg Lys Ser Lys Ile His Gln Glu Ser Val Asn Arg Trp Ser
20 25 30
Asp Cys Gly Cys Lys Ser Cys Lys Ser Trp Thr Lys Asn Glu Asp Gly
35 40 45
Asn Leu His Val Val Val Lys Asp Ser Thr Ser Arg Glu Thr Glu Tyr
50 55 60
Ser Val Gln Glu Pro Ser Glu Asn Val Ile Phe Ile His Gly Phe Met
65 70 75 80
Gly Ser Ser His Phe Trp Thr Glu Thr Val Phe Glu His Ile Gln Lys
85 90 95
Asp Asp Tyr Arg Leu Leu Ala Ile Asp Leu Leu Gly Phe Gly Glu Ser
100 105 110
Pro Lys Pro Arg Asp Ser Leu Tyr Thr Leu Lys Asp His Val Asp Thr
115 120 125
Ile Glu Arg Ser Val Ile Lys Pro Tyr Gln Leu Asp Ser Phe His Val
130 135 140
Val Ala His Ser Met Gly Cys Leu Ile Ala Leu Ala Leu Ala Lys
145 150 155 160
His Ser Asn Ile Val Lys Ser Val Thr Leu Val Ala Pro Pro Tyr Phe
165 170 175
Pro Ser Ser Val Asp Gly Ser Val Leu Asn Arg Ile Ala Arg Lys Arg
180 185 190
Leu Trp Pro Pro Leu Ala Phe Gly Thr Ala Val Met Ser Trp Tyr Glu
195 200 205
His Ile Gly Arg Cys Val Cys Phe Ile Ile Cys Lys His His Lys Ile
210 215 220
Trp Glu Trp Leu Ile Lys Leu Cys Ile Gly Lys Arg Glu Ile His Trp
225 230 235 240
Lys Ile Lys Asp Ile Thr Arg His Thr His His Ser Ala Trp His Ser
245 250 255
Met His Asn Val Ile Cys Gly Gly Ser Lys Val Ala Asp Glu His Leu
260 265 270
Glu Thr Leu Ile Lys Ser Gly Val Lys Ile His Leu Met Gln Gly Asp
275 280 285
Cys Asp Gln Ile Val Pro Ser His Cys Ser Gly Asn Met Lys Arg Thr

	290		295		300												
Phe	Pro	Ala	Val	Glu	Val	Asp	Ile	Ile	Thr	Gly	Ala	Asp	His	Asp	Ser		
305					310					315					320		
Met	Ile	Ser	Gly	Arg	Gly	Glu	Glu	Phe	Ala	Glu	Lys	Leu	Glu	Ser	Ile		
				325					330					335			
Trp	Cys	Ser	Phe	Lys	Glu	Ser	Gly										
				340													

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..265
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

Met	Gly	Ser	Ser	His	Phe	Trp	Thr	Glu	Thr	Val	Phe	Glu	His	Ile	Gln		
1			5						10				15				
Lys	Asp	Asp	Tyr	Arg	Leu	Leu	Ala	Ile	Asp	Leu	Leu	Gly	Phe	Gly	Glu		
			20					25					30				
Ser	Pro	Lys	Pro	Arg	Asp	Ser	Leu	Tyr	Thr	Leu	Lys	Asp	His	Val	Asp		
		35					40					45					
Thr	Ile	Glu	Arg	Ser	Val	Ile	Lys	Pro	Tyr	Gln	Leu	Asp	Ser	Phe	His		
		50					55				60						
Val	Val	Ala	His	Ser	Met	Gly	Cys	Leu	Ile	Ala	Leu	Ala	Leu	Ala	Ala		
		65			70				75				80				
Lys	His	Ser	Asn	Ile	Val	Lys	Ser	Val	Thr	Leu	Val	Ala	Pro	Pro	Tyr		
			85						90				95				
Phe	Pro	Ser	Ser	Val	Asp	Gly	Ser	Val	Leu	Asn	Arg	Ile	Ala	Arg	Lys		
			100				105					110					
Arg	Leu	Trp	Pro	Pro	Leu	Ala	Phe	Gly	Thr	Ala	Val	Met	Ser	Trp	Tyr		
		115					120					125					
Glu	His	Ile	Gly	Arg	Cys	Val	Cys	Phe	Ile	Ile	Cys	Lys	His	His	Lys		
		130				135					140						
Ile	Trp	Glu	Trp	Leu	Ile	Lys	Leu	Cys	Ile	Gly	Lys	Arg	Glu	Ile	His		
		145				150				155				160			
Trp	Lys	Ile	Lys	Asp	Ile	Thr	Arg	His	Thr	His	His	Ser	Ala	Trp	His		
			165						170					175			
Ser	Met	His	Asn	Val	Ile	Cys	Gly	Gly	Ser	Lys	Val	Ala	Asp	Glu	His		
			180					185					190				
Leu	Glu	Thr	Leu	Ile	Lys	Ser	Gly	Val	Lys	Ile	His	Leu	Met	Gln	Gly		
		195					200					205					
Asp	Cys	Asp	Gln	Ile	Val	Pro	Ser	His	Cys	Ser	Gly	Asn	Met	Lys	Arg		
		210				215					220						
Thr	Phe	Pro	Ala	Val	Glu	Val	Asp	Ile	Ile	Thr	Gly	Ala	Asp	His	Asp		
		225				230				235				240			
Ser	Met	Ile	Ser	Gly	Arg	Gly	Glu	Glu	Phe	Ala	Glu	Lys	Leu	Glu	Ser		
			245						250					255			
Ile	Trp	Cys	Ser	Phe	Lys	Glu	Ser	Gly									
			260				265										

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1054 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1054

(D) OTHER INFORMATION: / Ceres Seq. ID 1567417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

gaggtcggtt	gtctgttgga	tttctcttct	ccttcttctc	tcatttttct	catctgttct	60
ctcaacacaaa	agctcatcat	ttcaaaaaact	tcgggtgccca	ggaacacagaa	caggccctga	120
agctttcgct	tttgattcca	cgggaaaagg	attctacacc	ggagtccaccg	gcggtaaaaat	180
cctcaaatat	cttccaaga	aaggttatgt	cgactttgcc	cagatcacaa	actcttcgaa	240
gtctctgttg	tgcgacggag	caacttggaa	cactaacgtc	gaaaaatgtg	gtcgaccacgc	300
cggaatagcc	ttcaaacaga	aaacaggtga	tctttacgtc	gtagatgctg	cattgggtct	360
ccacgtcacc	cctgcgcgtg	ggggtttggc	taagaagatc	gccgacagtg	tcggCggcaa	420
gcctcttttg	ttctttgacg	ggcTtgacGt	agatcccact	accggcgtgc	tctatttccac	480
ttctctcagc	ttcaactattg	gccctaggga	tgtgttgaaa	gcagtgcgcaa	caaaagactc	540
gaocggtaag	ttcttcaaat	acgatccatc	aaaaaaggtc	gtgactgtat	tgatggaagg	600
tcttagcggc	tcagccggat	gtgccgttag	ctcagatggt	tcattgtgct	tggttggtca	660
gttcaacaaa	agtaacatca	agaggtattg	gatcaaaagg	tccaaagctg	gtactttctga	720
agactttcac	aactcggctc	cgaaccctga	caacatcaag	aggatcggtt	ctactggaaa	780
cttttggggt	gcttcgggtc	tgaactcagc	caccggaccg	acaaaCccct	cggcggttaa	840
agtcagttct	gcgggtaaa	tgcttcagac	cattccctca	aaagacaaagt	ttgggggatac	900
tttgcttagt	gaagttaaac	aatacaaaagg	acagctttat	atcggaagctc	tttttggctcc	960
tttgcgggR	aattcttaag	ctttaaagtg	aacatgttat	tagtatgggt	tagaattaaa	1020
gtgattgaat	cgaaataaat	atggttacaa	aggc			

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..325

(D) OTHER INFORMATION: / Ceres Seq. ID 1567418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

Arg	Ser	Phe	Val	Ser	Leu	Ile	Ser	Leu	Leu	Leu	Leu	Ser	Phe	Ser
1				5					10				15	
Ser	Ser	Val	Leu	Ser	Thr	Lys	Lys	Ser	Ser	Phe	Gln	Lys	Leu	Pro Val
			20					25				30		
Pro	Gly	Asn	Arg	Thr	Gly	Pro	Glu	Ala	Phe	Ala	Phe	Asp	Ser	Thr Gly
			35				40					45		
Lys	Gly	Phe	Tyr	Thr	Gly	Val	Thr	Gly	Gly	Lys	Ile	Leu	Lys	Tyr Leu
			50			55					60			
Pro	Lys	Lys	Gly	Tyr	Val	Asp	Phe	Ala	Gln	Ile	Thr	Asn	Ser	Ser Lys
65					70				75					80
Ser	Ser	Leu	Cys	Asp	Gly	Ala	Leu	Gly	Thr	Asn	Val	Glu	Lys	Cys
			85					90					95	
Gly	Arg	Pro	Ala	Gly	Ile	Ala	Phe	Asn	Thr	Lys	Thr	Gly	Asp	Leu Tyr
			100					105					110	
Val	Val	Asp	Ala	Ala	Leu	Gly	Leu	His	Val	Ile	Pro	Arg	Arg	Gly Gly
		115				120						125		
Leu	Ala	Lys	Lys	Ile	Ala	Asp	Ser	Val	Gly	Gly	Lys	Pro	Phe	Leu Phe
		130				135					140			
Leu	Asp	Gly	Leu	Asp	Val	Asp	Pro	Thr	Thr	Gly	Val	Val	Tyr	Phe Thr
145					150				155					160
Ser	Phe	Ser	Ser	Thr	Phe	Gly	Pro	Arg	Asp	Val	Leu	Lys	Ala	Val Ala
				165					170					175
Thr	Lys	Asp	Ser	Thr	Gly	Lys	Phe	Phe	Lys	Tyr	Asp	Pro	Ser	Lys Lys
				180				185				190		
Val	Val	Thr	Val	Leu	Met	Glu	Gly	Leu	Ser	Gly	Ser	Ala	Gly	Cys Ala
		195				200					205			
Val	Ser	Ser	Asp	Gly	Ser	Phe	Val	Leu	Val	Gly	Gln	Phe	Thr	Lys Ser

210	215	220
Asn Ile Lys Arg Tyr Trp	Ile Lys Gly Ser Lys	Ala Gly Thr Ser Glu
225	230	240
Asp Phe Thr Asn Ser Val	Ser Asn Pro Asp Asn	Ile Lys Arg Ile Gly
245	250	255
Ser Thr Gly Asn Phe Trp	Val Ala Ser Val Val	Asn Ser Ala Thr Gly
260	265	270
Pro Thr Asn Pro Ser Ala	Val Lys Val Ser Ser	Ala Gly Lys Val Leu
275	280	285
Gln Thr Ile Pro Leu Lys	Asp Lys Phe Gly Asp	Thr Leu Val Ser Glu
290	295	300
Val Asn Glu Tyr Lys Gly	Gln Leu Tyr Ile Gly	Ala Leu Phe Gly Pro
305	310	315
Phe Ala Xaa Asn Ser		
325		

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1469

(D) OTHER INFORMATION: / Ceres Seq. ID 1567419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

atcaatagtt	caataactaag	aaacccggcct	atatatatat	ttgtgggtcac	taattttctcc	60
aaaaaacagt	tgcccttcgt	aaaaagatgg	aacctcagag	aaaacactcg	acagcccttc	120
acacgtgtca	tccctgccc	cgaaacattc	catacagaa	ctacgccgtg	tttctactgt	180
gtggcatcat	agctctcatg	tatcaccatg	tacactcact	tgtaaacgca	aacaacactc	240
taataaacat	tctctctctc	ctctccgata	tgtttctcgc	cttcatgtgg	gcaaccacaa	300
cttccctccg	cttaaacccg	gttcatcgga	ccgagtagcc	tgaaaaatat	gctgctaacc	360
cgagGactt	tccaaagctg	gaocgttttta	tatgcacggc	tgatccgtac	aaggagcctc	420
cgatgatggt	ggttaacacc	gctttatcgg	tgatggctta	cgatgatccg	tctcataaga	480
tctcagtgtg	cgtatccggc	gatggaggat	cttccctgac	tttgtttgct	cttatggagg	540
ctgccaaagt	ctctaagcat	tggttgccct	tttgcaagaa	taacaatgtt	caagatcgct	600
ctccctgaat	tattttttct	tcaaaagtac	attcttggag	tgatgaagct	gaaaaactta	660
agatgatgtg	cgaagacatg	agaagttagg	tgcaacatgt	ggttgagagt	ggaaaagtgt	720
agBactcgct	tatttgcatt	cgatcaattt	agttgtgtgt	tcgatctgtg	gacagataaa	780
ttoactcgtc	atgaccatct	taccattatt	aaagtgctac	aacataacga	aacagagatg	840
atgccaaacc	tatatatagt	ttaacagaaa	aaagatgaa	tttaccacca	ctatttcaaa	900
gcgggtgctc	ttaatacttt	gtttacagta	ctcgcgtgga	tgacaaactc	accaactcatt	960
ctaacactag	actgtgacat	gtactcaaac	aatctctacg	caccacttca	tgctctgtgc	1020
tatttttttag	accctaaagt	caatttttgt	ttaggatttg	tgcaattttc	tcaaaaattt	1080
caaggaataa	acaaaaatga	tatttatgca	tccgagctca	aaagcccat	tgacatcaac	1140
acggttgggt	ttgatggact	tatgggacca	gttcatatgg	gaactgggtg	tttcttcaat	1200
cgacggcgct	tttatgggoc	tccgactagt	ttgaacttgc	ctgaCgatg	aaaaacttgg	1260
gccaaatcgg	attgcgcata	aaacatttaa	aaacccaaat	attttggcgt	tggtcacacga	1320
gtgtagcagg	tgtaactacg	agtgcaaac	caatttggga	tccaaggtta	gattaaattg	1380
aacttttagct	tattttttat	tatgtgtatt	ttttgtttat	gtttacagat	tttgtttctt	1440
ttacatcaac	tagctctctc	aaaatccat				

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..221

(D) OTHER INFORMATION: / Ceres Seq. ID 1567420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

Met Glu Pro Gln Arg Lys His Ser Thr Ala Leu His Thr Cys His Pro
1 5 10 15
Cys Arg Arg Thr Ile Pro Tyr Arg Ile Tyr Ala Val Phe His Leu Cys
20 25 30
Gly Ile Ile Ala Leu Met Tyr His His Val His Ser Leu Val Asn Ala
35 40 45
Asn Asn Thr Leu Ile Thr Cys Leu Leu Leu Ser Asp Ile Val Leu
50 55 60
Ala Phe Met Trp Ala Thr Thr Thr Ser Leu Arg Leu Asn Pro Val His
65 70 75 80
Arg Thr Glu Tyr Pro Glu Lys Tyr Ala Ala Lys Pro Glu Asp Phe Pro
85 90 95
Lys Leu Asp Val Phe Ile Cys Thr Ala Asp Pro Tyr Lys Glu Pro Pro
100 105 110
Met Met Val Val Asn Thr Ala Leu Ser Val Met Ala Tyr Glu Tyr Pro
115 120 125
Ser His Lys Ile Ser Val Tyr Val Ser Asp Asp Gly Gly Ser Ser Leu
130 135 140
Thr Leu Phe Ala Leu Met Glu Ala Ala Lys Phe Ser Lys His Trp Leu
145 150 155 160
Pro Phe Cys Lys Asn Asn Asn Val Gln Asp Arg Ser Pro Glu Val Tyr
165 170 175
Phe Ser Ser Lys Ser His Ser Trp Ser Asp Glu Ala Glu Asn Leu Lys
180 185 190
Met Met Tyr Glu Asp Met Lys Ser Arg Val Glu His Val Val Glu Ser
195 200 205
Gly Lys Val Glu Xaa Cys Val Tyr Cys Met Arg Ser Ile
210 215 220

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..184

(D) OTHER INFORMATION: / Ceres Seq. ID 1567421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

Met Tyr His His Val His Ser Leu Val Asn Ala Asn Asn Thr Leu Ile
1 5 10 15
Thr Cys Leu Leu Leu Leu Ser Asp Ile Val Leu Ala Phe Met Trp Ala
20 25 30
Thr Thr Thr Ser Leu Arg Leu Asn Pro Val His Arg Thr Glu Tyr Pro
35 40 45
Glu Lys Tyr Ala Ala Lys Pro Glu Asp Phe Pro Lys Leu Asp Val Phe
50 55 60
Ile Cys Thr Ala Asp Pro Tyr Lys Glu Pro Pro Met Met Val Val Asn
65 70 75 80
Thr Ala Leu Ser Val Met Ala Tyr Glu Tyr Pro Ser His Lys Ile Ser
85 90 95
Val Tyr Val Ser Asp Asp Gly Gly Ser Ser Leu Thr Leu Phe Ala Leu
100 105 110
Met Glu Ala Ala Lys Phe Ser Lys His Trp Leu Pro Phe Cys Lys Asn
115 120 125
Asn Asn Val Gln Asp Arg Ser Pro Glu Val Tyr Phe Ser Ser Lys Ser
130 135 140

His Ser Trp Ser Asp Glu Ala Glu Asn Leu Lys Met Met Tyr Glu Asp
145 150 155 160
Met Lys Ser Arg Val Glu His Val Val Glu Ser Gly Lys Val Glu Xaa
165 170 175
Cys Val Tyr Cys Met Arg Ser Ile
180

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..194

(D) OTHER INFORMATION: / Ceres Seq. ID 1567422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

Met Trp Leu Arg Val Glu Lys Leu Xaa Thr Ala Phe Ile Ala Cys Asp
1 5 10 15
Gln Phe Ser Cys Val Phe Asp Leu Trp Thr Asp Lys Phe Thr Arg His
20 25 30
Asp His Pro Thr Ile Ile Lys Val Leu Gln His Asn Glu Thr Glu Met
35 40 45
Met Pro Asn Leu Ile Tyr Val Ser Arg Glu Lys Ser Lys Val Ser Pro
50 55 60
His His Phe Lys Ala Gly Ala Leu Asn Thr Leu Leu Arg Val Ser Ala
65 70 75 80
Val Met Thr Asn Ser Pro Ile Ile Leu Thr Leu Asp Cys Asp Met Tyr
85 90 95
Ser Asn Asn Pro Thr Ala Pro Leu His Ala Leu Cys Tyr Phe Leu Asp
100 105 110
Pro Lys Ile Asn Phe Gly Leu Gly Phe Val Gln Phe Pro Gln Lys Phe
115 120 125
Gln Gly Ile Asn Lys Asn Asp Ile Tyr Ala Ser Glu Leu Lys Arg Pro
130 135 140
Phe Asp Ile Asn Thr Val Gly Phe Asp Gly Leu Met Gly Pro Val His
145 150 155 160
Met Gly Thr Gly Cys Phe Phe Asn Arg Arg Ala Phe Tyr Gly Pro Pro
165 170 175
Thr Ser Leu Thr Leu Pro Asp Asp Arg Lys Thr Trp Ala Lys Ser Asp
180 185 190
Cys Arg

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1865 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1865

(D) OTHER INFORMATION: / Ceres Seq. ID 1567445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

ctgattatttt ccaatgacttt tttctctgtg ctgattcgtt tgtttcggcg attcaactct 60
tcttcaacgc cctgagagtc acgcacgaga attggattga tggtttttca cacgcaggag 120
aggcgattcgt ttgtcttctt ctgtcccgct tgacctgttt cgaatcgaaga tggtagattat 180
gcagcagctg attctaaatt agggcatttta aatccgcctt ccaggtgaat ttttgaanaa 240
taattaaagg gtgttcttga atggacttga aaatggataa tgttatattgg ggaagattta 300


```

aacttggtcg gaagatcggt ggtggctctt ttggagaact tttcttggc gtaagtttgc 360
aaaccggaga ggaagcagct gtttaagctg agcctgcgaa aactaagcat ccccaacttc 420
attatgagtc gaagatatac atgctctctc aaggaggagag tggcatcccc agccttaagt 480
ggtttggggt tcaaggagac tacaatgcga ttgtcattga tctgcttggg ccaggtttgg 540
aagacttgtt caactactgc aataggaggg ttactttgaa ggcagttttg atgcttgcag 600
atcaactgat tagcagagtt gaatatatgc attcaagggg gtttcttcac cgtgacatca 660
aaactgcaca tttcttgatg ggacttggtc gcaaaagcaa ccaggttgat atcatgtatt 720
ttgggcttgc aaagaagtat agggatctcc aaacacatag gcatactccc tatagagaaa 780
acaagaacct tacgggcaca gctcggtatg ctagtgtcaa cactcaccta ggagtggagc 840
aaagttaggag ggatgactcg gagtctcttg gttacgtact catgtatttc ctgagaggaa 900
gcttaccgtg gcaggagact aaagctggca caaagaagca aaagtatgac agaattagcg 960
agaagaagt atcaactctc atagaggtct tgtgcaagtc atatccacc ccgaattctgat 1020
catactttca atactgcaga tctctgcgat tcgaagacAa accgagactac tcatatctaa 1080
agagactttt ccagagactg tttatccgtg aaggttatca gtttgattat gtattcgact 1140
ggactgcatt gaaacacct cagagtagtg ccaggtccca ttccagtaca catgaaaggc 1200
atcgtaaccg taaaccaggg atgggtgcgg gaccgtctgc tgaaaaacct gaaaggattt 1260
cagtagggaa catcccgcat aaattctcag tgcggctcga agcattttggc gaagggaacg 1320
ttagaggacc cagtcoccat caaaaccata ccagacatcg aactcttgac gaaattccct 1380
caatgaaacc tgctgtgaat atggtatctg agaaaggag aaacacttcc agatacggca 1440
gtgcttgcag gagagcagta gcctcaggaa gttagaccaag ctcatcaggt gaacaaggg 1500
agagccggga ctgcagccgc gtgacctcaa gcggtggcgg tgtccgacca tcagctttcc 1560
aaagaaccca agcagcagct gctgtgagtg gatacagatc aaagacagca tctgccttta 1620
accgcgaccg agtagccgt tcaagaacag caccgacgca ggctctcaga agctctgagc 1680
ttctttcgat ccgcaaatga agccttcac aattggctct ttgctgtaa ttggattott 1740
ctttacatat gttgtttgt cctttgttcc caagaaactc ccaatttttc atgtattatt 1800
aaattctctg gattttgtat caatttttcc acattttatt gtaactcatga caatttgtg 1860
agttt

```

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 479 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..479

(D) OTHER INFORMATION: / Ceres Seq. ID 1567446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

```

Met Asp Leu Lys Met Asp Asn Val Ile Gly Gly Lys Phe Lys Leu Gly
1      5      10      15
Arg Lys Ile Gly Gly Gly Ser Phe Gly Glu Leu Phe Leu Ala Val Ser
20     25     30
Leu Gln Thr Gly Glu Glu Ala Ala Val Lys Leu Glu Pro Ala Lys Thr
35     40     45     50
Lys His Pro Gln Leu His Tyr Glu Ser Lys Ile Tyr Met Leu Leu Gln
55     60
Gly Gly Ser Gly Ile Pro Ser Leu Lys Trp Phe Gly Val Gln Gly Asp
65     70     75     80
Tyr Asn Ala Met Val Ile Asp Leu Leu Gly Pro Ser Leu Glu Asp Leu
85     90     95
Phe Asn Tyr Cys Asn Arg Leu Thr Leu Lys Ala Val Leu Met Leu
100    105    110
Ala Asp Gln Leu Ile Ser Arg Val Glu Tyr Met His Ser Arg Gly Phe
115    120    125
Leu His Arg Asp Ile Lys Pro Asp Asn Phe Leu Met Gly Leu Gly Arg
130    135    140
Lys Ala Asn Gln Val Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys Tyr
145    150    155    160
Arg Asp Leu Gln Thr His Arg His Ile Pro Tyr Arg Glu Asn Lys Asn
165    170    175

```

Leu Thr Gly Thr Ala Arg Tyr Ala Ser Val Asn Thr His Leu Gly Val
180 185 190
Glu Gln Ser Arg Arg Asp Asp Leu Glu Ser Leu Gly Tyr Val Leu Met
195 200 205
Tyr Phe Leu Arg Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Gly Thr
210 215 220
Lys Lys Gln Lys Tyr Asp Arg Ile Ser Glu Lys Lys Val Ser Thr Pro
225 230 235 240
Ile Glu Val Leu Cys Lys Ser Tyr Pro Pro Glu Phe Val Ser Tyr Phe
245 250 255
Gln Tyr Cys Arg Ser Leu Arg Phe Glu Asp Lys Pro Asp Tyr Ser Tyr
260 265 270
Leu Lys Arg Leu Phe Arg Asp Leu Phe Ile Arg Glu Gly Tyr Gln Phe
275 280 285
Asp Tyr Val Phe Asp Trp Thr Ala Leu Lys His Pro Gln Ser Ser Ala
290 295 300
Arg Ser His Ser Ser Thr His Glu Arg His Arg Thr Gly Lys Pro Gly
305 310 315 320
Met Gly Ala Gly Pro Ser Ala Glu Lys Pro Glu Arg Ile Ser Val Gly
325 330 335
Asn Ile Arg Asp Lys Phe Ser Gly Ala Val Glu Ala Phe Ala Arg Arg
340 345 350
Asn Val Arg Gly Pro Ser Pro His Gln Asn His Thr Arg His Arg Thr
355 360 365
Leu Asp Glu Ile Pro Ser Met Lys Pro Ala Val Asn Met Val Ser Glu
370 375 380
Lys Gly Arg Asn Thr Ser Arg Tyr Gly Ser Ala Ser Arg Arg Ala Val
385 390 395 400
Ala Ser Gly Ser Arg Pro Ser Ser Ser Gly Glu Gln Arg Glu Ser Arg
405 410 415
Asp Ser Ser Arg Val Ala Ser Ser Gly Gly Val Arg Pro Ser Val
420 425 430
Phe Gln Arg Thr Gln Ala Ala Ala Val Ser Gly Tyr Glu Ser Lys
435 440 445
Thr Ala Ser Ala Phe Asn Arg Asp Arg Val Ala Ala Ser Arg Thr Ala
450 455 460
Arg Asp Glu Ala Leu Arg Ser Phe Glu Leu Leu Ser Ile Arg Lys
465 470 475

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..475
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

Met Asp Asn Val Ile Gly Gly Lys Phe Lys Leu Gly Arg Lys Ile Gly
1 5 10 15
Gly Gly Ser Phe Gly Glu Leu Phe Leu Ala Val Ser Leu Gln Thr Gly
20 25 30
Glu Glu Ala Ala Val Lys Leu Glu Pro Ala Lys Thr Lys His Pro Gln
35 40 45
Leu His Tyr Glu Ser Lys Ile Tyr Met Leu Leu Gln Gly Gly Ser Gly
50 55 60
Ile Pro Ser Leu Lys Trp Phe Gly Val Gln Gly Asp Tyr Asn Ala Met
65 70 75 80
Val Ile Asp Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Asn Tyr Cys

(1) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..419

- (D) OTHER INFORMATION: / Ceres Seq. ID 1567448

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

```

Met Leu Leu Gln Gly Gly Ser Gly Ile Pro Ser Leu Lys Trp Phe Gly
1      5      10      15
Val Gln Gly Asp Tyr Asn Ala Met Val Ile Asp Leu Leu Gly Pro Ser
20      25      30
Leu Glu Asp Leu Phe Asn Tyr Cys Asn Arg Arg Leu Thr Lys Ala
35      40      45
Val Leu Met Leu Ala Asp Gln Leu Ile Ser Arg Val Glu Tyr Met His
50      55      60
Ser Arg Gly Phe Leu His Arg Asp Ile Lys Pro Asp Asn Phe Leu Met
65      70      75      80
Gly Leu Gly Arg Lys Ala Asn Gln Val Tyr Ile Ile Asp Phe Gly Leu
85      90      95
Ala Lys Lys Tyr Arg Asp Leu Gln Thr His Arg His Ile Pro Tyr Arg
100     105     110
Glu Asn Lys Asn Leu Thr Gly Thr Ala Arg Tyr Ala Ser Val Asn Thr
115     120     125
His Leu Gly Val Glu Gln Ser Arg Arg Asp Asp Leu Glu Ser Leu Gly
130     135     140
Tyr Val Leu Met Tyr Phe Leu Arg Gly Ser Leu Pro Trp Gln Gly Leu
145     150     155     160
Lys Ala Gly Thr Lys Lys Gln Lys Tyr Asp Arg Ile Ser Glu Lys Lys
165     170     175
Val Ser Thr Pro Ile Glu Val Leu Cys Lys Ser Tyr Pro Pro Glu Phe
180     185     190
Val Ser Tyr Phe Gln Tyr Cys Arg Ser Leu Arg Phe Glu Asp Lys Pro
195     200     205
Asp Tyr Ser Tyr Leu Lys Arg Leu Phe Arg Asp Leu Phe Ile Arg Glu
210     215     220
Gly Tyr Gln Phe Asp Tyr Val Phe Asp Trp Thr Ala Leu Lys His Pro
225     230     235     240
Gln Ser Ser Ala Arg Ser His Ser Ser Thr His Glu Arg His Arg Thr
245     250     255
Gly Lys Pro Gly Met Gly Ala Gly Pro Ser Ala Glu Lys Pro Glu Arg
260     265     270
Ile Ser Val Gly Asn Ile Arg Asp Lys Phe Ser Gly Ala Val Glu Ala
275     280     285
Phe Ala Arg Arg Asn Val Arg Gly Pro Ser Pro His Gln Asn His Thr
290     295     300
Arg His Arg Thr Leu Asp Glu Ile Pro Ser Met Lys Pro Ala Val Asn
305     310     315     320
Met Val Ser Glu Lys Gly Arg Asn Thr Ser Arg Tyr Gly Ser Ala Ser
325     330     335
Arg Arg Ala Val Ala Ser Gly Ser Arg Pro Ser Ser Ser Gly Glu Gln
340     345     350
Arg Glu Ser Arg Asp Ser Ser Arg Val Ala Ser Ser Gly Gly Val
355     360     365
Arg Pro Ser Val Phe Gln Arg Thr Gln Ala Ala Ala Val Ser Gly
370     375     380
Tyr Glu Ser Lys Thr Ala Ser Ala Phe Asn Arg Asp Arg Val Ala Ala
385     390     395     400
Ser Arg Thr Ala Arg Asp Glu Ala Leu Arg Ser Phe Glu Leu Leu Ser
405     410     415
Ile Arg Lys

```

(2) INFORMATION FOR SEQ ID NO:610:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 697 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..697
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

aacgaatctt	gtttagtaaa	aagcgcaGct	gcaaaaaaaaa	tcgagtagag	aagaagtagg	60
cagacaaaga	agaagaagaa	gaagttctcg	gcgtgcttca	atggcgatat	cagtagcagc	120
ttcgtctctt	atggccgtga	tggttccacg	tggtcccgcc	gtatccaccc	gttgctccgc	180
cgtcccttat	cttctctctc	gctcctttgg	ccgatcctct	ttcaccgttc	cgttgaagct	240
tgtttcaggg	aatggattgc	aaaaaagtga	attgtagaag	acaagagctt	cttcagaaga	300
gaactcgctc	attgatacca	acgaactcat	cacagatttg	aaggaaaagt	gggatggctt	360
tgagaacaaa	tctactgtac	ttatatatgg	aggaggagcc	attgttgctg	tttggttatc	420
ttccattgtt	gttggtgcca	tcaactctgt	tctcttgctt	ccgaaaagta	tggaacttgt	480
cgtctcgggt	tacactggat	ggtttgtota	cagatacctt	ctcttcaagt	caagcagaaa	540
ggaaattggct	gaggatattg	aatccttgaa	gaagaagatg	gcaggaaagc	aatagattca	600
ttttcaaaaa	aaacagagtt	tctctctgta	tgttttctcg	taatatcgtg	ttatattata	660
caatgtctct	gtttcaaat	tgtatctggt	gcattctc			

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

Met	Ala	Ile	Ser	Val	Ala	Ala	Ser	Ser	Ser	Met	Ala	Val	Met	Val	Pro	
1			5					10				15				
Arg	Val	Pro	Ala	Val	Ser	Thr	Arg	Cys	Ser	Ala	Val	Pro	Tyr	Leu	Pro	
		20						25				30				
Pro	Arg	Ser	Phe	Gly	Arg	Ser	Ser	Phe	Thr	Val	Pro	Leu	Lys	Leu	Val	
		35					40					45				
Ser	Gly	Asn	Gly	Leu	Gln	Lys	Val	Glu	Leu							
		50				55										

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

Met	Val	Leu	Arg	Thr	Asn	Leu	Leu	Tyr	Leu	Tyr	Met	Glu	Glu	Glu	Pro	
1			5					10				15				
Leu	Leu	Leu	Phe	Gly	Tyr	Leu	Pro	Leu	Leu	Val	Pro	Ser	Thr	Leu		
		20					25					30				
Phe	Leu	Cys	Phe	Arg	Lys	Leu	Trp	Asn	Leu	Ser	Val	Ser	Gly	Thr	Leu	
		35					40					45				
Asp	Gly	Leu	Ser	Thr	Asp	Thr	Phe	Ser	Ser	Ser	Gln	Ala	Glu	Arg	Asn	
		50				55						60				
Trp	Leu	Arg	Ile	Leu	Asn	Pro										
		65				70										

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..60
(D) OTHER INFORMATION: / Ceres Seq. ID 1567452
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:
Met Glu Glu Glu Pro Leu Leu Leu Phe Gly Tyr Leu Pro Leu Leu Leu
1 5 10 15
Val Pro Ser Thr Leu Phe Leu Cys Phe Arg Lys Leu Trp Asn Leu Ser
20 25 30
Val Ser Gly Thr Leu Asp Gly Leu Ser Thr Asp Thr Phe Ser Ser Ser
35 40 45
Gln Ala Glu Arg Asn Trp Leu Arg Ile Leu Asn Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1122
(D) OTHER INFORMATION: / Ceres Seq. ID 1567453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

attttttgat	atgtaaaatt	tatcgaaaac	gttccatttc	aatatgtaga	caaaagcggag	60
aagtatattg	tggaggcggc	aagcaaggga	gcagagctag	tggtgttccc	ggaggggttt	120
atcgggtctc	atcctcgagg	ttttaggttc	gggttagcgg	ttggcgctca	taacgaagaa	180
gggcgtgatg	agtttcggaa	gtaccatgct	tctgctatc	atgttctctg	ccctgaagta	240
gcaagattgg	ctgacgtggc	taggaaaaac	catgtgtact	tggtaatggg	agccatagag	300
aaggaagggg	ataccctcta	tgcacacagt	cttttcttta	gtcccacagg	tcagttcttg	360
ggcaagcacc	gtaaaactcat	gcccacaagt	tgggaacgtt	gcatttgggg	ccaaggggac	420
ggatacacca	tcgccgttta	cgacactccc	attggaaaac	tcgggtctgc	tatttctgtg	480
gagaatagga	tgccctctca	cagaactgca	ttgtacgcc	aaggcattga	gctttattgt	540
gcacctactg	ctgatgggtc	gaaagaatgg	caatcgtcga	tgcttcacat	tcgcgatcgaa	600
ggtggaatgt	tgctctgttc	ggcttgccaa	ttctgccagc	gtaaaacatt	ccctgatcat	660
ctcgactact	tgtttaacga	ttggtacgac	gacaaaagac	atgattctat	tgcttcccaa	720
ggtggaagtg	tcattatttc	acctttggga	caagttctcg	ccggaccaaa	ctttgaatca	780
gaagggtctg	tcacagctga	tattgatctt	ggtgatatag	caagagccaa	gttatacttc	840
gattcggttg	gacattactc	gagaccagat	gttttacaat	tgaccgtaaa	tgagcacccg	900
aggaaaatcg	ttacattcgt	gacgaaggtg	gagaaaagct	aggatgactc	aaacaaatag	960
taagagacct	gaagttcgta	tctgctggag	ttagtgcatt	cgtatggagt	caagtcacaa	1020
atgtttctgt	gcgttttcat	tttatgttca	agtttatatta	ctttttctct	tcaatggtaa	1080
gactatgga	gtcaagtaat	aatggtaaga	cttatgttgt	tg		

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..224
(D) OTHER INFORMATION: / Ceres Seq. ID 1567454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

```

Met Gly Ala Ile Glu Lys Glu Gly Tyr Thr Leu Tyr Cys Thr Val Leu
1      5      10      15
Phe Phe Ser Pro Gln Gly Gln Phe Leu Gly Lys His Arg Lys Leu Met
20     25     30
Pro Thr Ser Leu Glu Arg Cys Ile Trp Gly Gln Gly Asp Gly Ser Thr
35     40     45
Ile Pro Val Tyr Asp Thr Pro Ile Gly Lys Leu Gly Ala Ala Ile Cys
50     55     60
Trp Glu Asn Arg Met Pro Leu Tyr Arg Thr Ala Leu Tyr Ala Lys Gly
65     70     75     80
Ile Glu Leu Tyr Cys Ala Pro Thr Ala Asp Gly Ser Lys Glu Trp Gln
85     90     95
Ser Ser Met Leu His Ile Ala Ile Glu Gly Gly Cys Phe Val Leu Ser
100    105    110
Ala Cys Gln Phe Cys Gln Arg Lys His Phe Pro Asp His Pro Asp Tyr
115    120    125
Leu Phe Thr Asp Trp Tyr Asp Asp Lys Glu His Asp Ser Ile Val Ser
130    135    140
Gln Gly Gly Ser Val Ile Ile Ser Pro Leu Gly Gln Val Leu Ala Gly
145    150    155    160
Pro Asn Phe Glu Ser Glu Gly Leu Val Thr Ala Asp Ile Asp Leu Gly
165    170    175
Asp Ile Ala Arg Ala Lys Leu Tyr Phe Asp Ser Val Gly His Tyr Ser
180    185    190
Arg Pro Asp Val Leu His Leu Thr Val Asn Glu His Pro Arg Lys Ser
195    200    205
Val Thr Phe Val Thr Lys Val Glu Lys Ala Glu Asp Asp Ser Asn Lys
210    215    220

```

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1567455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

```

Met Pro Thr Ser Leu Glu Arg Cys Ile Trp Gly Gln Gly Asp Gly Ser
1      5      10      15
Thr Ile Pro Val Tyr Asp Thr Pro Ile Gly Lys Leu Gly Ala Ala Ile
20     25     30
Cys Trp Glu Asn Arg Met Pro Leu Tyr Arg Thr Ala Leu Tyr Ala Lys
35     40     45
Gly Ile Glu Leu Tyr Cys Ala Pro Thr Ala Asp Gly Ser Lys Glu Trp
50     55     60
Gln Ser Ser Met Leu His Ile Ala Ile Glu Gly Gly Cys Phe Val Leu
65     70     75     80
Ser Ala Cys Gln Phe Cys Gln Arg Lys His Phe Pro Asp His Pro Asp
85     90     95
Tyr Leu Phe Thr Asp Trp Tyr Asp Asp Lys Glu His Asp Ser Ile Val
100    105    110
Ser Gln Gly Gly Ser Val Ile Ile Ser Pro Leu Gly Gln Val Leu Ala
115    120    125
Gly Pro Asn Phe Glu Ser Glu Gly Leu Val Thr Ala Asp Ile Asp Leu
130    135    140
Gly Asp Ile Ala Arg Ala Lys Leu Tyr Phe Asp Ser Val Gly His Tyr

```

145				150						155					160
Ser	Arg	Pro	Asp	Val	Leu	His	Leu	Thr	Val	Asn	Glu	His	Pro	Arg	Lys
				165						170					175
Ser	Val	Thr	Phe	Val	Thr	Lys	Val	Glu	Lys	Ala	Glu	Asp	Asp	Ser	Asn
				180						185				190	

Lys

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

Met	Pro	Leu	Tyr	Arg	Thr	Ala	Leu	Tyr	Ala	Lys	Gly	Ile	Glu	Leu	Tyr
1			5						10				15		
Cys	Ala	Pro	Thr	Ala	Asp	Gly	Ser	Lys	Glu	Trp	Gln	Ser	Ser	Met	Leu
			20					25					30		
His	Ile	Ala	Ile	Glu	Gly	Gly	Cys	Phe	Val	Leu	Ser	Ala	Cys	Gln	Phe
			35				40					45			
Cys	Gln	Arg	Lys	His	Phe	Pro	Asp	His	Pro	Asp	Tyr	Leu	Phe	Thr	Asp
			50				55				60				
Trp	Tyr	Asp	Asp	Lys	Glu	His	Asp	Ser	Ile	Val	Ser	Gln	Gly	Gly	Ser
					70				75				80		
Val	Ile	Ile	Ser	Pro	Leu	Gly	Gln	Val	Leu	Ala	Gly	Pro	Asn	Phe	Glu
					85				90				95		
Ser	Glu	Gly	Leu	Val	Thr	Ala	Asp	Ile	Asp	Leu	Gly	Asp	Ile	Ala	Arg
			100				105					110			
Ala	Lys	Leu	Tyr	Phe	Asp	Ser	Val	Gly	His	Tyr	Ser	Arg	Pro	Asp	Val
			115				120					125			
Leu	His	Leu	Thr	Val	Asn	Glu	His	Pro	Arg	Lys	Ser	Val	Thr	Phe	Val
			130				135					140			
Thr	Lys	Val	Glu	Lys	Ala	Glu	Asp	Asp	Ser	Asn	Lys				
			145				150			155					

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1811
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

agctatcaat	ttaactggaga	agagatgggt	ggatcagagg	ttttggagga	atgtggagaa	60
aaaaaagca	agaaagagtc	aaagaagcga	gcgcgtaaac	tggagaagtt	gtcccgtaaa	120
cagtaacgag	aagaagccac	atcatcatct	ctttctctgg	aggaggagga	tgaatcgtgt	180
tcacgcaact	acggtgacgt	gactactaac	gagttgcagt	cggtctgtta	gggaaaagag	240
ctcaactgat	tgagcaacct	ggttgaagag	attgtggggg	cagaggtttc	gatcagaggt	300
cgactgcaca	agaatcgctt	agtcggtacc	aaattgtttg	tgatcttgag	ggaaaagtga	360
ttcacggttc	aatgcgtggg	ggaggagacc	agagttgggt	caaacatgat	taaatattgtc	420
aagcagcagt	gtcgtgtaac	tgttgttgag	cttatcgggt	tcgtctctca	ccctaagaag	480
ctctcacaag	gaaccaccca	gcaggttgaa	atacatgtca	gaaaaatgta	ctgcctcagc	540
agatccttgc	caaatattacc	acttgtttgt	gaggatgctg	ctcgtagtga	atcagatat	600

gaaaaatctg	gcaaggatgg	caaacaagct	gctcgtgtcc	ttcaggacac	acgtttgaat	660
aataggggtc	ttgacatcag	aacaccggct	aatcaagcca	tcttcogtat	tcagtgccaa	720
gtccaaattg	cgttcagaga	atacttacaa	tccaaggggt	ttcttgaat	ccacacaccg	780
aaatgtatcg	ctggcagtag	tgaaggaggt	tctgctgtgt	ttaggttgga	ctacaaaggg	840
cagctcgtct	gtctggctca	gtctcctcag	cttcataaag	agatggcgat	atgtgggtgac	900
atgcgacgcg	tctttgaggt	tggtcctgtt	ttcagagctg	aagactcctt	cactcataga	960
cacctgtgtg	aattcgttgg	tcttgatgtg	gagatggaga	ttcgaatgca	ctactctgtg	1020
ataatggatc	ttgtggggaga	gttgtttccg	ttcatattca	caaaaatgaa	agaaaaggtgc	1080
ccaaaggaaac	ttgaatctgt	cagaaagcaa	taccttttcc	aatctttgaa	gtttcttccg	1140
caaacattga	ggctaaccct	tgcagaaggg	attcaaatgc	ttaagggaagc	tggcgaggag	1200
gttgatctcc	ttggtgatct	aaatacagaa	tctgagagga	aacttggcca	gcttggcttg	1260
gaaaagtaca	agacggaggt	ctacatgctg	catcgctatc	catcgctctg	cagacccgttc	1320
tacacatgac	cctatgaaaa	tgatttctaac	tacagcaact	ctttcogatg	cttcatcaga	1380
ggagaggaga	tcattgtcag	agctcaacgt	atccatgacc	cagaactctt	ggagaagcgc	1440
gcaagagaaat	gcggcattga	tgtcaagaca	atatccacgt	acattgatgc	attcagggtac	1500
gggtgNaccA	cctcacgggt	gattcggagt	ggggctggag	cgtgtggttaa	tgctctattg	1560
tgccctcaat	aacatccgca	aaacttcgct	attccctcgt	gactctcaaa	ggctcactcc	1620
ctaataatcat	tgctcttccc	tggcgactct	caaaaggctcg	ctcccttaat	atctatcttt	1680
gataaattgtc	cccgctcccg	atttctaagt	tatttttttg	gtgcagttcg	ttagtggttt	1740
agttatcttt	aaactatgta	tgtgttgtaa	cctttaaatt	attaaggagc	agtactattt	1800
gggctttttc	g					

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 388 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..388

(D) OTHER INFORMATION: / Ceres Seq. ID 1567464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

Met	Ile	Lys	Phe	Val	Lys	Gln	Leu	Ser	Arg	Glu	Ser	Val	Glu	Leu
1			5					10					15	
Ile	Gly	Val	Val	Ser	His	Pro	Lys	Lys	Pro	Leu	Thr	Gly	Thr	Gln
			20					25					30	
Gln	Val	Glu	Ile	His	Val	Arg	Lys	Met	Tyr	Cys	Leu	Ser	Arg	Ser
			35					40					45	
Pro	Asn	Leu	Pro	Leu	Val	Val	Glu	Asp	Ala	Ala	Arg	Ser	Glu	Ser
			50					55					60	
Ile	Glu	Lys	Ser	Gly	Lys	Asp	Gly	Lys	Gln	Ala	Ala	Arg	Val	Leu
			65					70					75	
Asp	Thr	Arg	Leu	Asn	Asn	Arg	Val	Leu	Asp	Ile	Arg	Thr	Pro	Ala
			85					90					95	
Gln	Ala	Ile	Phe	Arg	Ile	Gln	Cys	Gln	Val	Gln	Ile	Ala	Phe	Arg
			100					105					110	
Tyr	Leu	Gln	Ser	Lys	Gly	Phe	Leu	Glu	Ile	His	Thr	Pro	Lys	Leu
			115					120					125	
Ala	Gly	Ser	Ser	Glu	Gly	Gly	Ser	Ala	Val	Phe	Arg	Leu	Asp	Tyr
			130					135					140	
Gly	Gln	Pro	Ala	Cys	Leu	Ala	Gln	Ser	Pro	Gln	Leu	His	Lys	Gln
			145					150					155	
Ala	Ile	Cys	Gly	Asp	Met	Arg	Arg	Val	Phe	Glu	Val	Gly	Pro	Val
			165					170					175	
Arg	Ala	Glu	Asp	Ser	Phe	Thr	His	Arg	His	Leu	Cys	Glu	Phe	Val
			180					185					190	
Leu	Asp	Val	Glu	Met	Glu	Ile	Arg	Met	His	Tyr	Ser	Glu	Ile	Met
			195					200					205	
Leu	Val	Gly	Glu	Leu	Phe	Pro	Phe	Ile	Phe	Thr	Lys	Ile	Glu	Glu
			210					215					220	

Cys Pro Lys Glu Leu Glu Ser Val Arg Lys Gln Tyr Pro Phe Gln Ser
225 230 235 240
Leu Lys Phe Leu Pro Gln Thr Leu Arg Leu Thr Phe Ala Glu Gly Ile
245 250 255
Gln Met Leu Lys Glu Ala Gly Glu Glu Val Asp Pro Leu Gly Asp Leu
260 265 270
Asn Thr Glu Ser Glu Arg Lys Leu Gly Gln Leu Val Leu Glu Lys Tyr
275 280 285
Lys Thr Glu Phe Tyr Met Leu His Arg Tyr Pro Ser Ala Val Arg Pro
290 295 300
Phe Tyr Thr Met Pro Tyr Glu Asn Asp Ser Asn Tyr Ser Asn Ser Phe
305 310 315 320
Asp Val Phe Ile Arg Gly Glu Glu Ile Met Ser Gly Ala Gln Arg Ile
325 330 335
His Asp Pro Glu Leu Leu Glu Lys Arg Ala Arg Glu Cys Gly Ile Asp
340 345 350
Val Lys Thr Ile Ser Thr Tyr Ile Asp Ala Phe Arg Tyr Gly Xaa Thr
355 360 365
Thr Ser Arg Trp Ile Arg Ser Gly Ala Cys Gly Asn Ala Leu
370 375 380
Met Cys Pro Gln
385

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1567465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

Met Tyr Cys Leu Ser Arg Ser Leu Pro Asn Leu Pro Leu Val Val Glu
1 5 10 15
Asp Ala Ala Arg Ser Glu Ser Asp Ile Glu Lys Ser Gly Lys Asp Gly
20 25 30
Lys Gln Ala Ala Arg Val Leu Gln Asp Thr Arg Leu Asn Asn Arg Val
35 40 45
Leu Asp Ile Arg Thr Pro Ala Asn Gln Ala Ile Phe Arg Ile Gln Cys
50 55 60
Gln Val Gln Ile Ala Phe Arg Glu Tyr Leu Gln Ser Lys Gly Phe Leu
65 70 75 80
Glu Ile His Thr Pro Lys Leu Ile Ala Gly Ser Ser Glu Gly Gly Ser
85 90 95
Ala Val Phe Arg Leu Asp Tyr Lys Gly Gln Pro Ala Cys Leu Ala Gln
100 105 110
Ser Pro Gln Leu His Lys Gln Met Ala Ile Cys Gly Asp Met Arg Arg
115 120 125
Val Phe Glu Val Gly Pro Val Phe Arg Ala Glu Asp Ser Phe Thr His
130 135 140
Arg His Leu Cys Glu Phe Val Gly Leu Asp Val Glu Met Glu Ile Arg
145 150 155 160
Met His Tyr Ser Glu Ile Met Asp Leu Val Gly Glu Leu Phe Pro Phe
165 170 175
Ile Phe Thr Lys Ile Glu Glu Arg Cys Pro Lys Glu Leu Glu Ser Val
180 185 190
Arg Lys Gln Tyr Pro Phe Gln Ser Leu Lys Phe Leu Pro Gln Thr Leu
195 200 205
Arg Leu Thr Phe Ala Glu Gly Ile Gln Met Leu Lys Glu Ala Gly Glu

210	215	220
Glu Val Asp Pro Leu Gly Asp Leu Asn Thr Glu Ser Glu Arg Lys Leu		
225	230	235
Gly Gln Leu Val Leu Glu Lys Tyr Lys Thr Glu Phe Tyr Met Leu His		240
	245	250
Arg Tyr Pro Ser Ala Val Arg Pro Phe Tyr Thr Met Pro Tyr Glu Asn		
	260	265
Asp Ser Asn Tyr Ser Asn Ser Phe Asp Val Phe Ile Arg Gly Glu Glu		
	275	280
Ile Met Ser Gly Ala Gln Arg Ile His Asp Pro Glu Leu Leu Glu Lys		
	290	295
Arg Ala Arg Glu Cys Gly Ile Asp Val Lys Thr Ile Ser Thr Tyr Ile		
305	310	315
Asp Ala Phe Arg Tyr Gly Xaa Thr Thr Ser Arg Trp Ile Arg Ser Gly		
	325	330
Ala Gly Ala Cys Gly Asn Ala Leu Met Cys Pro Gln		335
	340	345

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..229

(D) OTHER INFORMATION: / Ceres Seq. ID 1567466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

Met Ala Ile Cys Gly Asp Met Arg Arg Val Phe Glu Val Gly Pro Val		
1	5	10
Phe Arg Ala Glu Asp Ser Phe Thr His Arg His Leu Cys Glu Phe Val		
	20	25
Gly Leu Asp Val Glu Met Glu Ile Arg Met His Tyr Ser Glu Ile Met		
	35	40
Asp Leu Val Gly Glu Leu Phe Pro Phe Ile Phe Thr Lys Ile Glu Glu		
	50	55
Arg Cys Pro Lys Glu Leu Glu Ser Val Arg Lys Gln Tyr Pro Phe Gln		
65	70	75
Ser Leu Lys Phe Leu Pro Gln Thr Leu Arg Leu Thr Phe Ala Glu Gly		
	85	90
Ile Gln Met Leu Lys Glu Ala Gly Glu Glu Val Asp Pro Leu Gly Asp		
	100	105
Leu Asn Thr Glu Ser Glu Arg Lys Leu Gly Gln Leu Val Leu Glu Lys		
	115	120
Tyr Lys Thr Glu Phe Tyr Met Leu His Arg Tyr Pro Ser Ala Val Arg		
	130	135
Pro Phe Tyr Thr Met Pro Tyr Glu Asn Asp Ser Asn Tyr Ser Asn Ser		
145	150	155
Phe Asp Val Phe Ile Arg Gly Glu Glu Ile Met Ser Gly Ala Gln Arg		
	165	170
Ile His Asp Pro Glu Leu Leu Glu Lys Arg Ala Arg Glu Cys Gly Ile		
	180	185
Asp Val Lys Thr Ile Ser Thr Tyr Ile Asp Ala Phe Arg Tyr Gly Xaa		
	195	200
Thr Thr Ser Arg Trp Ile Arg Ser Gly Ala Gly Ala Cys Gly Asn Ala		
	210	215
Leu Met Cys Pro Gln		220
225		

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

aaaaacgcaa cgaagaacaa aatgggttca aagtcaccaa atattgtcgc acttggttta 60
ccctacttc ttactttta cactotttcc tctcaagttg aagtcgtgga atctacaggg 120
cgcaaacatt cgttttggg aaatcctatc gtgtggactc cacactcaa ttcatgtgga 180
ggttctcaag catcagtatt tgcttcttcc aagtggacga caggccgacc atgcagagct 240
agtCgtNect ccaggaacta atattcctgt tctgatcaa tctccatagt actttaattt 300
gagtttgagt tactctgtgt tcgaatttta aagtatatgt ggttttctgt tttagtttgc 360
tgttccaact ctcaagtgtg gaggaataat ataaact

(2) INFORMATION FOR SEQ ID NO:625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

Lys Asn Ala Thr Lys Asn Lys Met Gly Ser Lys Ser Pro Asn Ile Val
1 5 10 15
Ala Leu Val Leu Pro Leu Leu Leu Ile Leu Tyr Thr Leu Ser Ser Gln
20 25 30
Val Glu Val Val Glu Ser Thr Gly Arg Lys Leu Ser Phe Trp Gly Asn
35 40 45
Pro Ile Val Trp Thr Pro His Ser Asn Ser Cys Gly Gly Ser Pro Ala
50 55 60
Ser Val Phe Ala Ser Ser Lys Trp Thr Thr Gly Arg Pro Cys Arg Arg
65 70 75 80
Ser Arg Xaa Ser Arg Asn
85

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

Lys Thr Gln Arg Arg Thr Lys Trp Val Gln Ser His Gln Ile Leu Ser
1 5 10 15
His Leu Cys Tyr Pro Tyr Phe Leu Tyr Phe Thr Leu Phe Pro Leu Lys
20 25 30
Leu Lys Ser Trp Asn Leu Gln Gly Ala Asn Phe Arg Phe Gly Glu Ile
35 40 45
Leu Ser Cys Gly Leu His Thr Gln Ile His Val Glu Val Leu Gln His
50 55 60
Gln Tyr Leu Leu Leu Pro Ser Gly Arg Gln Ala Asp His Ala Asp Val
65 70 75 80
Val Xaa Pro Pro Gly Thr Asn Ile Pro Val Ser Asp Gln Ser Pro
85 90 95

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1567504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

```
Met Gly Ser Lys Ser Pro Asn Ile Val Ala Leu Val Leu Pro Leu Leu
1           5           10          15
Leu Ile Leu Tyr Thr Leu Ser Ser Gln Val Glu Val Val Glu Ser Thr
20          25          30
Gly Arg Lys Leu Ser Phe Trp Gly Asn Pro Ile Val Trp Thr Pro His
35          40          45
Ser Asn Ser Cys Gly Gly Ser Pro Ala Ser Val Phe Ala Ser Ser Lys
50          55          60
Trp Thr Thr Gly Arg Pro Cys Arg Arg Ser Arg Xaa Ser Arg Asn
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..750

(D) OTHER INFORMATION: / Ceres Seq. ID 1567513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

```
taataaaaaa ataaaaagta attagtga gaattaaagaa aaacaaagtc tattccatac      60
gaagaagagc ctcagggttaa ttttttataa gatgggttat tggaaagtcga aggtgtgtcc      120
aaggatgaag aaattgttcc agaagagtc ccacaaaaag gaagttgttg agggaggagaa      180
gccacgagag gtggaagtcg tggaggaggt gtcgtgaaaa ccgaagaacc ggccaaggaa      240
ggagaaacta aaccggagga aataattgca accggcgaga aagagataga aatagttgaa      300
gagaagaaag aagagcttaa accgggtgag gttccggtcc tgcagctgc ggaggagaag      360
aagccagccg tagaagagga gaagaagacg gcgcgggttg aagagaagaa gccagctgtg      420
gaagaggaga agaagcctgc cgtggaagag aagaaacctg tggaggagga gaaaaaagaa      480
gttggttccg ctgttccggg ggtgaaact ccttcgacta aggcctccga aactccggtg      540
gttgaactc cgcccaaggc tccggaaact ccggcgGCTg cgccacaaa ggcttgaaat      600
ttcttcattg tacatttttc taaaaaaata ttgattgtct ttgtgtgat aatttatttt      660
ctttgtttat ttgtcttatt atccatgtga atttcctcta taaattaatt tgcttgcttg      720
aattatatat tcttatgatc caaatcctcc
```

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..41

(D) OTHER INFORMATION: / Ceres Seq. ID 1567514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

```
Met Gly Tyr Trp Lys Ser Lys Val Val Pro Arg Met Lys Lys Leu Phe
1           5           10          15
Glu Lys Ser Pro Ala Lys Lys Glu Val Val Glu Glu Glu Lys Pro Arg
20          25          30
Glu Val Glu Val Val Glu Glu Val Ser
35          40
```

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..30
(D) OTHER INFORMATION: / Ceres Seq. ID 1567515
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:
Met Lys Lys Leu Phe Glu Lys Ser Pro Ala Lys Lys Glu Val Val Glu
1 5 10 15
Glu Glu Lys Pro Arg Glu Val Glu Val Val Glu Glu Val Ser 30
(2) INFORMATION FOR SEQ ID NO:631:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 591 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..591
(D) OTHER INFORMATION: / Ceres Seq. ID 1567520
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:
actcgggtccc atcatgccaag tagataaaca ctgaatcacc aaatcttggt tgagatttag 60
aaaaaaagga agctccaaga gatggcaaga gttgttaaaa tcgattctgc agagtcatgg 120
gatttctatg tgagccaagc caagaatcag aattgtccca ttgtggctca ttctactgca 180
ttaatggtga ttcttctgtg gtttatgaac tccttctctg aagagcttgc gtttaactat 240
aaggatgctc tgtttctaat agttgatggt gatgaagtta aggaagtggc aagtcaacta 300
gaggtaaagg cgatgccaac ttcttctgtt ttgaaggatg gtaatgcgat gcacaaactc 360
gtgggcgcaa accctgatga gattaagaaa cgggtcgatg gtttcgttca gtctcacgt 420
gtgtttcata ttgcttaaga gagatttata gatacgagca gaatactaaa taaagtttgt 480
gtgaagtgtg attagtttgt aactttggta tttggtttgt gtgaaAtatc aagtgttaagt 540
gtaaattttt ataaaaagca gtttgttat aaacaagaac tggatttatt c
(2) INFORMATION FOR SEQ ID NO:632:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..118
(D) OTHER INFORMATION: / Ceres Seq. ID 1567521
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:
Met Ala Arg Val Val Lys Ile Asp Ser Ala Glu Ser Trp Asp Phe Tyr
1 5 10 15
Val Ser Gln Ala Lys Asn Gln Asn Cys Pro Ile Val Ala His Phe Thr
20 25 30
Ala Leu Trp Cys Ile Pro Ser Val Phe Met Asn Ser Phe Phe Glu Glu
35 40 45
Leu Ala Phe Asn Tyr Lys Asp Ala Leu Phe Leu Ile Val Asp Val Asp
50 55 60
Glu Val Lys Glu Val Ala Ser Gln Leu Glu Val Lys Ala Met Pro Thr
65 70 75 80
Phe Leu Phe Leu Lys Asp Gly Asn Ala Met Asp Lys Leu Val Gly Ala
85 90 95
Asn Pro Asp Glu Ile Lys Lys Arg Val Asp Gly Phe Val Gln Ser Ser

100 105 110

Arg Val Val His Ile Ala
115

(2) INFORMATION FOR SEQ ID NO:633:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..77
(D) OTHER INFORMATION: / Ceres Seq. ID 1567522
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

Met	Asn	Ser	Phe	Phe	Glu	Glu	Leu	Ala	Phe	Asn	Tyr	Lys	Asp	Ala	Leu
1				5					10					15	
Phe	Leu	Ile	Val	Asp	Val	Asp	Glu	Val	Lys	Glu	Val	Ala	Ser	Gln	Leu
			20				25					30			
Glu	Val	Lys	Ala	Met	Pro	Thr	Phe	Leu	Phe	Leu	Lys	Asp	Gly	Asn	Ala
	35					40					45				
Met	Asp	Lys	Leu	Val	Gly	Ala	Asn	Pro	Asp	Glu	Ile	Lys	Lys	Arg	Val
	50				55						60				
Asp	Gly	Phe	Val	Gln	Ser	Ser	Arg	Val	Val	His	Ile	Ala			
65					70				75						

(2) INFORMATION FOR SEQ ID NO:634:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1352
(D) OTHER INFORMATION: / Ceres Seq. ID 1567526
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

aatcagtaaaa	acgaaaaagct	aatccaaaac	tctttaatta	ttgttaacaa	ctgatcaatg	60
gctgttaacaa	gctcttcttc	tacttgtgat	ggttttcttc	tcatcagcct	tattgttgct	120
gttttctcat	tggttggggc	atcatctgct	cagttaaacg	caacgtttta	ctcaggcagc	180
tgccctaacg	catctgccat	cgttgcgagc	actattcagc	aaagctcttca	atccgatgca	240
agaatcggag	gcagcctaata	cgccttccat	tttcacgact	gttttgttaa	tggttgcgat	300
gggtgcgtct	tgcttgacga	cacttcaagc	atccagagcg	agaagaacgc	tcctgccaat	360
gcaaaactcaa	ctagaggatt	caatgttgct	gatagtatca	agacagccct	cgagaatgct	420
tgctccggca	tggtttcttg	ctctgacatt	ttagctcttg	cttcagagcg	ctctgtgtct	480
ttggcaggag	gaccttcatg	gactgtgtta	ttagggaaga	gagatggtct	caccgcaaac	540
ttgtctggag	ccaattcgct	tcttccctct	cccttcgaag	gccttaacaa	catcacatca	600
aaatttgtag	ctgtcgggct	aaatacaacc	gatgtagtat	ccctgtctgg	agcgatcagc	660
ttggcgcgtg	gtcaatgcgt	aacCgttcaa	caatagaacta	ttcaacttca	acgggacagg	720
aaaccgccac	ccgactctga	actcaacact	tctcagcagt	cttcaacagc	tatgtctcca	780
aaacggcagc	aatacaggga	tcaccaatct	cgatctgagc	acacctgatg	cgttgcgata	840
caattactac	acgaaccttc	agagtaacaa	tggtcttctc	cagtcagacc	aggaactgtt	900
ctcaaacacc	ggttcagcca	cgcctccgat	tggttaattcc	tttgcaagta	accagaccct	960
gttttttgag	gcgtttgttc	agctctatga	caagatgggg	aacattagtc	ccttgactgg	1020
gagtagtgga	gagattagac	aagactgtaa	ggtggttaat	ggacagtcac	cagcccaactga	1080
agcaggggac	attcagttac	aatctgaagg	accagtgagt	gtagcagata	tgtgaacaaac	1140
gagtagatca	gtttccacgt	ttgtttatca	tatatgaata	ataactccta	ggccgaatca	1200
tttttgtaga	aaaaataagt	ttggttgagg	agaaaaatag	tgagtggtag	ggttgtgtgt	1260
tacacttttg	aaaattttta	tattctaaaa	cattattatg	cctaaatata	tgcatgcatg	1320
tataacgtct	atcgttttga	tacattttgt	gg			

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..212
(D) OTHER INFORMATION: / Ceres Seq. ID 1567527
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

Met	Ala	Val	Thr	Ser	Ser	Ser	Ser	Thr	Cys	Asp	Gly	Phe	Phe	Ile	Ile
1				5				10					15		
Ser	Leu	Ile	Val	Val	Ser	Ser	Leu	Phe	Gly	Ala	Ser	Ser	Ala	Gln	
		20					25					30			
Leu	Asn	Ala	Thr	Phe	Tyr	Ser	Gly	Thr	Cys	Pro	Asn	Ala	Ser	Ala	Ile
		35					40				45				
Val	Arg	Ser	Thr	Ile	Gln	Gln	Ala	Leu	Gln	Ser	Asp	Ala	Arg	Ile	Gly
	50				55				60						
Gly	Ser	Leu	Ile	Arg	Leu	His	Phe	His	Asp	Cys	Phe	Val	Asn	Gly	Cys
65				70					75					80	
Asp	Gly	Ser	Leu	Leu	Asp	Asp	Thr	Ser	Ser	Ile	Gln	Ser	Glu	Lys	
			85				90						95		
Asn	Ala	Pro	Ala	Asn	Ala	Asn	Ser	Thr	Arg	Gly	Phe	Asn	Val	Val	Asp
		100					105					110			
Ser	Ile	Lys	Thr	Ala	Leu	Glu	Asn	Ala	Cys	Pro	Gly	Ile	Val	Ser	Cys
		115					120					125			
Ser	Asp	Ile	Leu	Ala	Leu	Ala	Ser	Glu	Ala	Ser	Val	Ser	Leu	Ala	Gly
	130					135					140				
Gly	Pro	Ser	Trp	Thr	Val	Leu	Leu	Gly	Arg	Arg	Asp	Gly	Leu	Thr	Ala
145				150					155					160	
Asn	Leu	Ser	Gly	Ala	Asn	Ser	Ser	Leu	Pro	Pro	Phe	Glu	Gly	Leu	
			165					170					175		
Asn	Asn	Ile	Thr	Ser	Lys	Phe	Val	Ala	Val	Gly	Leu	Asn	Thr	Thr	Asp
		180					185						190		
Val	Val	Ser	Leu	Ser	Gly	Ala	His	Thr	Phe	Gly	Arg	Gly	Gln	Cys	Val
	195						200					205			
Thr	Val	Gln	Gln												
	210														

(2) INFORMATION FOR SEQ ID NO:636:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 716 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..716

(D) OTHER INFORMATION: / Ceres Seq. ID 1567532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

aagaattagg	gtttctcttt	gtcttcagca	gtcagtgccg	atccgtagGa	aaaaagtgtg	60
agaatctgcc	acocatgggtc	gtatgcacag	tccaggaaag	ggattttcag	ccctctgogtt	120
gccttacaaG	agatcgtctc	caagctggct	caagaccacc	tctcaggatg	ttgatgaatc	180
aattctgaaa	tttgccaaaa	agggtattgac	cccttccacg	attgggtgtg	ttctccgtga	240
ctctccaggt	atccctcagg	tcaagagtgt	tactggaagc	aagatcttga	ggatactcaa	300
agctcatggc	cttgctcctg	agatccctga	ggatctgtac	cattctaata	agaaggctgt	360
tgccatccgt	aaacatctcg	agagggaacg	gaaggacaag	gattccaagt	tcaggctcat	420
cttggtttag	agcaggattc	accgcctcgc	tgcgtattac	aagaagacca	agaagctccc	480
tcccgtctgg	aagtacgaat	ccactaccgc	gagcaccctt	gtgggttaag	ctggagctct	540
gaggaggatt	ctactagtct	gttgctctcc	tttggtttga	tgaattctca	actttagtct	600

taatgtttca gcaggatttt tgtgtttgcc tctcttcttt ttcggaatc ttatgtctcc 660
ttgtttaaga gaatcgtatg atcttgaatt tactattgaa tatgcttttg catccc

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

Met	Gly	Arg	Met	His	Ser	Arg	Gly	Lys	Gly	Ile	Ser	Ala	Ser	Ala	Leu
1			5				10					15			
Pro	Tyr	Lys	Arg	Ser	Ser	Pro	Ser	Trp	Leu	Lys	Thr	Thr	Ser	Gln	Asp
		20					25					30			
Val	Asp	Glu	Ser	Ile	Cys	Lys	Phe	Ala	Lys	Lys	Gly	Leu	Thr	Pro	Ser
	35					40					45				
Gln	Ile	Gly	Val	Ile	Leu	Arg	Asp	Ser	His	Gly	Ile	Pro	Gln	Val	Lys
	50				55					60					
Ser	Val	Thr	Gly	Ser	Lys	Ile	Leu	Arg	Ile	Leu	Lys	Ala	His	Gly	Leu
	65			70				75					80		
Ala	Pro	Glu	Ile	Pro	Glu	Asp	Leu	Tyr	His	Leu	Ile	Lys	Lys	Ala	Val
		85				90							95		
Ala	Ile	Arg	Lys	His	Leu	Glu	Arg	Asn	Arg	Lys	Asp	Lys	Asp	Ser	Lys
		100				105						110			
Phe	Arg	Leu	Ile	Leu	Val	Glu	Ser	Arg	Ile	His	Arg	Leu	Ala	Arg	Tyr
		115				120						125			
Tyr	Lys	Lys	Thr	Lys	Lys	Leu	Pro	Pro	Val	Trp	Lys	Tyr	Glu	Ser	Thr
	130				135						140				
Thr	Ala	Ser	Thr	Leu	Val	Ala									
145				150											

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

Met	His	Ser	Arg	Gly	Lys	Gly	Ile	Ser	Ala	Ser	Ala	Leu	Pro	Tyr	Lys
1				5			10					15			
Arg	Ser	Ser	Pro	Ser	Trp	Leu	Lys	Thr	Thr	Ser	Gln	Asp	Val	Asp	Glu
			20				25					30			
Ser	Ile	Cys	Lys	Phe	Ala	Lys	Lys	Gly	Leu	Thr	Pro	Ser	Gln	Ile	Gly
		35				40					45				
Val	Ile	Leu	Arg	Asp	Ser	His	Gly	Ile	Pro	Gln	Val	Lys	Ser	Val	Thr
	50				55					60					
Gly	Ser	Lys	Ile	Leu	Arg	Ile	Leu	Lys	Ala	His	Gly	Leu	Ala	Pro	Glu
	65				70					75				80	
Ile	Pro	Glu	Asp	Leu	Tyr	His	Leu	Ile	Lys	Lys	Ala	Val	Ala	Ile	Arg
		85				90						95			
Lys	His	Leu	Glu	Arg	Asn	Arg	Lys	Asp	Lys	Asp	Ser	Lys	Phe	Arg	Leu
		100				105						110			
Ile	Leu	Val	Glu	Ser	Arg	Ile	His	Arg	Leu	Ala	Arg	Tyr	Tyr	Lys	Lys

1	Ile	Arg	Arg	Leu	Ser	Phe	Val	Ser	Val	Ser	Ile	Phe	Ser	Pro	Arg	Ile
1	Ser	Asn	Arg	Phe	Phe	Thr	Ile	Ser	Leu	Arg	Ser	Tyr	Phe	Ser	Thr	Val
			20						25					30		
	Leu	Cys	Phe	Phe	Ser	Ile	Asp	Met	Ala	Gly	Lys	Gly	Gly	Lys	Gly	Leu
			35					40					45			
	Leu	Ala	Ala	Lys	Thr	Thr	Ala	Ala	Ala	Ala	Asn	Lys	Asp	Ser	Val	Lys
			50				55					60				
	Lys	Lys	Ser	Ile	Ser	Arg	Ser	Ser	Arg	Ala	Gly	Ile	Gln	Phe	Pro	Val
			65			70					75				80	
	Gly	Arg	Ile	His	Arg	Gln	Leu	Lys	Gln	Arg	Val	Ser	Ala	His	Gly	Arg
				85						90					95	
	Val	Gly	Ala	Thr	Ala	Ala	Val	Tyr	Thr	Ala	Ser	Ile	Leu	Glu	Tyr	Leu
			100						105					110		
	Thr	Ala	Glu	Val	Leu	Glu	Leu	Ala	Gly	Asn	Ala	Ser	Lys	Asp	Leu	Lys
			115					120					125			
	Val	Lys	Arg	Ile	Thr	Pro	Arg	His	Leu	Gln	Leu	Ala	Ile	Arg	Gly	Asp
			130				135				140					
	Glu	Glu	Leu	Asp	Thr	Leu	Ile	Lys	Gly	Thr	Ile	Ala	Gly	Gly	Gly	Val
			145			150					155				160	

Ile Pro His Ile His Lys Ser Leu Val Asn Lys Val Thr Lys Asp
165 170 175

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

```
Met Ala Gly Lys Gly Gly Lys Gly Leu Leu Ala Ala Lys Thr Thr Ala
1      5      10
Ala Ala Ala Asn Lys Asp Ser Val Lys Lys Lys Ser Ile Ser Arg Ser
20     25
Ser Arg Ala Gly Ile Gln Phe Pro Val Gly Arg Ile His Arg Gln Leu
35     40     45
Lys Gln Arg Val Ser Ala His Gly Arg Val Gly Ala Thr Ala Ala Val
50     55     60
Tyr Thr Ala Ser Ile Leu Glu Tyr Leu Thr Ala Glu Val Leu Glu Leu
65     70     75     80
Ala Gly Asn Ala Ser Lys Asp Leu Lys Val Lys Arg Ile Thr Pro Arg
85     90     95
His Leu Gln Leu Ala Ile Arg Gly Asp Glu Glu Leu Asp Thr Leu Ile
100    105    110
Lys Gly Thr Ile Ala Gly Gly Gly Val Ile Pro His Ile His Lys Ser
115    120    125
Leu Val Asn Lys Val Thr Lys Asp
130    135
```

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..566
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

```
tcaagccgtc aacaatgtcg aagcgaggcg gtggaggtac ctctggtaac aaattcagga      60
tgtcactggg tcttccgggt gcggcgacgg tgaactgtgc cgataacacc ggtgctaaga      120
atctctacat catttccggt aaaggatcac aaggctcgtc taatcgatta cctcttgcgt      180
gcgtcgagga catggtgatg gccaccgtca aaaagggtaa gcctgatctc agggaaaaagg      240
ttcttctctc cgtcatcgtt aggcacgcga aaccatggcg ccgaaaggat ggtgttttct      300
tgtacttcga agataatgct ggagtcattg tcaaccoccaa gggagaaatg aaaggttctg      360
caattactgg tcttattggg aaagagtggt ctgattcttg gccaaaggatt gctagtgtcg      420
ccaatgccat tgtctaatga tcagatcaat caattgcttg tatttgatgg atatgtctag      480
atacaaatgt gagaattttg gtacgaagat attttttatt tctgacaata tgtatctgac      540
attcaaatga ttggctatt ttTgac
```

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1567548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

Lys	Pro	Ser	Thr	Met	Ser	Lys	Arg	Gly	Arg	Gly	Gly	Thr	Ser	Gly	Asn	
1				5					10					15		
Lys	Phe	Arg	Met	Ser	Leu	Gly	Leu	Pro	Val	Ala	Ala	Thr	Val	Asn	Cys	
			20					25					30			
Ala	Asp	Asn	Thr	Gly	Ala	Lys	Asn	Leu	Tyr	Ile	Ile	Ser	Val	Lys	Gly	
		35					40					45				
Ile	Lys	Gly	Arg	Leu	Asn	Arg	Leu	Pro	Ser	Ala	Cys	Val	Gly	Asp	Met	
	50				55						60					
Val	Met	Ala	Thr	Val	Lys	Gly	Lys	Pro	Asp	Leu	Arg	Lys	Lys	Val		
65				70					75					80		
Leu	Pro	Ala	Val	Ile	Val	Arg	Gln	Arg	Lys	Pro	Trp	Arg	Arg	Lys	Asp	
			85					90						95		
Gly	Val	Phe	Met	Tyr	Phe	Glu	Asp	Asn	Ala	Gly	Val	Ile	Val	Asn	Pro	
		100					105						110			
Lys	Gly	Glu	Met	Lys	Gly	Ser	Ala	Ile	Thr	Gly	Pro	Ile	Gly	Lys	Glu	
		115					120					125				
Cys	Ala	Asp	Leu	Trp	Pro	Arg	Ile	Ala	Ser	Ala	Ala	Asn	Ala	Ile	Val	
130						135						140				

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1567549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

Met	Ser	Lys	Arg	Gly	Arg	Gly	Gly	Thr	Ser	Gly	Asn	Lys	Phe	Arg	Met	
1				5				10					15			
Ser	Leu	Gly	Leu	Pro	Val	Ala	Ala	Thr	Val	Asn	Cys	Ala	Asp	Asn	Thr	
			20					25					30			
Gly	Ala	Lys	Asn	Leu	Tyr	Ile	Ile	Ser	Val	Lys	Gly	Ile	Lys	Gly	Arg	
		35					40					45				
Leu	Asn	Arg	Leu	Pro	Ser	Ala	Cys	Val	Gly	Asp	Met	Val	Met	Ala	Thr	
	50				55						60					
Val	Lys	Lys	Gly	Lys	Pro	Asp	Leu	Arg	Lys	Lys	Val	Leu	Pro	Ala	Val	
65				70					75					80		
Ile	Val	Arg	Gln	Arg	Lys	Pro	Trp	Arg	Arg	Lys	Asp	Gly	Val	Phe	Met	
			85					90						95		
Tyr	Phe	Glu	Asp	Asn	Ala	Gly	Val	Ile	Val	Asn	Pro	Lys	Gly	Glu	Met	
		100					105						110			
Lys	Gly	Ser	Ala	Ile	Thr	Gly	Pro	Ile	Gly	Lys	Glu	Cys	Ala	Asp	Leu	
		115					120					125				
Trp	Pro	Arg	Ile	Ala	Ser	Ala	Ala	Asn	Ala	Ile	Val					
130						135					140					

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..125
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567550
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:
Met Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn
1 5 10 15
Thr Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly
 20 25 30
Arg Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala
 35 40 45
Thr Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Leu Pro Ala
 50 55 60
Val Ile Val Arg Gln Arg Lys Pro Trp Arg Arg Lys Asp Gly Val Phe
65 70 75 80
Met Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Glu
 85 90 95
Met Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala Asp
 100 105 110
Leu Trp Pro Arg Ile Ala Ser Ala Ala Asn Ala Ile Val
 115 120 125
(2) INFORMATION FOR SEQ ID NO:646:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..352
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567555
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:
cctagaaatt ttgtctctct cgccgccttg cgaaaagcat ttctgatctt actcttagga 60
taaaaaaatg tcgacagttg gagagcttgc ttgcagctac gctgttatga tctctgagga 120
cgagggtatc gctatcacgg ctgacaaaat cgcgaccttg gtgaaagctg ctggtgttag 180
tattgagtca tactggccaa tgctattcgc caagatggct gagaaacgta acgtgactga 240
tctcatcatg aacgttggtg ctggtgtgtg aggtgtgtgc ccggttgacg ctgtgtctcc 300
agctgctggc ggtgtgtcgg caSctgcaac cggagcacca ctctccacca cc
(2) INFORMATION FOR SEQ ID NO:647:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..95
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567556
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:
Met Ser Thr Val Gly Glu Leu Ala Cys Ser Tyr Ala Val Met Ile Leu
1 5 10 15
Glu Asp Glu Gly Ile Ala Ile Thr Ala Asp Lys Ile Ala Thr Leu Val
 20 25 30
Lys Ala Ala Gly Val Ser Ile Glu Ser Tyr Trp Pro Met Leu Phe Ala
 35 40 45
Lys Met Ala Glu Lys Arg Asn Val Thr Asp Leu Ile Met Asn Val Gly
 50 55 60
Ala Gly Gly Gly Gly Gly Ala Pro Val Ala Ala Ala Pro Ala Ala

(2) INFORMATION FOR SEO ID NO:648:

- (ii) MOLECULE TYPE: peptide

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..82

- (D) OTHER INFORMATION: / Ceres Seq. ID 1567557

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

(2) INFORMATION FOR SEQ ID NO:649:

- (ii) MOLECULE TYPE: peptide

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..51

- (D) OTHER INFORMATION: / Ceres Seq. ID 1567558

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

(2) INFORMATION FOR SEQ ID NO:650:

- (ii) MOLECULE TYPE: DNA (genomic)

- (A) NAME/KEY: -

- (B) LOCATION: 1..1465

- (D) OTHER INFORMATION: / Ceres Seq. ID 1567563

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

agattaaaaa ctctttaaaa actttttgtc ataaatcagg caaagaagta aaagaggctt 60
 aaaactctct ctctctcttg gtcttcttca ctcttaacga aaatggactc tctaactctc 120

```

ttcttcacgc ggcgactcgt cgcgcgtcgt atctactggt tctctcgcgt tctcgggtcca 180
gcagagcgta aaggcaaacg agccgtagat ctctctggcg gctcaatctc gcgcgagaaa 240
gtccaaagaca actacaaaac gactctggtct ttcttcgcgc gtccaaaaga aatcgaaaacc 300
gcgcgagaaa ttccagactt cgtcgacaca ttctacaatt tcgtccaccga catatacgag 360
tggggactgg gacaatcctt ccactttctca ccactcaatcc ccggaaaaac tcacaaaagac 420
gccacgcgcc tccacgaaga gatggccgta gatctgatcc aagtcaaac tgggtcaaaag 480
atcttagacg tcggatdcgg cgtcggcggt bcgatgcgag cgaattgcac tcactcgcga 540
gtcaacgtag tcgggattac gataaacgag tatcagggtga acagagctcg ttccacaaat 600
aagaaagctg gtctcgacgc gctttgcgag gtgctctgtg gtaacttctc ccagatgcgc 660
ttcgatgaca acagtttcga cgggtgctta tccatcgaa gacacgtgtca gcgcgcgaag 720
ctggaggaag tgtacgcaga gatctacagg gtgttgaaac ccggtactat gtagtgtctg 780
taccagtggtg ttacgcaggga gaaatttaag gcggaggatg acgaaAcacg tggaggtaat 840
ccaaggGatt gagagagggt atgcgttacc tgggcttagg cttacgtgga tattgctgag 900
acggctaaaa aggttggggt tgagatagtg aaggagaagg atctggcgag tccaccgcgt 960
gagccgtggt ggctagggt taagatgggt aggtctgctt attggaggaa tcacattgtg 1020
gttcagattt tgtcagcggt tggagttgct cctaaaggaa ctgttgatgt tcatgagatg 1080
ttgtttaaga ctgctgatta ttgaccaga ggaggtgaaa ccggaataatt ctctccgatg 1140
catatgattc tctgcagaaa accggagtcg ccggaggaga gttcttgaga aaggtagaaa 1200
ggaacacatca ccggaaaaaag tatggagaat ttctcaatt ttgttttatt ttaagttaa 1260
atcaacttgg ttattgtact atttttgtgt ttaatttgg ttgtgtttc aagaattatt 1320
agtttttttt tgtttttgtg catatgagaa tottactctt gatttctccg ccgtagtgcc 1380
gcgcgacat agggattatt tagtattttt aagtgtgttt aagattgatt aacaagttag 1440
taaaaaaaa tgtactagg tctgcg

```

(2) INFORMATION FOR SEQ ID NO:651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..249

(D) OTHER INFORMATION: / Ceres Seq. ID 1567564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

```

Met Asp Ser Leu Thr Leu Phe Phe Thr Gly Ala Leu Val Ala Val Gly
1      5      10      15
Ile Tyr Trp Phe Leu Cys Val Leu Gly Pro Ala Glu Arg Lys Gly Lys
20     25     30
Arg Ala Val Asp Leu Ser Gly Gly Ser Ile Ser Ala Glu Lys Val Gln
35     40     45
Asp Asn Tyr Lys Gln Tyr Trp Ser Phe Phe Arg Arg Pro Lys Glu Ile
50     55     60
Glu Thr Ala Glu Lys Val Pro Asp Phe Val Asp Thr Phe Tyr Asn Leu
65     70     75     80
Val Thr Asp Ile Tyr Glu Trp Gly Trp Gly Gln Ser Phe His Phe Ser
85     90     95
Pro Ser Ile Pro Gly Lys Ser His Lys Asp Ala Thr Arg Leu His Glu
100    105    110
Glu Met Ala Val Asp Leu Ile Gln Val Lys Pro Gly Gln Lys Ile Leu
115    120    125
Asp Val Gly Xaa Gly Val Gly Gly Xaa Met Arg Ala Ile Ala Ser His
130    135    140
Ser Arg Ala Asn Val Val Gly Ile Thr Ile Asn Glu Tyr Gln Val Asn
145    150    155    160
Arg Ala Arg Leu His Asn Lys Lys Ala Gly Leu Asp Ala Leu Cys Glu
165    170    175
Val Val Cys Gly Asn Phe Leu Gln Met Pro Phe Asp Asp Asn Ser Phe
180    185    190
Asp Gly Ala Tyr Ser Ile Glu Ala Thr Cys His Ala Pro Lys Leu Glu
195    200    205

```


Glu Val Tyr Ala Glu Ile Tyr Arg Val Leu Lys Pro Gly Ser Met Tyr
210 215 220
Val Ser Tyr Glu Trp Val Thr Thr Glu Lys Phe Lys Ala Glu Asp Asp
225 230 235 240
Glu Thr Arg Gly Gly Asn Pro Arg Asp
245

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1567565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

Met Ala Val Asp Leu Ile Gln Val Lys Pro Gly Gln Lys Ile Leu Asp
1 5 10 15
Val Gly Xaa Gly Val Gly Gly Xaa Met Arg Ala Ile Ala Ser His Ser
20 25 30
Arg Ala Asn Val Val Gly Ile Thr Ile Asn Glu Tyr Gln Val Asn Arg
35 40 45
Ala Arg Leu His Asn Lys Lys Ala Gly Leu Asp Ala Leu Cys Glu Val
50 55 60
Val Cys Gly Asn Phe Leu Gln Met Pro Phe Asp Asn Ser Phe Asp
65 70 75 80
Gly Ala Tyr Ser Ile Glu Ala Thr Cys His Ala Pro Lys Leu Glu Glu
85 90 95
Val Tyr Ala Glu Ile Tyr Arg Val Leu Lys Pro Gly Ser Met Tyr Val
100 105 110
Ser Tyr Glu Trp Val Thr Thr Glu Lys Phe Lys Ala Glu Asp Asp Glu
115 120 125
Thr Arg Gly Gly Asn Pro Arg Asp
130 135

(2) INFORMATION FOR SEQ ID NO:653:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1629 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1629

(D) OTHER INFORMATION: / Ceres Seq. ID 1567581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

aatttthtTC gaacaccgaa aacactttcg aacctataaa gacagaacac tgtgtcaatt 60
ttcattacct ggggaacaaaa cgcaaaatca aagacaataa ttttttcccc gagagagaaa 120
atgcagaggt tgaagcagca gcagcagcag caacaagtta tgatgcagca agctcttatg 180
cagcaacagt ctctctacca tcttggtctc cttgccccgc cacagataga accaatccca 240
agtggaaatc tccccctcg ttttgatcca agtacttgcc gcagtgtgta cgttggaaac 300
atccatattc aggtgacgga acctctgctt caagagggtt ttgctggcac tggctcctgta 360
gaaagctgta aactaatatg gaaagaaaag tcttcttatg ggtttgtgca ctactttgat 420
cgaagatctg ctggtcttgc aatctcttct ctcaatggaa ggcatcttgt tgggcaacct 480
atcaagggtta actgggctta tgcgagtgcc cagaggaggag atacatcaag tcaactcaat 540
ataatttgta gggattttag tccggagggtt actgatgcaa tgctgtttac ttgcttctct 600
gtctaccgga cttgctcgga tgcaagagtt atgtgggagc agaaaaactgg cgcttcaaga 660
ggatttggat ttgtttcctt ccgtaaccaa caggatgcc agactgcaat agatgagata 720
actgggaaat ggcttggttc caggcagata cgttgcaact gggcgacaaa gggagccact 780

tcctgtgagg	acaaacagag	ctctgattcc	aaaagcgtcg	tggaacttac	cagtggtgtgc	840
tcggaggatg	gtaaaagatac	tactaatggt	gaagctcctg	agaacaatgc	tcagtacaca	900
actgtttacg	tcggttaact	tgctccagag	gtgtcccaagg	ttgatettcca	ccgccaactc	960
cattcccttg	gtcgtggggg	catagaggaa	gtccgtgttc	aaagagacaa	aggtttcgga	1020
tttgtgagat	actctactca	tgtagaggca	gccctcgcta	ttcagatggg	aaacacacat	1080
tcctacctta	gtggcaggca	aataaagtgt	tcttggggaa	gcaagccaac	tcacgacagga	1140
acagettcaa	acccgcttcc	tcacacagct	cctgcaccaa	tcocgggatt	ctcagcgagat	1200
gatctcttgg	cttacgagag	gcaactagcg	atgagcaaga	ttgcaggaaat	gaatccgatg	1260
atgcatcacc	cgcaggagaca	acatgtcttt	aaacaagctg	caatggggagc	cactggttca	1320
aaccaggcaa	tatatgacgg	tggttaccag	aacgcgcagc	agctcatgta	ctaccagtaa	1380
gatctctctc	ggagccgtta	cttgagcgaa	gagttcttct	ttttctctct	ttttgttatg	1440
taacgtctctt	attgtatctt	tttctttctt	tctaacttat	gttctgttta	taatgttatc	1500
atgtagctgt	gggtttgtgg	tttgtgttcc	acgttttttc	ttttgttaac	tactacggtt	1560
tacgtttttg	cacatcttca	actctttctt	ctttctcttt	ctctaactta	atcttatatta	1620
ttgggtcgc						

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 459 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..459

(D) OTHER INFORMATION: / Ceres Seq. ID 1567582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

Asn	Xaa	Ser	Arg	Thr	Pro	Lys	Thr	Leu	Ser	Asn	Pro	Lys	Arg	Gln	Asn
1						5					10			15	
Thr	Val	Ser	Ile	Phe	Ile	Thr	Trp	Glu	Gln	Asn	Ala	Lys	Ser	Lys	Thr
						20				25			30		
Ile	Ile	Phe	Ser	Pro	Arg	Glu	Lys	Met	Gln	Arg	Leu	Lys	Gln	Gln	Gln
						35				40			45		
Gln	Gln	Gln	Gln	Val	Met	Met	Gln	Gln	Ala	Leu	Met	Gln	Gln	Gln	Ser
						50				55			60		
Leu	Tyr	His	Pro	Gly	Leu	Leu	Ala	Pro	Pro	Gln	Ile	Glu	Pro	Ile	Pro
						65				70			75		80
Ser	Gly	Asn	Leu	Pro	Pro	Gly	Phe	Asp	Pro	Ser	Thr	Cys	Arg	Ser	Val
						85				90			95		
Tyr	Val	Gly	Asn	Ile	His	Ile	Gln	Val	Thr	Glu	Pro	Leu	Leu	Gln	Glu
						100				105			110		
Val	Phe	Ala	Gly	Thr	Gly	Pro	Val	Glu	Ser	Cys	Lys	Leu	Ile	Arg	Lys
						115				120			125		
Glu	Lys	Ser	Ser	Tyr	Gly	Phe	Val	His	Tyr	Phe	Asp	Arg	Arg	Ser	Ala
						130				135			140		
Gly	Leu	Ala	Ile	Leu	Ser	Leu	Asn	Gly	Arg	His	Leu	Phe	Gly	Gln	Pro
						145				150			155		160
Ile	Lys	Val	Asn	Trp	Ala	Tyr	Ala	Ser	Gly	Gln	Arg	Glu	Asp	Thr	Ser
						165				170			175		
Ser	His	Phe	Asn	Ile	Phe	Val	Gly	Asp	Leu	Ser	Pro	Glu	Val	Thr	Asp
						180				185			190		
Ala	Met	Leu	Phe	Thr	Cys	Phe	Ser	Val	Tyr	Pro	Thr	Cys	Ser	Asp	Ala
						195				200			205		
Arg	Val	Met	Trp	Asp	Gln	Lys	Thr	Gly	Arg	Ser	Arg	Gly	Phe	Gly	Phe
						210				215			220		
Val	Ser	Phe	Arg	Asn	Gln	Gln	Asp	Ala	Gln	Thr	Ala	Ile	Asp	Glu	Ile
						225				230			235		240
Thr	Gly	Lys	Trp	Leu	Gly	Ser	Arg	Gln	Ile	Arg	Cys	Asn	Trp	Ala	Thr
						245				250			255		
Lys	Gly	Ala	Thr	Ser	Gly	Glu	Asp	Lys	Gln	Ser	Ser	Asp	Ser	Lys	Ser
						260				265			270		

Val	Val	Glu	Leu	Thr	Ser	Gly	Val	Ser	Glu	Asp	Gly	Lys	Asp	Thr	Thr		
		275					280					285					
Asn	Gly	Glu	Ala	Pro	Glu	Asn	Asn	Ala	Gln	Tyr	Thr	Thr	Val	Tyr	Val		
		290				295					300						
Gly	Asn	Leu	Ala	Pro	Glu	Val	Ser	Gln	Val	Asp	Leu	His	Arg	His	Phe		
		305			310					315					320		
His	Ser	Leu	Gly	Ala	Gly	Val	Ile	Glu	Glu	Val	Arg	Val	Gln	Arg	Asp		
			325						330				335				
Lys	Gly	Phe	Gly	Phe	Val	Arg	Tyr	Ser	Thr	His	Val	Glu	Ala	Ala	Leu		
			340					345					350				
Ala	Ile	Gln	Met	Gly	Asn	Thr	His	Ser	Tyr	Leu	Ser	Gly	Arg	Gln	Met		
		355					360					365					
Lys	Cys	Ser	Trp	Gly	Ser	Lys	Pro	Thr	Pro	Ala	Gly	Thr	Ala	Ser	Asn		
		370				375					380						
Pro	Leu	Pro	Pro	Pro	Ala	Pro	Ala	Pro	Ile	Pro	Gly	Phe	Ser	Ala	Ser		
		385			390				395								
Asp	Leu	Leu	Ala	Tyr	Glu	Arg	Gln	Leu	Ala	Met	Ser	Lys	Met	Ala	Gly		
			405					410					415				
Met	Asn	Pro	Met	Met	His	His	Pro	Gln	Gly	Gln	His	Ala	Phe	Lys	Gln		
			420					425					430				
Ala	Ala	Met	Gly	Ala	Thr	Gly	Ser	Asn	Gln	Ala	Ile	Tyr	Asp	Gly	Gly		
		435				440						445					
Tyr	Gln	Asn	Ala	Gln	Gln	Leu	Met	Tyr	Tyr	Gln							
		450			455												

(2) INFORMATION FOR SEQ ID NO:655:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 419 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..419

(D) OTHER INFORMATION: / Ceres Seq. ID 1567583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

Met	Gln	Arg	Leu	Lys	Gln	Gln	Gln	Gln	Gln	Gln	Val	Met	Met	Gln		
1				5					10			15				
Gln	Ala	Leu	Met	Gln	Gln	Gln	Ser	Leu	Tyr	His	Pro	Gly	Leu	Leu	Ala	
		20					25					30				
Pro	Pro	Gln	Ile	Glu	Pro	Ile	Pro	Ser	Gly	Asn	Leu	Pro	Pro	Gly	Phe	
		35				40				45						
Asp	Pro	Ser	Thr	Cys	Arg	Ser	Val	Tyr	Val	Gly	Asn	Ile	His	Ile	Gln	
		50			55					60						
Val	Thr	Glu	Pro	Leu	Leu	Gln	Glu	Val	Phe	Ala	Gly	Thr	Gly	Pro	Val	
		65			70				75					80		
Glu	Ser	Cys	Lys	Leu	Ile	Arg	Lys	Glu	Lys	Ser	Ser	Tyr	Gly	Phe	Val	
			85					90					95			
His	Tyr	Phe	Asp	Arg	Arg	Ser	Ala	Gly	Leu	Ala	Ile	Leu	Ser	Leu	Asn	
		100						105				110				
Gly	Arg	His	Leu	Phe	Gly	Gln	Pro	Ile	Lys	Val	Asn	Trp	Ala	Tyr	Ala	
		115				120					125					
Ser	Gly	Gln	Arg	Glu	Asp	Thr	Ser	Ser	His	Phe	Asn	Ile	Phe	Val	Gly	
		130				135					140					
Asp	Leu	Ser	Pro	Glu	Val	Thr	Asp	Ala	Met	Leu	Phe	Thr	Cys	Phe	Ser	
		145			150					155					160	
Val	Tyr	Pro	Thr	Cys	Ser	Asp	Ala	Arg	Val	Met	Trp	Asp	Gln	Lys	Thr	
			165					170					175			
Gly	Arg	Ser	Arg	Gly	Phe	Gly	Phe	Val	Ser	Phe	Arg	Asn	Gln	Gln	Asp	
			180					185					190			
Ala	Gln	Thr	Ala	Ile	Asp	Glu	Ile	Thr	Gly	Lys	Trp	Leu	Gly	Ser	Arg	

Met	Met	Gln	Gln	Ala	Leu	Met	Gln	Gln	Gln	Ser	Leu	Tyr	His	Pro	Gly
1				5				10						15	
Leu	Leu	Ala	Pro	Pro	Gln	Ile	Glu	Pro	Ile	Pro	Ser	Gly	Asn	Leu	Pro
			20					25					30		
Pro	Gly	Phe	Asp	Pro	Ser	Thr	Cys	Arg	Ser	Val	Tyr	Val	Gly	Asn	Ile
		35					40					45			
His	Ile	Gln	Val	Thr	Glu	Pro	Leu	Gln	Glu	Val	Phe	Ala	Gly	Thr	
		50				55						60			
Gly	Pro	Val	Glu	Ser	Cys	Lys	Leu	Ile	Arg	Lys	Glu	Lys	Ser	Ser	Tyr
65					70					75				80	
Gly	Phe	Val	His	Tyr	Phe	Asp	Arg	Arg	Ser	Ala	Gly	Leu	Ala	Ile	Leu
			85						90					95	
Ser	Leu	Asn	Gly	Arg	His	Leu	Phe	Gly	Gln	Pro	Ile	Lys	Val	Asn	Trp
			100					105					110		
Ala	Tyr	Ala	Ser	Gly	Gln	Arg	Glu	Asp	Thr	Ser	Ser	His	Phe	Asn	Ile
		115					120					125			
Phe	Val	Gly	Asp	Leu	Ser	Pro	Glu	Val	Thr	Asp	Ala	Met	Leu	Phe	Thr
		130				135					140				
Cys	Phe	Ser	Val	Tyr	Pro	Thr	Cys	Ser	Asp	Ala	Arg	Val	Met	Trp	Asp
145					150					155				160	

Gln Lys Thr Gly Arg Ser Arg Gly Phe Gly Phe Val Ser Phe Arg Asn
165 170 175
Gln Gln Asp Ala Gln Thr Ala Ile Asp Glu Ile Thr Gly Lys Trp Leu
180 185 190
Gly Ser Arg Gln Ile Arg Cys Asn Trp Ala Thr Lys Gly Ala Thr Ser
195 200 205
Gly Glu Asp Lys Gln Ser Ser Asp Ser Lys Ser Val Val Glu Leu Thr
210 215 220
Ser Gly Val Ser Glu Asp Gly Lys Asp Thr Trp Asn Gly Glu Ala Pro
225 230 235
Glu Asn Asn Ala Gln Tyr Thr Thr Val Tyr Val Gly Asn Leu Ala Pro
245 250 255
Glu Val Ser Gln Val Asp Leu His Arg His Phe His Ser Leu Gly Ala
260 265 270
Gly Val Ile Glu Glu Val Arg Val Gln Arg Asp Lys Gly Phe Gly Phe
275 280 285
Val Arg Tyr Ser Thr His Val Glu Ala Ala Leu Ala Ile Gln Met Gly
290 295 300
Asn Thr His Ser Tyr Leu Ser Gly Arg Gln Met Lys Cys Ser Trp Gly
305 310 315
Ser Lys Pro Thr Pro Ala Gly Thr Ala Ser Asn Pro Leu Pro Pro Pro
325 330 335
Ala Pro Ala Pro Ile Pro Gly Phe Ser Ala Ser Asp Leu Leu Ala Tyr
340 345 350
Glu Arg Gln Leu Ala Met Ser Lys Met Ala Gly Met Asn Pro Met Met
355 360 365
His His Pro Gln Gly Gln His Ala Phe Lys Gln Ala Ala Met Gly Ala
370 375 380
Thr Gly Ser Asn Gln Ala Ile Tyr Asp Gly Gly Tyr Gln Asn Ala Gln
385 390 395
Gln Leu Met Tyr Tyr Gln
405

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1190 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1190

(D) OTHER INFORMATION: / Ceres Seq. ID 1567589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

agaaaccctga	aaaatccttta	ttgtagcagc	tgagagcaata	tatatcccaa	tttgcgcgcaa	60
ctagggtttt	ctcttcctca	cgcaaaagcaa	tacatcgagc	tctcccaactg	attcagcagc	120
tctttgaact	actcttcgac	aatggcgaggaa	cgttggtggag	aacgttggtgt	tgagcgtggt	180
ggagaaactg	gtgatttcgg	acgaggatcc	ggaggcccggtg	gaggtcgctgg	agatcgttga	240
gggctgtggc	gtggaggccg	tggttggtcgt	cgtggagggtc	gtgccactga	agaagagaaaa	300
tggtttccag	tgaccaagct	tggttcgtcac	gtggcggctg	gtcatatcaa	gcagatagag	360
cagatctcat	ttcattcaact	cccgggttaag	gagtaccaga	tcattgatat	gctcatcggt	420
ccaacattga	aggatgaggt	aatgaaaaatc	atgccgggttc	agaaaaaac	cagggtcgtgt	480
caaaaggcata	gattcaaggc	ctttgttgtc	gttgagagatg	gtaattgtcoa	tggttggtgtg	540
ggagtgaagt	gctctaagga	agttgctacg	gccattagag	gagcgattat	tctcgctaa	600
ctgtctgttg	ttccagtgag	gagaggttac	tggttgtaaca	agattgggaa	gccacatacgt	660
gttccttgta	aggtgactgg	gaagtgtgga	tctgtgacac	tgagagaggt	tcacgctcct	720
agaggttctg	gtattgtggc	tgctagaggt	cctaagaag	ttcttcaatt	cgctggaatt	780
gatgatgttt	gcactctctc	caggggatcc	acaaaaactc	ttggaaaCtt	cgctcagggt	840
acattcgatt	tccttcagaa	gacttacgga	ttccttacc	cagaggtctg	gaaggagaca	900
agattctcta	gatcaccata	ccaagagcac	actgatttcc	tggtgtccaa	ggctctcttc	960
accagcaaac	ccgaccaggt	ggttgaagac	caagcctaaa	caatgcttcc	acctgtgtgt	1020

ctttttggat tataatcctt catgagttaa ttttggttga acctttggta gtatatgttg 1080
ctggattgtg cacccttctgt tttcatctcc tcttccaac tactttattt ttgcttatgg 1140
atcttaatgt tctagttttg cttttacttt tgttgagaaa agttaaatcc

(2) INFORMATION FOR SEQ ID NO:658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..285

(D) OTHER INFORMATION: / Ceres Seq. ID 1567590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

Met Ala Glu Arg Gly Gly Glu Arg Gly Val Glu Arg Gly Gly Glu Arg
1 5 10 15
Gly Asp Phe Gly Arg Gly Phe Gly Gly Arg Gly Gly Arg Gly Asp Arg
20 25 30
Gly Gly Arg Gly Arg Gly Gly Arg Gly Gly Arg Gly Gly Arg Ala
35 40 45
Ser Glu Glu Glu Lys Trp Val Pro Val Thr Lys Leu Gly Arg His Val
50 55 60
Ala Ala Gly His Ile Lys Gln Ile Glu Gln Ile Tyr Leu His Ser Leu
65 70 75 80
Pro Val Lys Glu Tyr Gln Ile Ile Asp Met Leu Ile Gly Pro Thr Leu
85 90 95
Lys Asp Glu Val Met Lys Ile Met Pro Val Gln Lys Gln Thr Arg Ala
100 105 110
Gly Gln Arg Thr Arg Phe Lys Ala Phe Val Val Val Gly Asp Gly Asn
115 120 125
Gly His Val Gly Leu Gly Val Lys Cys Ser Lys Glu Val Ala Thr Ala
130 135 140
Ile Arg Gly Ala Ile Ile Leu Ala Lys Leu Ser Val Val Pro Val Arg
145 150 155 160
Arg Gly Tyr Trp Gly Asn Lys Ile Gly Lys Pro His Thr Val Pro Cys
165 170 175
Lys Val Thr Gly Lys Cys Gly Ser Val Thr Val Arg Met Val Pro Ala
180 185 190
Pro Arg Gly Ser Gly Ile Val Ala Ala Arg Val Pro Lys Lys Val Leu
195 200 205
Gln Phe Ala Gly Ile Asp Asp Val Phe Thr Ser Ser Arg Gly Ser Thr
210 215 220
Lys Thr Leu Gly Asn Phe Val Lys Ala Thr Phe Asp Cys Leu Gln Lys
225 230 235 240
Thr Tyr Gly Phe Leu Thr Pro Glu Phe Trp Lys Glu Thr Arg Phe Ser
245 250 255
Arg Ser Pro Tyr Gln Glu His Thr Asp Phe Leu Ala Ser Lys Ala Leu
260 265 270
Ser Thr Ser Lys Pro Asp Pro Val Val Glu Asp Gln Ala
275 280 285

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196

(D) OTHER INFORMATION: / Ceres Seq. ID 1567591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

Met Leu Ile Gly Pro Thr Leu Lys Asp Glu Val Met Lys Ile Met Pro
1 5 10 15
Val Gln Lys Gln Thr Arg Ala Gly Gln Arg Thr Arg Phe Lys Ala Phe
20 25 30
Val Val Val Gly Asp Gly Asn Gly His Val Gly Leu Gly Val Lys Cys
35 40 45
Ser Lys Glu Val Ala Thr Ala Ile Arg Gly Ala Ile Ile Leu Ala Lys
50 55 60
Leu Ser Val Val Pro Val Arg Arg Gly Tyr Trp Gly Asn Lys Ile Gly
65 70 75 80
Lys Pro His Thr Val Pro Cys Lys Val Thr Gly Lys Cys Gly Ser Val
85 90 95
Thr Val Arg Met Val Pro Ala Pro Arg Gly Ser Gly Ile Val Ala Ala
100 105 110
Arg Val Pro Lys Lys Val Leu Gln Phe Ala Gly Ile Asp Asp Val Phe
115 120 125
Thr Ser Ser Arg Gly Ser Thr Lys Thr Leu Gly Asn Phe Val Lys Ala
130 135 140
Thr Phe Asp Cys Leu Gln Lys Thr Tyr Gly Phe Leu Thr Pro Glu Phe
145 150 155 160
Trp Lys Glu Thr Arg Phe Ser Arg Ser Pro Tyr Gln Glu His Thr Asp
165 170 175
Phe Leu Ala Ser Lys Ala Leu Ser Thr Ser Lys Pro Asp Pro Val Val
180 185 190
Glu Asp Gln Ala
195

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1567592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

Met Lys Ile Met Pro Val Gln Lys Gln Thr Arg Ala Gly Gln Arg Thr
1 5 10 15
Arg Phe Lys Ala Phe Val Val Val Gly Asp Gly Asn Gly His Val Gly
20 25 30
Leu Gly Val Lys Cys Ser Lys Glu Val Ala Thr Ala Ile Arg Gly Ala
35 40 45
Ile Ile Leu Ala Lys Leu Ser Val Val Pro Val Arg Arg Gly Tyr Trp
50 55 60
Gly Asn Lys Ile Gly Lys Pro His Thr Val Pro Cys Lys Val Thr Gly
65 70 75 80
Lys Cys Gly Ser Val Thr Val Arg Met Val Pro Ala Pro Arg Gly Ser
85 90 95
Gly Ile Val Ala Ala Arg Val Pro Lys Lys Val Leu Gln Phe Ala Gly
100 105 110
Ile Asp Asp Val Phe Thr Ser Ser Arg Gly Ser Thr Lys Thr Leu Gly
115 120 125
Asn Phe Val Lys Ala Thr Phe Asp Cys Leu Gln Lys Thr Tyr Gly Phe
130 135 140
Leu Thr Pro Glu Phe Trp Lys Glu Thr Arg Phe Ser Arg Ser Pro Tyr
145 150 155 160
Gln Glu His Thr Asp Phe Leu Ala Ser Lys Lys Ala Leu Ser Thr Ser Lys

165 170 175

Pro Asp Pro Val Val Glu Asp Gln Ala
180 185

(2) INFORMATION FOR SEQ ID NO:661:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1236 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1236
(D) OTHER INFORMATION: / Ceres Seq. ID 1567593
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

aaaccaca	acataatttc	acatatctct	ctttctttct	cttgaaggaa	agacgaagat	60
ctccaagtcc	caagtgtgta	acacaagacg	taaacatggg	tcactctggg	ttcttagtta	120
tgattatggt	aggagtcagt	gcttctctcg	tgagcgtcta	cgggtggcgt	tggatcaacg	180
ctcacgccc	ttttacgggt	gggtggtgat	cttcgggcac	aatgggtggt	gcttgtggat	240
atggttaatt	atatagccaa	ggctacggga	cgagcacggc	ggctctaagc	acagScctct	300
ttcaacaagt	gacttagctg	tggttcttgc	tttgagataa	gatgtgaaaa	cgatggtaaa	360
tggtgtttac	ctggctcaat	cggtgtaacc	gctacaaact	tcgtcccgcc	aaataacggc	420
ttagcgaaac	ataatggcgg	ttggtgtaat	ctcctcttgc	aacactttga	ccttgctcac	480
cctgtttttc	aacgcattgc	tcagtacaga	gctggaaatc	tcctgttttc	ctacagaagg	540
gttctcttgc	ggagaaagg	aggaaataaga	ttcacgataa	acggccactc	atactcaac	600
cttgtgtcga	tcacaaacgt	cggtggtgcc	ggagacgttc	actcgccggc	gatcaagggt	660
tcaagaacag	tgtggcaagc	taigtcaagg	aactgggggc	aaaattggca	aagcaactct	720
tacctcaacg	gtcaagcact	ttcctttaag	gtcaccacca	cgacggccgc	cacagtgtgc	780
tccttcaacg	cgcgtctctc	cggctgggtc	tatggccaga	cttttgcggc	tggacagttc	840
cgttaaaaag	ggcaagttgg	ttaactcttc	ttccatttat	ctaaagtaaa	ctcattttgt	900
tggttatatt	gysctcttga	aaaaactcgg	ttattgagag	agtgatgcgt	cgagggtctg	960
gttttgcaga	aggccttgat	gacgtctaatt	cttttttggg	acctctttat	ttttctttct	1020
tgaaactagt	ttttgttaag	aaagaaaaaa	caagttatag	tagttaattg	attactgatg	1080
cagaggtgga	gttttaacta	ccaccgcgta	gtagtagtta	tgagtgtttt	attttaaggt	1140
gtgagagaga	gttagattat	caagatttgt	caattttatt	atgtttgttt	gtaataatag	1200
aatcttttac	ttcagttta	gaaaattggg	ggattg			

(2) INFORMATION FOR SEQ ID NO:662:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..104
(D) OTHER INFORMATION: / Ceres Seq. ID 1567594
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

Thr	Gln	Gln	His	Asn	Phe	Thr	Tyr	Leu	Ser	Phe	Phe	Leu	Leu	Lys	Glu
1				5					10					15	
Arg	Arg	Arg	Ser	Pro	Ser	Pro	Lys	Leu	Leu	Thr	Gln	Asp	Val	Asn	Met
				20				25					30		
Gly	His	Leu	Gly	Phe	Leu	Val	Met	Ile	Met	Val	Gly	Val	Met	Ala	Ser
			35				40					45			
Ser	Val	Ser	Val	Tyr	Gly	Gly	Gly	Trp	Ile	Asn	Ala	His	Ala	Thr	Phe
			50				55				60				
Tyr	Gly	Gly	Gly	Asp	Ala	Ser	Gly	Thr	Met	Gly	Gly	Ala	Cys	Gly	Tyr
			65			70				75				80	
Gly	Asn	Leu	Tyr	Ser	Gln	Gly	Tyr	Gly	Thr	Ser	Thr	Ala	Ala	Leu	Ser
					85				90					95	
Thr	Xaa	Ser	Leu	Gln	Gln	Trp	Thr								

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(2) INFORMATION FOR SEQ ID NO:663:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..73
(D) OTHER INFORMATION: / Ceres Seq. ID 1567595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

Met	Gly	His	Leu	Gly	Phe	Leu	Val	Met	Ile	Met	Val	Gly	Val	Met	Ala
1			5						10					15	
Ser	Ser	Val	Ser	Val	Tyr	Gly	Gly	Gly	Trp	Ile	Asn	Ala	His	Ala	Thr
			20					25					30		
Phe	Tyr	Gly	Gly	Gly	Asp	Ala	Ser	Gly	Thr	Met	Gly	Gly	Ala	Cys	Gly
			35					40					45		
Tyr	Gly	Asn	Leu	Tyr	Ser	Gln	Gly	Tyr	Gly	Thr	Ser	Thr	Ala	Ala	Leu
			50			55					60				
Ser	Thr	Xaa	Ser	Leu	Gln	Trp	Thr								
65					70										

(2) INFORMATION FOR SEQ ID NO:664:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..65
(D) OTHER INFORMATION: / Ceres Seq. ID 1567596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

Met	Ile	Met	Val	Gly	Val	Met	Ala	Ser	Ser	Val	Ser	Val	Tyr	Gly	Gly
1				5					10					15	
Gly	Trp	Ile	Asn	Ala	His	Ala	Thr	Phe	Tyr	Gly	Gly	Gly	Asp	Ala	Ser
			20					25					30		
Gly	Thr	Met	Gly	Gly	Ala	Cys	Gly	Tyr	Gly	Asn	Leu	Tyr	Ser	Gln	Gly
			35				40					45			
Tyr	Gly	Thr	Ser	Thr	Ala	Ala	Leu	Ser	Thr	Xaa	Ser	Leu	Gln	Gln	Trp
			50			55					60				
Thr															
65															

(2) INFORMATION FOR SEQ ID NO:665:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 606 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..606
(D) OTHER INFORMATION: / Ceres Seq. ID 1567605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

cagttccacg	gaacacatggt	ggaaggaagt	ttctttgaag	acttgaacat	cccaaacaga	60
gcaaacaca	acaacagcag	caacaatcaa	acgttttttc	aaggggaacaa	caacaacaac	120
aatgtgttta	agttcgacac	tcgagatcac	aacaactttg	aagctgcaca	taacaacaac	180
aataacagta	gcggcaacag	gttcacagctt	gtgttttgatt	ccacaccggt	cgacatggcg	240

tcattcgatt acagagatga tatgtcgtatg ccaggagtag taggaacgat ggatggaatg	300
cagcagaagc agcaagatgt atccatatgg ttctaaagtc ttggtagtag atttcattctt	360
ctcttatttt tatcttttgg ttctttacat tcaactcaacc atgtaatat ttctcctggg	420
tctctctgtc tctatcgtctt gttatgatgt gtctgtaaga gtctctaaaa actctctgtt	480
actgtgtgtc ttgtctcggg cttggtgaat ctctctgtca tcatcagctt ttagttaacac	540
acccgacttg gggatgaacg aacactaaat gtaagtgttc ataataaaa tatatttgca	600

Agctcc

(2) INFORMATION FOR SEQ ID NO:666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

Gln	Phe	Pro	Gly	Asn	Met	Val	Glu	Gly	Ser	Phe	Phe	Glu	Asp	Leu	Asn
1			5						10				15		
Ile	Pro	Asn	Arg	Ala	Asn	Asn	Asn	Asn	Ser	Ser	Asn	Asn	Gln	Thr	Phe
			20					25					30		
Phe	Gln	Gly	Asn	Asn	Asn	Asn	Asn	Val	Phe	Lys	Phe	Asp	Thr	Ala	
		35					40				45				
Asp	His	Asn	Asn	Phe	Glu	Ala	Ala	His	Asn	Asn	Asn	Asn	Asn	Ser	Ser
		50				55					60				
Gly	Asn	Arg	Phe	Gln	Leu	Val	Phe	Asp	Ser	Thr	Pro	Phe	Asp	Met	Ala
		65			70				75					80	
Ser	Phe	Asp	Tyr	Arg	Asp	Asp	Met	Ser	Met	Pro	Gly	Val	Val	Gly	Thr
			85					90					95		
Met	Asp	Gly	Met	Gln	Gln	Lys	Gln	Gln	Asp	Val	Ser	Ile	Trp	Phe	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

Met	Val	Glu	Gly	Ser	Phe	Phe	Glu	Asp	Leu	Asn	Ile	Pro	Asn	Arg	Ala
1			5						10					15	
Asn	Asn	Asn	Asn	Ser	Ser	Asn	Asn	Gln	Thr	Phe	Phe	Gln	Gly	Asn	Asn
			20					25					30		
Asn	Asn	Asn	Asn	Val	Phe	Lys	Phe	Asp	Thr	Ala	Asp	His	Asn	Asn	Phe
		35				40					45				
Glu	Ala	Ala	His	Asn	Asn	Asn	Asn	Asn	Ser	Ser	Gly	Asn	Arg	Phe	Gln
		50				55					60				
Leu	Val	Phe	Asp	Ser	Thr	Pro	Phe	Asp	Met	Ala	Ser	Phe	Asp	Tyr	Arg
		65			70				75					80	
Asp	Asp	Met	Ser	Met	Pro	Gly	Val	Val	Gly	Thr	Met	Asp	Gly	Met	Gln
			85						90				95		
Gln	Lys	Gln	Gln	Asp	Val	Ser	Ile	Trp	Phe						
			100					105							

(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1448 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1448

(D) OTHER INFORMATION: / Ceres Seq. ID 1567608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

```
aaaaagatgg  tgcacttcag  atgcttgcca  caaatattga  gtatgatgag  cataaaggac  60
gcattgctat  tggacagacta  cagcagggg  tactgcgcaa  aggaatggat  gtcagggtgt  120
gcactttcga  agattcctgt  agattttcaa  gagtttagta  gctttttgta  tatgagaaat  180
tctacagagt  acctactgat  tcaagtgaag  ctggagatat  ttgcgctgta  tgtggcatag  240
acaacattca  gattggggag  actattgctg  ataaagtaca  tgggaagcct  ctacctacaa  300
tcaaagttag  agagccaact  gtgaaaatgt  ccttctctgt  aaacacctct  ccattttctg  360
tcctgtgagg  gaagtattga  acaagcagga  acttacgaga  tcgttttaac  ctggaacttg  420
aaagaaatct  agctatgaaa  gtggaagatg  gtgagacagc  agacacattc  attgttagtg  480
ccgtggtaca  ttacacatta  ccattcctgat  agaaaaatg  cgaagagaag  gatattgaatt  540
tatggttgcc  cccccgaag  ttatcaacaa  aagggttaac  gataaattgc  tggagccata  600
tgagatagca  actgttgaag  taccagagcg  tcacatgggg  cctgttgttg  aacttcttgg  660
caaaaggcgt  ggacagatgt  ttgatatgca  ggggtgttgg  tcggaaggaa  caactttctt  720
gcggtacaaa  atccccacac  gtggacttct  tggattgagg  aacgcaattt  taacagcttc  780
tcgctggaca  cgtatcctta  acactgtatt  tgacagttta  tggaccttgg  cgcggtgata  840
ttagcccgag  cgatctaggt  tcgctggttg  cctttgaaga  tggaaacata  acatcatatg  900
ccctggccgg  tcgcgaggag  agagggcaca  tgtttgttag  ttctggagtg  gatgtataca  960
aaggctcagat  agttgggatc  caccGagaga  cccggcgact  tgggtcttaa  tatctgcgaag  1020
aagaaggcag  cgacaacaac  aagatccaac  aaagatgtaa  cagtgattct  tgacactccc  1080
ttaacatata  gtctggacga  ctgcatcgaa  tacattgaag  aggatgagtt  ggtggaggtt  1140
acaccttcta  gtattaggat  gtgcaagaat  cagaaaatgg  caagaaaagg  caggcagtaa  1200
aacccttttt  tgcaagctgg  gtttggagga  aattgaagaa  agctctctac  taaaaaaaaa  1260
gaaagctagt  ttctagtgtt  atttatagcg  ttgtttgatt  gttatacata  gctttattct  1320
tatagcaaa  ggtgagtcct  gatgttatcc  aattaatgtt  tttttggaat  atctccatgc  1380
cctttgatca  tctgatactt  aaagctgtac  aactctgaa  gttgtgcact  agcagatatt  1440
aaagtgtg
```

(2) INFORMATION FOR SEQ ID NO:669:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..168

(D) OTHER INFORMATION: / Ceres Seq. ID 1567609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

```
Lys Asp Gly Ala Leu Gln Met Leu Ala Thr Asn Ile Glu Tyr Asp Glu
1      5      10      15
His Lys Gly Arg Ile Ala Ile Gly Arg Leu His Ala Gly Val Leu Arg
20      25      30
Lys Gly Met Asp Val Arg Val Cys Thr Ser Glu Asp Ser Cys Arg Phe
35      40      45
Ala Arg Val Ser Glu Leu Phe Val Tyr Glu Lys Phe Tyr Arg Val Pro
50      55      60
Thr Asp Ser Val Glu Ala Gly Asp Ile Cys Ala Val Cys Gly Ile Asp
65      70      75      80
Asn Ile Gln Ile Gly Glu Thr Ile Ala Asp Lys Val His Gly Lys Pro
85      90      95
Leu Pro Thr Ile Lys Val Glu Glu Pro Thr Val Lys Met Ser Phe Ser
100     105     110
```

Val Asn Thr Ser Pro Phe Ser Gly Arg Glu Gly Lys Tyr Val Thr Ser
115 120 125
Arg Asn Leu Arg Asp Arg Leu Asn Arg Glu Leu Glu Arg Asn Leu Ala
130 135 140
Met Lys Val Glu Asp Gly Glu Thr Ala Asp Thr Phe Ile Val Ser Ala
145 150 155 160
Val Val His Tyr Thr Leu Pro Ser
165

(2) INFORMATION FOR SEQ ID NO:670:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..162
(D) OTHER INFORMATION: / Ceres Seq. ID 1567610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

Met Leu Ala Thr Asn Ile Glu Tyr Asp Glu His Lys Gly Arg Ile Ala
1 5 10 15
Ile Gly Arg Leu His Ala Gly Val Leu Arg Lys Gly Met Asp Val Arg
20 25 30
Val Cys Thr Ser Glu Asp Ser Cys Arg Phe Ala Arg Val Ser Glu Leu
35 40 45
Phe Val Tyr Glu Lys Phe Tyr Arg Val Pro Thr Asp Ser Val Glu Ala
50 55 60
Gly Asp Ile Cys Ala Val Cys Gly Ile Asp Asn Ile Gln Ile Gly Glu
65 70 75 80
Thr Ile Ala Asp Lys Val His Gly Lys Pro Leu Pro Thr Ile Lys Val
85 90 95
Glu Glu Pro Thr Val Lys Met Ser Phe Ser Val Asn Thr Ser Pro Phe
100 105 110
Ser Gly Arg Glu Gly Lys Tyr Val Thr Ser Arg Asn Leu Arg Asp Arg
115 120 125
Leu Asn Arg Glu Leu Glu Arg Asn Leu Ala Met Lys Val Glu Asp Gly
130 135 140
Glu Thr Ala Asp Thr Phe Ile Val Ser Ala Val His Tyr Thr Leu
145 150 155 160
Pro Ser

(2) INFORMATION FOR SEQ ID NO:671:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..134
(D) OTHER INFORMATION: / Ceres Seq. ID 1567611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

Met Asp Val Arg Val Cys Thr Ser Glu Asp Ser Cys Arg Phe Ala Arg
1 5 10 15
Val Ser Glu Leu Phe Val Tyr Glu Lys Phe Tyr Arg Val Pro Thr Asp
20 25 30
Ser Val Glu Ala Gly Asp Ile Cys Ala Val Cys Gly Ile Asp Asn Ile
35 40 45
Gln Ile Gly Glu Thr Ile Ala Asp Lys Val His Gly Lys Pro Leu Pro

(2) INFORMATION FOR SEO ID NO:672:

(A) LENGTH: 1143 base pa

- (ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

(2) INFORMATION FOR SEQ ID NO:673:

(A) LENGTH: 327 amino ac

- (ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

Lys	Met	Asp	Gln	Ala	Lys	Gly	Lys	Val	Cys	Val	Thr	Gly	Ala	Ser	Gly
1			5						10					15	
Phe	Leu	Ala	Ser	Trp	Leu	Val	Lys	Arg	Leu	Leu	Leu	Glu	Gly	Tyr	Glu
		20						25					30		
Val	Ile	Gly	Thr	Val	Arg	Asp	Pro	Gly	Asn	Glu	Lys	Lys	Leu	Ala	His
	35					40						45			

```

Leu Trp Lys Leu Glu Gly Ala Lys Glu Arg Leu Arg Leu Val Lys Ala
50 55 60
Asp Leu Met Glu Glu Gly Ser Phe Asp Asn Ala Ile Met Gly Cys Gln
65 70 75 80
Gly Val Phe His Thr Ala Ser Pro Val Leu Lys Pro Thr Ser Asn Pro
85 90 95
Glu Glu Glu Ile Leu Arg Pro Ala Ile Glu Gly Thr Leu Asn Val Leu
100 105 110
Arg Ser Cys Arg Lys Asn Pro Ser Leu Lys Arg Val Val Leu Thr Ser
115 120 125
Ser Ser Ser Thr Val Arg Ile Arg Asp Asp Phe Asp Pro Lys Ile Pro
130 135 140
Leu Asp Glu Ser Ile Trp Thr Ser Val Glu Leu Cys Lys Arg Phe Gln
145 150 155 160
Val Trp Tyr Ala Leu Ser Lys Thr Leu Ala Glu Gln Ala Ala Trp Lys
165 170 175
Phe Ser Glu Glu Asn Gly Ile Asp Leu Val Thr Val Leu Pro Ser Phe
180 185 190
Leu Val Gly Pro Ser Leu Pro Pro Asp Leu Cys Ser Thr Ala Ser Asp
195 200 205
Val Leu Gly Leu Leu Lys Gly Glu Thr Glu Lys Phe Gln Trp His Gly
210 215 220
Gln Met Gly Tyr Val His Ile Asp Asp Val Ala Arg Thr His Ile Val
225 230 235 240
Val Phe Glu His Glu Ala Ala Gln Gly Arg Tyr Ile Cys Ser Ser Asn
245 250 255
Val Ile Ser Leu Glu Glu Leu Val Ser Phe Leu Ser Ala Arg Tyr Pro
260 265 270
Ser Leu Pro Ile Pro Lys Arg Phe Glu Lys Leu Asn Arg Leu His Tyr
275 280 285
Asp Phe Asp Thr Ser Lys Ile Gln Ser Leu Gly Leu Lys Phe Lys Ser
290 295 300
Leu Glu Glu Met Phe Asp Asp Cys Ile Ala Ser Leu Val Glu Gln Gly
305 310 315 320
Tyr Leu Ser Thr Val Leu Pro
325

```

(2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..326

- (D) OTHER INFORMATION: / Ceres Seq. ID 1567624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

```

Met Asp Gln Ala Lys Gly Lys Val Cys Val Thr Gly Ala Ser Gly Phe
1 5 10 15
Leu Ala Ser Trp Leu Val Lys Arg Leu Leu Leu Glu Gly Tyr Glu Val
20 25 30
Ile Gly Thr Val Arg Asp Pro Gly Asn Glu Lys Lys Leu Ala His Leu
35 40 45
Trp Lys Leu Glu Gly Ala Lys Glu Arg Leu Arg Leu Val Lys Ala Asp
50 55 60
Leu Met Glu Glu Gly Ser Phe Asp Asn Ala Ile Met Gly Cys Gln Gly
65 70 75 80
Val Phe His Thr Ala Ser Pro Val Leu Lys Pro Thr Ser Asn Pro Glu
85 90 95
Glu Glu Ile Leu Arg Pro Ala Ile Glu Gly Thr Leu Asn Val Leu Arg

```

(2) INFORMATION FOR SEQ ID NO:675:

(A) LENGTH: 261 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..261

(D) OTHER INFORMATION: / Ceres Seq. ID 1567625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

Met	Glu	Glu	Gly	Ser	Phe	Asp	Asn	Ala	Ile	Met	Gly	Cys	Gln	Gly	Val
1				5					10				15		
Phe	His	Thr	Ala	Ser	Pro	Val	Leu	Lys	Pro	Thr	Ser	Asn	Pro	Glu	Glu
			20					25				30			
Glu	Ile	Leu	Arg	Pro	Ala	Ile	Glu	Gly	Thr	Leu	Asn	Val	Leu	Arg	Ser
		35				40					45				
Cys	Arg	Lys	Asn	Pro	Ser	Leu	Lys	Arg	Val	Val	Leu	Thr	Ser	Ser	Ser
	50					55				60					
Ser	Thr	Val	Arg	Ile	Arg	Asp	Asp	Phe	Asp	Pro	Lys	Ile	Pro	Leu	Asp
65				70						75				80	
Glu	Ser	Ile	Trp	Thr	Ser	Val	Glu	Leu	Cys	Lys	Arg	Phe	Gln	Val	Trp
			85					90					95		
Tyr	Ala	Leu	Ser	Lys	Thr	Leu	Ala	Glu	Gln	Ala	Ala	Trp	Lys	Phe	Ser
			100					105					110		
Glu	Glu	Asn	Gly	Ile	Asp	Leu	Val	Thr	Val	Leu	Pro	Ser	Phe	Leu	Val
		115				120					125				
Gly	Pro	Ser	Leu	Pro	Pro	Asp	Leu	Cys	Ser	Thr	Ala	Ser	Asp	Val	Leu
	130					135					140				
Gly	Leu	Leu	Lys	Gly	Glu	Thr	Glu	Lys	Phe	Gln	Trp	His	Gly	Gln	Met
145					150					155				160	

Gly	Tyr	Val	His	Ile	Asp	Asp	Val	Ala	Arg	Thr	His	Ile	Val	Val	Phe
				165					170					175	
Glu	His	Glu	Ala	Ala	Gln	Gly	Arg	Tyr	Ile	Cys	Ser	Ser	Asn	Val	Ile
			180				185						190		
Ser	Leu	Glu	Glu	Leu	Val	Ser	Phe	Leu	Ser	Ala	Arg	Tyr	Pro	Ser	Leu
	195						200					205			
Pro	Ile	Pro	Lys	Arg	Phe	Glu	Lys	Leu	Asn	Arg	Leu	His	Tyr	Asp	Phe
	210					215					220				
Asp	Thr	Ser	Lys	Ile	Gln	Ser	Leu	Gly	Leu	Lys	Phe	Lys	Ser	Leu	Glu
	225				230				235					240	
Glu	Met	Phe	Asp	Asp	Cys	Ile	Ala	Ser	Leu	Val	Glu	Gln	Gly	Tyr	Leu
			245					250						255	
Ser	Thr	Val	Leu	Pro											
			260												

(2) INFORMATION FOR SEQ ID NO:676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1160

(D) OTHER INFORMATION: / Ceres Seq. ID 1567629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

aaagtggagc	gacgtgcgtc	tgcttcgtct	cattacaaaag	cagaagaaac	acaaacagag	60
tcagagatct	taagagttaa	agactaatcc	caacaatggc	gtctctcaaa	gtcccaagca	120
atgttctctc	tcccgaaagt	gacgccgagc	aaactccaaa	ggctttttca	ggatggggta	180
ccaacgagaa	gctgatacata	tcaataactag	ctcacaggaa	cgcagcacaa	cgcagcttga	240
tcocgacgct	ttatgcagct	acotacaagt	aggatcttct	caaagcatta	gacaaagagc	300
ttttctagcga	ctttgagaga	gctgtgatgt	tgtggactct	tgatccacca	gagagagatg	360
cttattttggc	taaagaatcc	accaagatgt	tcaccaagaa	caattggggtt	cttgttgaaa	420
tcgcttgcac	aaggcctgct	cttgagotta	tcaaggtcaa	gcaagcttac	caagctcgat	480
acaagaaatc	aatcgaggaa	gatgtcgctc	aacacacatc	tggtgacott	cgtaagctct	540
tgcttctctc	tgtgagcact	ttcaggatgt	aaggagatga	tgtgaacatg	atgcttgcaa	600
gatctgaagc	taagatactt	cacgagaagg	tctcagagaa	atctctacgt	gacgatgact	660
tcacatcaga	attgacaaca	agaagcaaa	cacagctcgg	tgcaaacactc	aaccactaca	720
acaacgagta	tggaaacgct	attaacaaga	acttgaagga	agagtcggac	gacaatgact	780
acatgaaact	actaagagct	gtaatcacat	gtttgacata	cctcgagaag	cattttgaga	840
aggttctctc	tctatcaatc	aacaaaatgg	gaacagacga	atggggacta	acccgagctc	900
tgactacacg	aactgaaagt	gacatggaac	gcacaaaga	ggaatatcag	cgaagaaca	960
gcattctctt	ggaccgtGct	atcgccaagg	acacttctgg	tgactatgag	gacatgcttg	1020
ttgctcttct	cggacatggc	gatgcttgaa	actgtttcaa	cttctcgagt	cctctcttct	1080
cttaactgat	ggtttgtttt	aaataaaaa	gttgtgaaac	tggttctgca	actatttatc	1140
aatgatcggt	tgagtgtgtc					

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..317

(D) OTHER INFORMATION: / Ceres Seq. ID 1567630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

Met	Ala	Ser	Leu	Lys	Val	Pro	Ser	Asn	Val	Pro	Leu	Pro	Glu	Asp	Asp
1			5								10			15	
Ala	Glu	Gln	Leu	His	Lys	Ala	Phe	Ser	Gly	Trp	Gly	Thr	Asn	Glu	Lys

20	25	30
Leu Ile Ile Ser Ile Leu Ala His Arg Asn Ala Ala Gln Arg Ser Leu		
35	40	45
Ile Arg Ser Val Tyr Ala Ala Thr Tyr Asn Glu Asp Leu Leu Lys Ala		
50	55	60
Leu Asp Lys Glu Leu Ser Ser Asp Phe Glu Arg Ala Val Met Leu Trp		
65	70	75
Thr Leu Asp Pro Pro Glu Arg Asp Ala Tyr Leu Ala Lys Glu Ser Thr		
85	90	95
Lys Met Phe Thr Lys Asn Asn Trp Val Leu Val Glu Ile Ala Cys Thr		
100	105	110
Arg Pro Ala Leu Glu Leu Ile Lys Val Lys Gln Ala Tyr Gln Ala Arg		
115	120	125
Tyr Lys Lys Ser Ile Glu Glu Asp Val Ala Gln His Thr Ser Gly Asp		
130	135	140
Leu Arg Lys Leu Leu Leu Pro Leu Val Ser Thr Phe Arg Tyr Glu Gly		
145	150	155
Asp Asp Val Asn Met Met Leu Ala Arg Ser Glu Ala Lys Ile Leu His		
165	170	175
Glu Lys Val Ser Glu Lys Ser Tyr Ser Asp Asp Phe Ile Arg Ile		
180	185	190
Leu Thr Thr Arg Ser Lys Ala Gln Leu Gly Ala Thr Leu Asn His Tyr		
195	200	205
Asn Asn Glu Tyr Gly Asn Ala Ile Asn Lys Asn Leu Lys Glu Glu Ser		
210	215	220
Asp Asp Asn Asp Tyr Met Lys Leu Leu Arg Ala Val Ile Thr Cys Leu		
225	230	235
Thr Tyr Pro Glu Lys His Phe Glu Lys Val Leu Arg Leu Ser Ile Asn		
245	250	255
Lys Met Gly Thr Asp Glu Trp Gly Leu Thr Arg Val Val Thr Thr Arg		
260	265	270
Thr Glu Val Asp Met Glu Arg Ile Lys Glu Glu Tyr Gln Arg Arg Asn		
275	280	285
Ser Ile Pro Leu Asp Arg Ala Ile Ala Lys Asp Thr Ser Gly Asp Tyr		
290	295	300
Glu Asp Met Leu Val Ala Leu Leu Gly His Gly Asp Ala		
305	310	315

(2) INFORMATION FOR SEQ ID NO:678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..240

(D) OTHER INFORMATION: / Ceres Seq. ID 1567631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

Met Leu Trp Thr Leu Asp Pro Pro Glu Arg Asp Ala Tyr Leu Ala Lys		
1	5	10
Glu Ser Thr Lys Met Phe Thr Lys Asn Asn Trp Val Leu Val Glu Ile		
20	25	30
Ala Cys Thr Arg Pro Ala Leu Glu Leu Ile Lys Val Lys Gln Ala Tyr		
35	40	45
Gln Ala Arg Tyr Lys Lys Ser Ile Glu Glu Asp Val Ala Gln His Thr		
50	55	60
Ser Gly Asp Leu Arg Lys Leu Leu Leu Pro Leu Val Ser Thr Phe Arg		
65	70	75
Tyr Glu Gly Asp Asp Val Asn Met Met Leu Ala Arg Ser Glu Ala Lys		
85	90	95

Ile	Leu	His	Glu	Lys	Val	Ser	Glu	Lys	Ser	Tyr	Ser	Asp	Asp	Asp	Phe
	100							105					110		
Ile	Arg	Ile	Leu	Thr	Thr	Arg	Ser	Lys	Ala	Gln	Leu	Gly	Ala	Thr	Leu
	115						120					125			
Asn	His	Tyr	Asn	Asn	Glu	Tyr	Gly	Asn	Ala	Ile	Asn	Lys	Asn	Leu	Lys
	130					135					140				
Glu	Glu	Ser	Asp	Asp	Asn	Asp	Tyr	Met	Lys	Leu	Leu	Arg	Ala	Val	Ile
	145				150				155					160	
Thr	Cys	Leu	Thr	Tyr	Pro	Glu	Lys	His	Phe	Glu	Lys	Val	Leu	Arg	Leu
			165						170					175	
Ser	Ile	Asn	Lys	Met	Gly	Thr	Asp	Glu	Trp	Gly	Leu	Thr	Arg	Val	Val
			180					185					190		
Thr	Thr	Arg	Thr	Glu	Val	Asp	Met	Glu	Arg	Ile	Lys	Glu	Glu	Tyr	Gln
		195					200					205			
Arg	Arg	Asn	Ser	Ile	Pro	Leu	Asp	Arg	Ala	Ile	Ala	Lys	Asp	Thr	Ser
	210					215					220				
Gly	Asp	Tyr	Glu	Asp	Met	Leu	Val	Ala	Leu	Leu	Gly	His	Gly	Asp	Ala
	225				230					235				240	

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..220

(D) OTHER INFORMATION: / Ceres Seq. ID 1567632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

Met	Phe	Thr	Lys	Asn	Asn	Trp	Val	Leu	Val	Glu	Ile	Ala	Cys	Thr	Arg
1			5						10				15		
Pro	Ala	Leu	Glu	Leu	Ile	Lys	Val	Lys	Gln	Ala	Tyr	Gln	Ala	Arg	Tyr
		20					25					30			
Lys	Lys	Ser	Ile	Glu	Glu	Asp	Val	Ala	Gln	His	Thr	Ser	Gly	Asp	Leu
		35				40					45				
Arg	Lys	Leu	Leu	Leu	Pro	Leu	Val	Ser	Thr	Phe	Arg	Tyr	Glu	Gly	Asp
	50				55				60						
Asp	Val	Asn	Met	Met	Leu	Ala	Arg	Ser	Glu	Ala	Lys	Ile	Leu	His	Glu
	65			70				75					80		
Lys	Val	Ser	Glu	Lys	Ser	Tyr	Ser	Asp	Asp	Asp	Phe	Ile	Arg	Ile	Leu
		85					90					95			
Thr	Thr	Arg	Ser	Lys	Ala	Gln	Leu	Gly	Ala	Thr	Leu	Asn	His	Tyr	Asn
		100					105					110			
Asn	Glu	Tyr	Gly	Asn	Ala	Ile	Asn	Lys	Asn	Leu	Lys	Glu	Glu	Ser	Asp
		115				120					125				
Asp	Asn	Asp	Tyr	Met	Lys	Leu	Leu	Arg	Ala	Val	Ile	Thr	Cys	Leu	Thr
	130					135					140				
Tyr	Pro	Glu	Lys	His	Phe	Glu	Lys	Val	Leu	Arg	Leu	Ser	Ile	Asn	Lys
	145				150				155					160	
Met	Gly	Thr	Asp	Glu	Trp	Gly	Leu	Thr	Arg	Val	Val	Thr	Thr	Arg	Thr
			165					170					175		
Glu	Val	Asp	Met	Glu	Arg	Ile	Lys	Glu	Glu	Tyr	Gln	Arg	Arg	Asn	Ser
		180					185					190			
Ile	Pro	Leu	Asp	Arg	Ala	Ile	Ala	Lys	Asp	Thr	Ser	Gly	Asp	Tyr	Glu
		195				200						205			
Asp	Met	Leu	Val	Ala	Leu	Leu	Gly	His	Gly	Asp	Ala				
	210				215						220				

(2) INFORMATION FOR SEQ ID NO:680:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 628 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..628
(D) OTHER INFORMATION: / Ceres Seq. ID 1567661
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:
ttgtctcttt ctcaaacata tctcaactta ttgtttgaat ataaaaagag atatcaaaaa 60
gaagagaga ccaaaaaaca acaaaaatc tctaataaaa atggcttcca aagctatctt 120
cttctctttt ttgtctgtct cgcgcgtgtg ttgtctttct ctggcaggtt tgcgcgcgcg 180
tgatgctgac gacttcgac gtttccagat tcaaggatca gtttactgtg acaactgtccg 240
tgtccaattc gttaccgcgc tcagcaaat cctcgaaggc gcgaaaagta agttggagtg 300
caggagcaga acaaacggaa ccataacatt gaccaaaagaa gctgttaccg acaaaacagg 360
aagctacaaa atggaagtaa ccggtgacca cgaggaagaa gttttgcgagc ttgttttgg 420
ccaatcacca gacagtgggt gcagtgatgt cagcacagag gcttacttac gtaacgcgcgc 480
taagatcagt ttaacggcga atgacggaat cgtctccac gagacacgta ttgttaacc 540
ctctcggtttc atggttcaga ctcMattggc tgattgtcct gctgccttca aggagcttgg 600
(2) INFORMATION FOR SEQ ID NO:681:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..207
(D) OTHER INFORMATION: / Ceres Seq. ID 1567662
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:
Cys Pro Leu Leu Lys His Ile Ser Thr Tyr Cys Leu Asn Ile Lys Arg
1 5 10
Asp Ile Lys Lys Lys Arg Arg Pro Lys Thr Lys Gln Lys Ser Leu Ile
20 25 30
Lys Met Ala Ser Lys Ala Ile Phe Phe Ser Phe Phe Val Val Ser Ala
35 40 45
Val Cys Leu Ser Ser Leu Ala Gly Phe Ala Ala Ala Asp Ala Asp Asp
50 55 60
Phe Asp Arg Phe Gln Ile Gln Gly Ser Val Tyr Cys Asp Thr Cys Arg
65 70 75 80
Val Gln Phe Val Thr Arg Leu Ser Lys Phe Leu Glu Gly Ala Lys Val
85 90 95
Lys Leu Glu Cys Arg Ser Arg Thr Asn Gly Thr Ile Thr Leu Thr Lys
100 105 110
Glu Ala Val Thr Asp Lys Thr Gly Ser Tyr Lys Met Glu Val Thr Gly
115 120 125
Asp His Glu Glu Glu Val Cys Glu Leu Val Leu Val Gln Ser Pro Asp
130 135 140
Ser Gly Cys Ser Asp Val Ser Thr Glu Ala Tyr Leu Arg Asn Ala Ala
145 150 155 160
Lys Ile Ser Leu Thr Ala Asn Asp Gly Ile Val Ser His Glu Thr Arg
165 170 175
Ile Val Asn Pro Leu Gly Phe Met Val Gln Thr Xaa Leu Ala Asp Cys
180 185 190
Pro Ala Ala Phe Lys Glu Leu Gly Ile Val Pro Asp Val Thr Phe
195 200 205
(2) INFORMATION FOR SEQ ID NO:682:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..174
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567663
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

Met	Ala	Ser	Lys	Ala	Ile	Phe	Phe	Ser	Phe	Val	Val	Ser	Ala	Val
1			5					10				15		
Cys	Leu	Ser	Ser	Leu	Ala	Gly	Phe	Ala	Ala	Asp	Ala	Asp	Asp	Phe
			20				25					30		
Asp	Arg	Phe	Gln	Ile	Gln	Gly	Ser	Val	Tyr	Cys	Asp	Thr	Cys	Arg
			35				40					45		
Gln	Phe	Val	Thr	Arg	Leu	Ser	Lys	Phe	Leu	Glu	Gly	Ala	Lys	Val
			50				55					60		
Leu	Glu	Cys	Arg	Ser	Arg	Thr	Asn	Gly	Thr	Ile	Thr	Leu	Thr	Lys
			65				70			75				80
Ala	Val	Thr	Asp	Lys	Thr	Gly	Ser	Tyr	Lys	Met	Glu	Val	Thr	Gly
				85					90					95
His	Glu	Glu	Glu	Val	Cys	Glu	Leu	Val	Leu	Val	Gln	Ser	Pro	Asp
				100					105				110	
Gly	Cys	Ser	Asp	Val	Ser	Thr	Glu	Ala	Tyr	Leu	Arg	Asn	Ala	Ala
				115				120					125	
Ile	Ser	Leu	Thr	Ala	Asn	Asp	Gly	Ile	Val	Ser	His	Glu	Thr	Arg
				130			135					140		
Val	Asn	Pro	Leu	Gly	Phe	Met	Val	Gln	Thr	Xaa	Leu	Ala	Asp	Cys
					150					155				160
Ala	Ala	Phe	Lys	Glu	Leu	Gly	Ile	Val	Pro	Asp	Val	Thr	Phe	
					165					170				

(2) INFORMATION FOR SEQ ID NO:683:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 569 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..569
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567674
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

aaaatctcga	aacctctaatt	attctaagat	tctaatttgt	gaagtttgtg	aggttttagg	60
gatgggttac	aatttctaca	tgagagtgtg	tgaggttgtt	gatgatgctt	caacggatgc	120
aatcatatcg	tggagcgaaa	gcaacaacag	tttcattatc	tggaaagtgt	gagagtttta	180
cagaaggatt	ctgcctaaat	atgtagactt	gggcacaaac	ctctcacggt	ttttctccaa	240
ccttcgttct	catgggttca	aaatagttaa	aggaagaact	ggagtattgg	aatttggaac	300
tgaagatttt	gtcagagata	aactggagct	tatgaagaag	atggttagcg	ataaacgtaa	360
agcaaggaaa	gcagctaaat	ccaaagcaag	gaaagctaga	gttcaagtcg	agtttctctt	420
ccaacacttg	caaatttgat	ccattaaatc	agttctcttt	tttatgtata	tattcatctc	480
caagtagatc	aagtcttaaga	acttttccaat	agtatgtatc	tctctttata	ggaaccCtct	540
tttatgctct	agttcttgat	Tcttctctc				

(2) INFORMATION FOR SEQ ID NO:684:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1567675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

Lys	Ser	Arg	Asn	Pro	Asn	Tyr	Ser	Lys	Ile	Leu	Ile	Cys	Glu	Val	Cys
1			5					10						15	
Glu	Val	Leu	Gly	Met	Gly	Tyr	Asn	Phe	Tyr	Met	Arg	Val	Tyr	Glu	Val
			20					25					30		
Val	Asp	Asp	Ala	Ser	Thr	Asp	Ala	Ile	Ser	Trp	Ser	Glu	Ser	Asn	
		35					40				45				
Asn	Ser	Phe	Ile	Ile	Trp	Asn	Val	Gly	Glu	Phe	Tyr	Arg	Arg	Ile	Leu
	50					55				60					
Pro	Lys	Tyr	Val	Asp	Leu	Gly	Thr	Asn	Leu	Ser	Arg	Phe	Phe	Ser	Asn
	65				70					75				80	
Leu	Arg	Ser	His	Gly	Phe	Lys	Ile	Val	Lys	Gly	Arg	Thr	Gly	Val	Leu
			85						90					95	
Glu	Phe	Gly	His	Glu	Asp	Phe	Val	Arg	Asp	Lys	Leu	Glu	Leu	Met	Lys
			100					105					110		
Lys	Met	Val	Ser	Asp	Lys	Arg	Lys	Ala	Arg	Lys	Ala	Ala	Lys	Ser	Lys
		115				120						125			
Ala	Arg	Lys	Ala	Arg	Val	Gln	Val	Glu	Phe	Leu	Phe	Gln	His	Leu	Gln
	130					135					140				

Ile
145

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1567676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

Met	Gly	Tyr	Asn	Phe	Tyr	Met	Arg	Val	Tyr	Glu	Val	Asp	Asp	Ala	
1			5					10					15		
Ser	Thr	Asp	Ala	Ile	Ile	Ser	Trp	Ser	Glu	Ser	Asn	Asn	Ser	Phe	Ile
			20					25					30		
Ile	Trp	Asn	Val	Gly	Glu	Phe	Tyr	Arg	Arg	Ile	Leu	Pro	Lys	Tyr	Val
		35					40					45			
Asp	Leu	Gly	Thr	Asn	Leu	Ser	Arg	Phe	Phe	Ser	Asn	Leu	Arg	Ser	His
	50					55				60					
Gly	Phe	Lys	Ile	Val	Lys	Gly	Arg	Thr	Gly	Val	Leu	Glu	Phe	Gly	His
	65				70				75					80	
Glu	Asp	Phe	Val	Arg	Asp	Lys	Leu	Glu	Leu	Met	Lys	Lys	Met	Val	Ser
			85						90					95	
Asp	Lys	Arg	Lys	Ala	Arg	Lys	Ala	Ala	Lys	Ser	Lys	Ala	Arg	Lys	Ala
			100				105						110		
Arg	Val	Gln	Val	Glu	Phe	Leu	Phe	Gln	His	Leu	Gln	Ile			
		115				120									

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1567677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

```
Met Arg Val Tyr Glu Val Val Asp Asp Ala Ser Thr Asp Ala Ile Ile
1      5      10      15
Ser Trp Ser Glu Ser Asn Asn Ser Phe Ile Ile Trp Asn Val Gly Glu
20      25      30
Phe Tyr Arg Arg Ile Leu Pro Lys Tyr Val Asp Leu Gly Thr Asn Leu
35      40      45
Ser Arg Phe Phe Ser Asn Leu Arg Ser His Gly Phe Lys Ile Val Lys
50      55      60
Gly Arg Thr Gly Val Leu Glu Phe Gly His Glu Asp Phe Val Arg Asp
65      70      75      80
Lys Leu Glu Leu Met Lys Lys Met Val Ser Asp Lys Arg Lys Ala Arg
85      90      95
Lys Ala Ala Lys Ser Lys Ala Arg Lys Ala Arg Val Gln Val Glu Phe
100      105      110
Leu Phe Gln His Leu Gln Ile
115
```

(2) INFORMATION FOR SEQ ID NO:687:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1133 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1133

(D) OTHER INFORMATION: / Ceres Seq. ID 1567687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

```
aacagatcaa ggatgaatta gatgtgtttt ccaaggaagc tgtgtctttc gaagccaagc      60
gcatcaaaagg tctaagagca gtgtttggag aagtctaccc cgatcccgtc agagtgggtg      120
caattgggag gaaggttgag gatctcttgg ctgatactga aaacaatgaa tgggtcattgc      180
tttcttcoga gttttgtgga ggaaccacac taacaaacac ccgcgaagcc aaagcatttg      240
ctctctatc ggagaaggga attgctaaag gtattcgtag ggtaactgct gtgactactg      300
aatgtgtctt tgatgcattg aatgcggcgt ccttacttga aagagaagta gaggatgcct      360
ccagagcgga ggggaagtga ttgaaaaaga aagtttctgc ttgaaaaagc cgagttagatg      420
cagcaattat cccagcagct aaaaagcgag atattaggac taagattgct tcgcttcaga      480
atgaagtaag aaaagctcag aaaaaaatag cggaaacaaa cctgaaaaaa tctgtcaaat      540
tagcaacaga ggcagctgag tccgcagcat cagatgggaa gactttctgc ataattccagc      600
tggatgtggg tcttgatgca gcagctgtgc gagaggccgt ttcaaaagtc atgaaaaaga      660
agggatgtgc gataatggtg ttcagcacag atgaaagcac aaacaagcgc gttgtgtgtg      720
caggagtgcc agaaaaatca gaccagtta agccgttaga cgtcactgaa tggttgacaa      780
ctgcatctgg tctctataaa ggaaggtgcg ggaaagggaa aggtgtgtct gcatcaggcg      840
agggaaacga tgctctccaa gtgcaggcgg ctttgatata ggcttcatca ttgcatcaaa      900
tgaagctcaa ctgatttggt cgaggagtta cataatctgt gaggtcagaa taacctctac      960
ttaatttgct ttcatttgta accgttttac acatgtttta agaatctgtt aaatttctct      1020
gttcttggtg tggaaattgt ggtatgacac tcttttagtc aaagtaccac atgctgtgta      1080
taattccttg tgaatatgat tcttcccgct tgcgttgaaa ttggtatttt ttt
```

(2) INFORMATION FOR SEQ ID NO:688:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..303

(D) OTHER INFORMATION: / Ceres Seq. ID 1567688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

Gln	Ile	Lys	Asp	Glu	Leu	Asp	Val	Phe	Ser	Lys	Glu	Ala	Val	Leu	Ser	
1			5						10					15		
Glu	Ala	Lys	Arg	Ile	Lys	Gly	Leu	Arg	Ala	Val	Phe	Gly	Glu	Val	Tyr	
			20					25					30			
Pro	Asp	Pro	Val	Arg	Val	Val	Ser	Ile	Gly	Arg	Lys	Val	Glu	Asp	Leu	
			35				40					45				
Leu	Ala	Asp	Pro	Glu	Asn	Asn	Glu	Trp	Ser	Leu	Leu	Ser	Ser	Glu	Phe	
			50			55					60					
Cys	Gly	Gly	Thr	His	Ile	Thr	Asn	Thr	Arg	Glu	Ala	Lys	Ala	Phe	Ala	
			65		70				75					80		
Leu	Leu	Ser	Glu	Lys	Gly	Ile	Ala	Lys	Gly	Ile	Arg	Arg	Val	Thr	Ala	
			85						90				95			
Val	Thr	Thr	Glu	Cys	Ala	Phe	Asp	Ala	Leu	Asn	Ala	Ala	Ser	Leu	Leu	
			100				105						110			
Glu	Arg	Glu	Val	Glu	Asp	Ala	Ser	Arg	Ala	Glu	Gly	Ser	Ala	Leu	Glu	
			115				120					125				
Lys	Lys	Val	Ser	Ala	Leu	Lys	Ser	Arg	Val	Asp	Ala	Ala	Ile	Ile	Pro	
			130			135					140					
Ala	Ala	Lys	Lys	Ala	Asp	Ile	Arg	Thr	Lys	Ile	Ala	Ser	Leu	Gln	Asn	
			145		150				155					160		
Glu	Val	Arg	Lys	Ala	Gln	Lys	Lys	Ile	Ala	Glu	Gln	Asn	Leu	Lys	Lys	
			165					170					175			
Ser	Val	Lys	Leu	Ala	Thr	Glu	Ala	Ala	Glu	Ser	Ala	Ala	Ser	Asp	Gly	
			180					185					190			
Lys	Thr	Phe	Cys	Ile	Ile	Gln	Leu	Asp	Val	Gly	Leu	Asp	Ala	Ala	Ala	
			195				200					205				
Val	Arg	Glu	Ala	Val	Ser	Lys	Val	Met	Glu	Lys	Lys	Gly	Met	Ser	Ile	
			210			215					220					
Met	Val	Phe	Ser	Thr	Asp	Glu	Ser	Thr	Asn	Lys	Ala	Val	Val	Cys	Ala	
			225			230			235					240		
Gly	Val	Pro	Glu	Lys	Ser	Asp	Gln	Phe	Lys	Pro	Leu	Asp	Val	Thr	Glu	
			245					250					255			
Trp	Leu	Thr	Thr	Ala	Leu	Gly	Pro	Leu	Lys	Gly	Arg	Cys	Gly	Lys	Gly	
			260			265							270			
Lys	Gly	Gly	Leu	Ala	Ser	Gly	Gln	Gly	Thr	Asp	Ala	Ser	Gln	Val	Gln	
			275			280						285				
Ala	Ala	Leu	Asp	Met	Ala	Ser	Ser	Phe	Ala	Ser	Met	Lys	Leu	Asn		
			290			295					300					

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1326 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1326

(D) OTHER INFORMATION: / Ceres Seq. ID 1567700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

aaaaagcact	ctgtgtgcct	ctgc aaatta	acaatttcct	cagaacaatt	acatttcgat	60
tcgattcgat	tctcttatct	tcttgatctc	tggtttgtca	tctgtggtgg	atctccagat	120
gttggttttg	agaattttgt	cgcgagtaac	cgcgaacgcg	ggcatacgct	catctctatc	180
cgccgtcact	cttcgcgcga	ggaatcagac	tcctgttttc	tcgagccggt	ttcactccct	240
agctcacgat	ttctgcgcat	agcttggttc	agctcagatg	tctatgatgg	attcgtttgc	300
actgc aaagg	tccaattttt	cttctctctc	ctcgcttgaa	tcagatgaga	agaagaccga	360
cactgaggcc	tcaaagacaa	gtgaagagaa	acctaagcgt	gaggc aaacc	aaccaggctc	420
tgactctgaa	tctaagatt	ctgtgacaga	tcttgcaaaa	agaaagcgga	aggtgtctaa	480

aggagctgca	tcttcatctt	ctgaatcaga	tctcgagagt	gatgatgatg	aattgtcagc	540
cgatgatttg	gtgaagctcg	tagctgagaa	ggaagagcta	ctgtctcgaga	aggaagaaga	600
gattaagcag	ttgaaagaca	aagttctctg	cacttatgct	gagatggaga	atgtcatgga	660
cagaacaaga	cgtgatgctg	aaaacaccaa	aaagatgccc	gtacagaatt	ttgcaaaagc	720
ccatttggat	gtggcggaata	atcttggaa	agcttctctg	gttgctcaaa	aaagcttctc	780
aaagcttgac	acctcagaag	attctgctgg	agcagctcca	ctattaaaga	ccctttttaga	840
aggagtggag	atgactgaga	aacagctctg	tgaggtattt	aagaaatttg	gtatggagaa	900
gtatgatccg	ataaacgagc	catttgatcc	aaacagacat	aacgcagtgt	tccaagtccc	960
tgatgcttct	aagccagaag	gcacagttgc	tcattgtctg	aagtctggat	acacgctgta	1020
tgaccgagtt	ataagaccag	ctgaggtttg	tgttaccacg	ggaggagaga	accaagaaga	1080
aaagaagaag	tctgatgctt	aagaagaagt	cagctggttt	tcataaaatt	tgtaacgggt	1140
ctatgtttcc	attaacatct	tctcgagtct	tcagatcata	gtthtctttt	gtggttttgt	1200
tTatcattta	gatgaacaag	atctcccata	agttTgctgg	acatggcatt	tgcaagggaa	1260
atctcgcttb	tgtgtctgtt	tTctctatc	tccatgctat	aattgaacga	ggaataatc	1320
atctt						

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..327

(D) OTHER INFORMATION: / Ceres Seq. ID 1567701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

Met	Leu	Val	Leu	Arg	Ile	Leu	Ser	Arg	Val	Thr	Arg	Asn	Ala	Gly	Ile
1			5						10					15	
Arg	Ser	Ser	Leu	Ser	Ala	Val	Thr	Leu	Pro	Ala	Arg	Asn	Gln	Thr	Pro
			20					25					30		
Val	Phe	Ser	Ser	Arg	Phe	His	Ser	Leu	Ala	His	Asp	Phe	Ser	His	Lys
			35				40				45				
Leu	Val	Pro	Ala	Gln	Met	Ser	Met	Met	Asp	Ser	Phe	Ala	Leu	Gln	Arg
			50			55					60				
Phe	Asn	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Glu	Ser	Asp	Glu	Lys	Lys	Thr
			65			70			75					80	
His	Thr	Glu	Ala	Ser	Lys	Thr	Ser	Glu	Glu	Lys	Pro	Thr	Ala	Glu	Ala
			85						90				95		
Asn	Gln	Pro	Gly	Leu	Asp	Ser	Glu	Ser	Lys	Asp	Ser	Val	Thr	Asp	Ser
			100				105						110		
Ala	Lys	Arg	Lys	Arg	Lys	Gly	Ala	Lys	Gly	Ala	Ala	Ser	Ser	Ser	Ser
			115				120				125				
Glu	Ser	Asp	Ser	Glu	Ser	Asp	Asp	Asp	Glu	Leu	Ser	Ala	Asp	Asp	Leu
			130			135					140				
Val	Lys	Leu	Val	Ala	Glu	Lys	Glu	Glu	Leu	Leu	Ser	Glu	Lys	Glu	Glu
			145			150				155				160	
Glu	Ile	Lys	Gln	Leu	Lys	Asp	Lys	Val	Leu	Arg	Thr	Tyr	Ala	Glu	Met
			165						170				175		
Glu	Asn	Val	Met	Asp	Arg	Thr	Arg	Arg	Asp	Ala	Glu	Asn	Thr	Lys	Lys
			180					185					190		
Tyr	Ala	Val	Gln	Asn	Phe	Ala	Lys	Ser	Leu	Leu	Asp	Val	Ala	Asp	Asn
			195				200				205				
Leu	Gly	Arg	Ala	Ser	Ser	Val	Val	Lys	Glu	Ser	Phe	Ser	Lys	Leu	Asp
			210			215					220				
Thr	Ser	Glu	Asp	Ser	Ala	Gly	Ala	Ala	Pro	Leu	Leu	Lys	Thr	Leu	Leu
			225			230				235				240	
Glu	Gly	Val	Glu	Met	Thr	Glu	Lys	Gln	Leu	Ala	Glu	Val	Phe	Lys	Lys
			245					250					255		
Phe	Gly	Met	Glu	Lys	Tyr	Asp	Pro	Ile	Asn	Glu	Pro	Phe	Asp	Pro	Asn
			260					265					270		

Arg His Asn Ala Val Phe Gln Val Pro Asp Ala Ser Lys Pro Glu Gly
275 280 285
Thr Val Ala His Val Leu Lys Ser Gly Tyr Thr Leu Tyr Asp Arg Val
290 295 300
Ile Arg Pro Ala Glu Val Gly Val Thr Gln Gly Gly Glu Asn Gln Glu
305 310 315 320
Glu Lys Lys Glu Ser Asp Ala
325

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..274

(D) OTHER INFORMATION: / Ceres Seq. ID 1567702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

Met Ser Met Met Asp Ser Phe Ala Leu Gln Arg Phe Asn Phe Ser Ser
1 5 10 15
Ser Thr Ser Pro Glu Ser Asp Glu Lys Lys Thr His Thr Glu Ala Ser
20 25 30
Lys Thr Ser Glu Glu Lys Pro Thr Ala Glu Ala Asn Gln Pro Gly Leu
35 40 45
Asp Ser Glu Ser Lys Asp Ser Val Thr Asp Ser Ala Lys Arg Lys Arg
50 55 60
Lys Gly Ala Lys Gly Ala Ala Ser Ser Ser Ser Glu Ser Asp Ser Glu
65 70 75 80
Ser Asp Asp Asp Glu Leu Ser Ala Asp Asp Leu Val Lys Leu Val Ala
85 90 95
Glu Lys Glu Glu Leu Leu Ser Glu Lys Glu Glu Glu Ile Lys Gln Leu
100 105 110
Lys Asp Lys Val Leu Arg Thr Tyr Ala Glu Met Glu Asn Val Met Asp
115 120 125
Arg Thr Arg Arg Asp Ala Glu Asn Thr Lys Lys Tyr Ala Val Gln Asn
130 135 140
Phe Ala Lys Ser Leu Leu Asp Val Ala Asp Asn Leu Gly Arg Ala Ser
145 150 155 160
Ser Val Val Lys Glu Ser Phe Ser Lys Leu Asp Thr Ser Glu Asp Ser
165 170 175
Ala Gly Ala Ala Pro Leu Leu Lys Thr Leu Leu Glu Gly Val Glu Met
180 185 190
Thr Glu Lys Gln Leu Ala Glu Val Phe Lys Lys Phe Gly Met Glu Lys
195 200 205
Tyr Asp Pro Ile Asn Glu Pro Phe Asp Pro Asn Arg His Asn Ala Val
210 215 220
Phe Gln Val Pro Asp Ala Ser Lys Pro Glu Gly Thr Val Ala His Val
225 230 235 240
Leu Lys Ser Gly Tyr Thr Leu Tyr Asp Arg Val Ile Arg Pro Ala Glu
245 250 255
Val Gly Val Thr Gln Gly Gly Glu Asn Gln Glu Glu Lys Lys Glu Ser
260 265 270
Asp Ala

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..272
(D) OTHER INFORMATION: / Ceres Seq. ID 1567703
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

Met	Met	Asp	Ser	Phe	Ala	Leu	Gln	Arg	Phe	Asn	Phe	Ser	Ser	Ser	Thr
1				5						10				15	
Ser	Pro	Glu	Ser	Asp	Glu	Lys	Lys	Thr	His	Thr	Glu	Ala	Ser	Lys	Thr
			20					25					30		
Ser	Glu	Glu	Lys	Pro	Thr	Ala	Glu	Ala	Asn	Gln	Pro	Gly	Leu	Asp	Ser
			35				40					45			
Glu	Ser	Lys	Asp	Ser	Val	Thr	Asp	Ser	Ala	Lys	Arg	Lys	Arg	Lys	Gly
			50			55					60				
Ala	Lys	Gly	Ala	Ala	Ser	Ser	Ser	Ser	Glu	Ser	Asp	Ser	Glu	Ser	Asp
65				70						75				80	
Asp	Asp	Glu	Leu	Ser	Ala	Asp	Asp	Leu	Val	Lys	Leu	Val	Ala	Glu	Lys
			85					90					95		
Glu	Glu	Leu	Leu	Ser	Glu	Lys	Glu	Glu	Glu	Ile	Lys	Gln	Leu	Lys	Asp
			100					105					110		
Lys	Val	Leu	Arg	Thr	Tyr	Ala	Glu	Met	Glu	Asn	Val	Met	Asp	Arg	Thr
			115				120					125			
Arg	Arg	Asp	Ala	Glu	Asn	Thr	Lys	Lys	Tyr	Ala	Val	Gln	Asn	Phe	Ala
			130			135					140				
Lys	Ser	Leu	Leu	Asp	Val	Ala	Asp	Asn	Leu	Gly	Arg	Ala	Ser	Ser	Val
			145			150				155				160	
Val	Lys	Glu	Ser	Phe	Ser	Lys	Leu	Asp	Thr	Ser	Glu	Asp	Ser	Ala	Gly
			165					170					175		
Ala	Ala	Pro	Leu	Leu	Lys	Thr	Leu	Leu	Glu	Gly	Val	Glu	Met	Thr	Glu
			180				185					190			
Lys	Gln	Leu	Ala	Glu	Val	Phe	Lys	Lys	Phe	Gly	Met	Glu	Lys	Tyr	Asp
		195					200				205				
Pro	Ile	Asn	Glu	Pro	Phe	Asp	Pro	Asn	Arg	His	Asn	Ala	Val	Phe	Gln
		210			215					220					
Val	Pro	Asp	Ala	Ser	Lys	Pro	Glu	Gly	Thr	Val	Ala	His	Val	Leu	Lys
			225		230				235					240	
Ser	Gly	Tyr	Thr	Leu	Tyr	Asp	Arg	Val	Ile	Arg	Pro	Ala	Glu	Val	Gly
			245					250					255		
Val	Thr	Gln	Gly	Gly	Glu	Asn	Gln	Glu	Glu	Lys	Lys	Glu	Ser	Asp	Ala
			260				265						270		

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1418 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1418

(D) OTHER INFORMATION: / Ceres Seq. ID 1567704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

ataggaactcg	acaaatagaa	gaagcagatt	cgttgctaac	gaaGtaaagg	attcttaacttt	60
tttagtcttt	gcttttagaa	taacttataa	ctacaagtca	gagagggggc	gagtaaatcg	120
gaaagatgac	ggcgccgatg	atcctgaccg	gaagtgatc	ggcgccggag	agagacgctc	180
ggatggcgca	cactgctatg	gcgtttgttc	agctctttaa	tggtggatgc	catgtgattc	240
ctaaagtatc	tcttaagtgt	ggagtcacac	agcttgtctt	ctgtgtatgc	cgtgatcttc	300
ttgtctctc	tattctcgct	cctcttgctt	acttcgcgca	aagaaagatc	agaactccaa	360

tgaataaaaag	ccttctcttgg	tcattctcttct	ttctggggctt	agcagggggta	tttgggaacc	420
agttgttatt	ttcttatcgtt	cttacatatac	caaataccac	ttatgctgct	ggcattcaac	480
catccatccc	ggcttttccc	ttctcttggg	ctgtcatgat	gggtacagaa	agagtgtaatt	540
tggtgagaat	cgaagggtcaa	actaagggttg	gaggcacact	tggtgtgtgt	atgggtgctg	600
tccttatggt	tgattttcga	ggtccggcct	tgtaggaga	taaagatgca	gactttgcga	660
tgaacaatga	aaatcagtgct	aaagggtcaac	ctgagcctac	tggttggtta	gtctctgggt	720
ttctcgatct	tggaatttgag	caatggcaca	ttggagtttt	atgcttgatt	ggaaactgca	780
tggttatggc	tacttttctt	gccattccagg	cggcactttt	gaagaagtat	ccggcgaattc	840
ttctctgttg	tgcaattatca	tactYcttgg	gcacagtact	aatgtgcaca	acagctttct	900
ttatggtaaa	ggagcccatg	gattgggaagc	taacacaatc	tgaggttctt	gcagttatat	960
atgcaggagt	tctgcataca	gcactaaact	atggactctt	gacttggctc	aataagatta	1020
ttggtcctgc	cttgggtgct	ctctacaatc	ctcttcaacc	cgtcgtcatca	gctttcctat	1080
cgagatactt	tctcgttagc	cccatttato	tcggaagcgt	tggtgggtgga	ttcttcatca	1140
ttctaggaact	ctatatggtc	acttgggcac	cgttttagaga	gcgaaaaaca	gcggtttccg	1200
ggatttggat	tgccgccccat	gggtctaaaaa	cctcagagcc	cttgatatatt	aatgggacag	1260
ttaacagact	aggacagtgg	ttttctggat	taaccagttc	ctctgtgaaa	cttcgcagact	1320
aaaaagatac	caaaaagtta	agattccagac	gagatcccat	tttacaacag	ctataacttt	1380
tggttaactt	tcactctctta	ttaatatctt	cttcgatt			

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..398

(D) OTHER INFORMATION: / Ceres Seq. ID 1567705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

Met	Thr	Ala	Pro	Met	Ile	Leu	Thr	Gly	Ser	Gly	Ser	Ala	Ala	Glu	Arg
1			5					10						15	
Asp	Ala	Arg	Met	Ala	His	Thr	Ala	Met	Ala	Phe	Val	Gln	Leu	Phe	Asn
			20					25						30	
Gly	Gly	Tyr	His	Val	Ile	Thr	Lys	Val	Ala	Leu	Asn	Val	Gly	Val	Asn
			35					40						45	
Gln	Leu	Val	Phe	Cys	Val	Cys	Arg	Asp	Leu	Leu	Ala	Leu	Ser	Ile	Leu
			50					55						60	
Ala	Pro	Leu	Ala	Tyr	Phe	Arg	Glu	Arg	Lys	Ile	Arg	Thr	Pro	Met	Asn
			65					70						75	
Lys	Ser	Leu	Leu	Leu	Ser	Phe	Phe	Phe	Leu	Gly	Leu	Ala	Gly	Val	Phe
			85					90						95	
Gly	Asn	Gln	Leu	Leu	Phe	Leu	Ile	Gly	Leu	Thr	Tyr	Thr	Asn	Pro	Thr
			100					105						110	
Tyr	Ala	Ala	Ile	Gln	Pro	Ser	Ile	Pro	Val	Phe	Thr	Phe	Leu	Leu	
			115					120						125	
Ala	Val	Met	Met	Gly	Thr	Glu	Arg	Val	Asn	Leu	Leu	Arg	Ile	Glu	Gly
			130					135						140	
Gln	Thr	Lys	Val	Gly	Gly	Thr	Leu	Val	Cys	Val	Met	Gly	Ala	Val	Phe
			145					150						155	
Met	Val	Val	Phe	Arg	Gly	Pro	Ala	Leu	Leu	Gly	Asp	Lys	Asp	Ala	Asp
			165					170						175	
Phe	Ala	Met	Asn	Asn	Glu	Ile	Ser	Ala	Lys	Gly	Gln	Pro	Glu	Pro	Thr
			180					185						190	
Gly	Trp	Leu	Val	Ser	Gly	Phe	Leu	Asp	Leu	Gly	Phe	Glu	Gln	Trp	His
			195					200						205	
Ile	Gly	Val	Leu	Cys	Leu	Ile	Gly	Asn	Cys	Met	Cys	Met	Ala	Thr	Phe
			210					215						220	
Leu	Ala	Ile	Gln	Ala	Pro	Leu	Leu	Lys	Lys	Tyr	Pro	Ala	Asn	Leu	Ser
			225					230						235	
Val	Ala	Ala	Leu	Ser	Tyr	Xaa	Phe	Gly	Thr	Val	Leu	Met	Cys	Thr	Thr

(2) INFORMATION FOR SEO ID NO:695:

(A) LENGTH: 394 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..394

(D) OTHER INFORMATION: / Ceres Seq. ID 1567706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

Met	Ile	Leu	Thr	Gly	Ser	Gly	Ser	Ala	Ala	Glu	Arg	Asp	Ala	Arg	Met
1				5					10					15	
Ala	His	Thr	Ala	Met	Ala	Phe	Val	Gln	Leu	Phe	Asn	Gly	Gly	Tyr	His
			20					25					30		
Val	Ile	Thr	Lys	Val	Ala	Leu	Asn	Val	Gly	Val	Asn	Gln	Leu	Val	Phe
		35					40					45			
Cys	Val	Cys	Arg	Asp	Leu	Leu	Ala	Leu	Ser	Ile	Leu	Ala	Pro	Leu	Ala
	50					55					60				
Tyr	Phe	Arg	Glu	Arg	Lys	Ile	Arg	Thr	Pro	Met	Asn	Lys	Ser	Leu	Leu
65					70					75				80	
Leu	Ser	Phe	Phe	Phe	Leu	Gly	Leu	Ala	Gly	Val	Phe	Gly	Asn	Gln	Leu
				85					90					95	
Leu	Phe	Leu	Ile	Gly	Leu	Thr	Tyr	Thr	Asn	Pro	Thr	Tyr	Ala	Ala	Ala
			100					105					110		
Ile	Gln	Pro	Ser	Ile	Pro	Val	Phe	Thr	Phe	Leu	Leu	Ala	Val	Met	Met
		115				120						125			
Gly	Thr	Glu	Arg	Val	Asn	Leu	Leu	Arg	Ile	Glu	Gly	Gln	Thr	Lys	Val
	130				135						140				
Gly	Gly	Thr	Leu	Val	Cys	Val	Met	Gly	Ala	Val	Phe	Met	Val	Val	Phe
145					150					155					160
Arg	Gly	Pro	Ala	Leu	Leu	Gly	Asp	Lys	Asp	Ala	Asp	Phe	Ala	Met	Asn
			165						170					175	
Asn	Glu	Ile	Ser	Ala	Lys	Gly	Gln	Pro	Glu	Pro	Thr	Gly	Trp	Leu	Val
			180					185					190		
Ser	Gly	Phe	Leu	Asp	Leu	Gly	Phe	Glu	Gln	Trp	His	Ile	Gly	Val	Leu
	195					200						205			
Cys	Leu	Ile	Gly	Asn	Cys	Met	Cys	Met	Ala	Thr	Phe	Leu	Ala	Ile	Gln
	210					215					220				
Ala	Pro	Leu	Leu	Lys	Lys	Tyr	Pro	Ala	Asn	Leu	Ser	Val	Ala	Ala	Leu
225					230					235					240

Ser Tyr Xaa Phe Gly Thr Val Leu Met Cys Thr Thr Ala Phe Phe Met
245 250 255
Val Lys Glu Pro Leu Asp Trp Lys Leu Thr Gln Ser Glu Val Leu Ala
260 265 270
Val Ile Tyr Ala Gly Val Ile Ala Ser Ala Leu Asn Tyr Gly Leu Leu
275 280 285
Thr Trp Ser Asn Lys Ile Ile Gly Pro Ala Leu Val Ala Leu Tyr Asn
290 295 300
Pro Leu Gln Pro Ala Ala Ser Ala Phe Leu Ser Arg Ile Phe Leu Gly
305 310 315 320
Ser Pro Ile Tyr Leu Gly Ser Val Val Gly Gly Phe Phe Ile Ile Leu
325 330 335
Gly Leu Tyr Met Val Thr Trp Ala Ser Phe Arg Glu Arg Lys Thr Ala
340 345 350
Val Ser Gly Ile Gly Ile Ala Pro His Gly Leu Lys Thr Ser Glu Pro
355 360 365
Leu Ile Phe Asn Gly Thr Val Asn Arg Leu Gly Gln Leu Phe Ser Gly
370 375 380
Leu Pro Ser Ser Ser Val Lys Ser Ala Asp
385 390

(2) INFORMATION FOR SEQ ID NO:696:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 379 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..379

(D) OTHER INFORMATION: / Ceres Seq. ID 1567707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

Met Ala His Thr Ala Met Ala Phe Val Gln Leu Phe Asn Gly Gly Tyr
1 5 10 15
His Val Ile Thr Lys Val Ala Leu Asn Val Gly Val Asn Gln Leu Val
20 25 30
Phe Cys Val Cys Arg Asp Leu Leu Ala Leu Ser Ile Leu Ala Pro Leu
35 40 45
Ala Tyr Phe Arg Glu Arg Lys Ile Arg Thr Pro Met Asn Lys Ser Leu
50 55 60
Leu Leu Ser Phe Phe Phe Leu Gly Leu Ala Gly Val Phe Gly Asn Gln
65 70 75 80
Leu Leu Phe Leu Ile Gly Leu Thr Tyr Thr Asn Pro Thr Tyr Ala Ala
85 90 95
Ala Ile Gln Pro Ser Ile Pro Val Phe Thr Phe Leu Leu Ala Val Met
100 105 110
Met Gly Thr Glu Arg Val Asn Leu Leu Arg Ile Glu Gly Gln Thr Lys
115 120 125
Val Gly Gly Thr Leu Val Cys Val Met Gly Ala Val Phe Met Val Val
130 135 140
Phe Arg Gly Pro Ala Leu Leu Gly Asp Lys Asp Ala Asp Phe Ala Met
145 150 155 160
Asn Asn Glu Ile Ser Ala Lys Gly Gln Pro Glu Pro Thr Gly Trp Leu
165 170 175
Val Ser Gly Phe Leu Asp Leu Gly Phe Glu Gln Trp His Ile Gly Val
180 185 190
Leu Cys Leu Ile Gly Asn Cys Met Cys Met Ala Thr Phe Leu Ala Ile
195 200 205
Gln Ala Pro Leu Leu Lys Lys Tyr Pro Ala Asn Leu Ser Val Ala Ala
210 215 220
Leu Ser Tyr Xaa Phe Gly Thr Val Leu Met Cys Thr Thr Ala Phe Phe

225	230	235	240
Met Val Lys Glu Pro Leu Asp Trp Lys	Leu Thr Gln Ser Glu Val Leu		
	245	250	255
Ala Val Ile Tyr Ala Gly Val Ile Ala Ser	Ala Leu Asn Tyr Gly Leu		
	260	265	270
Leu Thr Trp Ser Asn Lys Ile Ile Gly	Pro Ala Leu Val Ala Leu Tyr		
	275	280	285
Asn Pro Leu Gln Pro Ala Ala Ser Ala Phe	Leu Ser Arg Ile Phe Leu		
	290	295	300
Gly Ser Pro Ile Tyr Leu Gly Ser Val Val	Gly Phe Phe Ile Ile		
	305	310	315
Leu Gly Leu Tyr Met Val Thr Trp Ala Ser	Phe Arg Glu Arg Lys Thr		
	325	330	335
Ala Val Ser Gly Ile Gly Ile Ala Pro His	Gly Leu Lys Thr Ser Glu		
	340	345	350
Pro Leu Ile Phe Asn Gly Thr Val Asn Arg	Leu Gly Gln Leu Phe Ser		
	355	360	365
Gly Leu Pro Ser Ser Ser Val Lys Ser Ala	Asp		
	370	375	

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..713
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

atcaagataaa	gcttatagtt	atcactaaga	gttttgtcta	cgtacatttt	gtgatcaaaa	60
aagttaataaa	tcaaaagatg	gaaggcaaaa	ctgtgatctc	aagtctgctc	ataataagtc	120
ttgtctttagc	acagattcaa	gtagaagcaa	aaatctgctg	tcctaccaag	gatgatagat	180
ctgtgtattt	tgtatgcatg	ctttccgtgt	catcccaatt	ttattgtcta	ttaaagagta	240
aatgcaaaaa	tacatctcag	acgatatgtc	ctccgggata	tactaatgac	attctcgaaa	300
attctgtgtga	tgtctgcaat	gaatattgca	agctagggtg	tgcatcctct	gtgtgttgtg	360
ctttgaccac	tctccaaaac	tttgacgcaa	gtaaagtatt	gagtgaagcg	gttgaaacat	420
gcaccaagggc	atgtttctct	gtctgcaccg	gagGatctac	cgccgcagtt	aaaaagtgcct	480
aaacaagtat	attttaaagt	gaagggttgt	catcattcag	agtgccgtga	ctgtttttac	540
ggaataattg	tcgtctatcg	atgtatgttg	taaaaaaaa	tgctagacta	tggtgctagt	600
actgtttta	aagttgtttc	cggtttgcca	atgtgtcatg	agagtttttg	atcctagatt	660
gtatatccct	tctacttgtc	ttctcttaaa	taataataaa	tgtgtccttc	tcg	

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

Gln Asp Lys Leu Ile Val Ile Thr Lys Ser Phe Val Tyr Val His Phe	
1	5
Val Ile Lys Gln Val Ile Asn Gln Lys Met Glu Gly Lys Thr Val Ile	
20	25
Ser Ser Ser Leu Leu Ile Ile Ser Leu Val Leu Ala Gln Ile Gln Val Glu	
35	40
	45

Ala Lys Ile Cys Cys Pro Thr Lys Asp Asp Arg Ser Val Tyr Phe Val
50 55 60
Cys Met Leu Ser Val Ser Ser Gln Phe Tyr Cys Leu Lys Ser Lys
65 70 75 80
Cys Lys Asn Thr Ser Ser Gln Thr Ile Cys Pro Gly Tyr Thr Asn Asp
85 90 95
Ile Leu Glu Asn Ser Gly Asp Ala Val Asn Glu Tyr Cys Lys Leu Gly
100 105 110
Cys Ala Ser Ser Val Cys Gly Ala Leu Thr Thr Leu Gln Asn Phe Asp
115 120 125
Ala Ser Lys Val Leu Ser Glu Ala Val Glu Gln Cys Thr Lys Ala Cys
130 135 140
Ser Ser Val Cys Thr Gly Gly Ser Thr Ala Ala Val Lys Ser Ala
145 150 155

(2) INFORMATION FOR SEQ ID NO:699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

Met Glu Gly Lys Thr Val Ile Ser Ser Leu Leu Ile Ile Ser Leu Val
1 5 10 15
Leu Ala Gln Ile Gln Val Glu Ala Lys Ile Cys Cys Pro Thr Lys Asp
20 25 30
Asp Arg Ser Val Tyr Phe Val Cys Met Leu Ser Val Ser Ser Gln Phe
35 40 45
Tyr Cys Leu Leu Lys Ser Lys Cys Lys Asn Thr Ser Gln Thr Ile Cys
50 55 60
Pro Pro Gly Tyr Thr Asn Asp Ile Leu Glu Asn Ser Gly Asp Ala Val
65 70 75 80
Asn Glu Tyr Cys Lys Leu Gly Cys Ala Ser Ser Val Cys Gly Ala Leu
85 90 95
Thr Thr Leu Gln Asn Phe Asp Ala Ser Lys Val Leu Ser Glu Ala Val
100 105 110
Glu Gln Cys Thr Lys Ala Cys Ser Ser Val Cys Thr Gly Gly Ser Thr
115 120 125
Ala Ala Val Lys Ser Ala
130

(2) INFORMATION FOR SEQ ID NO:700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

Met Leu Ser Val Ser Ser Gln Phe Tyr Cys Leu Leu Lys Ser Lys Cys
1 5 10 15
Lys Asn Thr Ser Gln Thr Ile Cys Pro Gly Tyr Thr Asn Asp Ile
20 25 30
Leu Glu Asn Ser Gly Asp Ala Val Asn Glu Tyr Cys Lys Leu Gly Cys

35 40 45
Ala Ser Ser Val Cys Gly Ala Leu Thr Thr Leu Gln Asn Phe Asp Ala
50 55 60
Ser Lys Val Leu Ser Glu Ala Val Glu Gln Cys Thr Lys Ala Cys Ser
65 70 75 80
Ser Val Cys Thr Gly Gly Ser Thr Ala Ala Val Lys Ser Ala
85 90

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..587
(D) OTHER INFORMATION: / Ceres Seq. ID 1567715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

atatataaca	ataacacttt	gggtttttaga	ctttagatcac	gaatcaaaaa	catttgagat	60
aaaaAtcaga	aaagtaaaga	gacgaaaatg	gcggatcaac	aagcaggaac	aatcgtcgga	120
ggagttcgcg	atatgtatgc	aaatgctaag	gatcttcaag	tcgagagtct	cgctcgtttc	180
gctgtcgaag	agcataacaa	gaacgagaac	ttgactctgg	agtacaagag	gctccttggg	240
gcgaaaacac	aggttgtggc	aggaacaatg	caccatctaa	ctgtggagggt	ggctgatggt	300
gagaccaata	aggtctatga	ggccaagggt	ttggagaaag	cttggggagaa	tctcaagcag	360
ttggagaggt	tcaaccacct	tcacgatggt	taatccgatg	ccttgagctt	tctctgcggc	420
ttgagtgaag	tccttgtgtg	ctctcagacc	acgtgataag	agttctgggt	taaccaagtt	480
aactctctta	ataagtgaaa	tccagtcaca	tgtgtttgaa	ctggatttgt	gtgtatctct	540
tgactctcgt	ttgtgtattg	ctattagcaa	actctcactt	tttatcc		

(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..70
(D) OTHER INFORMATION: / Ceres Seq. ID 1567716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

Tyr	Ile	Thr	Ile	Thr	Leu	Trp	Val	Leu	Asp	Phe	Arg	Tyr	Glu	Ser	Lys	
1				5				10					15			
Thr	Phe	Glu	Ile	Lys	Ile	Arg	Lys	Val	Lys	Arg	Arg	Lys	Trp	Arg	Ile	
				20				25					30			
Asn	Lys	Gln	Glu	Gln	Ser	Ser	Glu	Glu	Phe	Ala	Ile	Leu	Met	Gln	Met	
				35				40					45			
Leu	Met	Ile	Phe	Lys	Ser	Arg	Val	Ser	Leu	Val	Ser	Leu	Ser	Met	Ser	
				50				55					60			
Ile	Thr	Arg	Thr	Arg	Thr											
65				70												

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1567717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

Met Ala Asp Gln Gln Ala Gly Thr Ile Val Gly Gly Val Arg Asp Ile
1 5 10 15
Asp Ala Asn Ala Asn Asp Leu Gln Val Glu Ser Leu Ala Arg Phe Ala
20 25 30
Val Asp Glu His Asn Lys Asn Glu Asn Leu Thr Leu Glu Tyr Lys Arg
35 40 45
Leu Leu Gly Ala Lys Thr Gln Val Val Ala Gly Thr Met His His Leu
50 55 60
Thr Val Glu Val Ala Asp Gly Glu Thr Asn Lys Val Tyr Glu Ala Lys
65 70 75 80
Val Leu Glu Lys Ala Trp Glu Asn Leu Lys Gln Leu Glu Ser Phe Asn
85 90 95
His Leu His Asp Val
100

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..587

(D) OTHER INFORMATION: / Ceres Seq. ID 1567721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

cttcgctctt atgtgtctct gccccaaatt aaaaactcag aaaccttaga aaattccgat 60
tcatacaactg agagagaaga agaattgaga aatgatgaag cgctcgatcc caacgttcaa 120
ccgcactctg gtgcagagag tcattccagcc cgctaaaacc gaaagcgcca ttctcttacc 180
tgagaaatcc tccaagtctg actcaggcaa ggtgatagct gttggacctg gatcaaggga 240
taaggacggg aaattgattc cggtctctgt gaaggaaggc gacactgttc ttcttccaga 300
gtacggtggt acacaggctca agctcggcga gaacgagtac catctcttcc gggacgagga 360
tgttttggga actttgcaagc aggattgaaa aggctaagct tgccaactta accacgaggg 420
ttcatgttgg tgtttgggt atgaggagaa gtcatttata aattagttaa tcttgaagat 480
gtggttggac ttgtttgctg ttatcattg aatctacctt tatgaacctg tcttgaatt 540
tttacaatat ggcataatc acatggataa ccCaagtgtt gcactctt

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51

(D) OTHER INFORMATION: / Ceres Seq. ID 1567722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

Leu Pro Ser Tyr Val Ser Leu Pro Gln Ile Lys Asn Ser Glu Thr Leu
1 5 10 15
Glu Asn Ser Asp Ser Ser Thr Glu Arg Glu Glu Glu Leu Arg Asn Asp
20 25 30
Glu Ala Ser Asp Pro Asn Val Gln Pro His Leu Gly Ala Glu Ser His
35 40 45
Pro Ala Arg
50

(2) INFORMATION FOR SEQ ID NO:706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..98
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1567723
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

Met	Met	Lys	Arg	Leu	Ile	Pro	Thr	Phe	Asn	Arg	Ile	Leu	Val	Gln	Arg
1				5					10					15	
Val	Ile	Gln	Pro	Ala	Lys	Thr	Glu	Ser	Gly	Ile	Leu	Leu	Pro	Glu	Lys
			20					25					30		
Ser	Ser	Lys	Leu	Asn	Ser	Gly	Lys	Val	Ile	Ala	Val	Gly	Pro	Gly	Ser
			35				40					45			
Arg	Asp	Lys	Asp	Gly	Lys	Leu	Ile	Pro	Val	Ser	Val	Lys	Glu	Gly	Asp
	50					55					60				
Thr	Val	Leu	Leu	Pro	Glu	Tyr	Gly	Gly	Thr	Gln	Val	Lys	Leu	Gly	Glu
65					70					75				80	
Asn	Glu	Tyr	His	Leu	Phe	Arg	Asp	Glu	Asp	Val	Leu	Gly	Thr	Leu	His
				85					90					95	

Glu Asp

- (2) INFORMATION FOR SEQ ID NO:707:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..97
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1567724
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

Met	Lys	Arg	Leu	Ile	Pro	Thr	Phe	Asn	Arg	Ile	Leu	Val	Gln	Arg	Val
1				5					10					15	
Ile	Gln	Pro	Ala	Lys	Thr	Glu	Ser	Gly	Ile	Leu	Leu	Pro	Glu	Lys	Ser
			20					25					30		
Ser	Lys	Leu	Asn	Ser	Gly	Lys	Val	Ile	Ala	Val	Gly	Pro	Gly	Ser	Arg
			35				40					45			
Asp	Lys	Asp	Gly	Lys	Leu	Ile	Pro	Val	Ser	Val	Lys	Glu	Gly	Asp	Thr
	50					55					60				
Val	Leu	Leu	Pro	Glu	Tyr	Gly	Gly	Thr	Gln	Val	Lys	Leu	Gly	Glu	Asn
65					70					75				80	
Glu	Tyr	His	Leu	Phe	Arg	Asp	Glu	Asp	Val	Leu	Gly	Thr	Leu	His	Glu
				85					90					95	

Asp

- (2) INFORMATION FOR SEQ ID NO:708:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1209
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1567738
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

ataccctcat	ttaaatggcg	gagattacaa	gggaaagaga	caactccaat	tcaaagctct	60
gattttttcc	accaatcccc	attttttccc	ttttacaatt	cttaagctag	ttttatactt	120
ttctttctcc	tttcatgttg	gttaagagaa	gccatggata	ccgagtttct	ccgaacccta	180
gatcgctcaga	ttcttttggg	tgtcttcggt	gcttttcgtc	ccgttggtgc	tggtgctgct	240
tatttttcta	catctctcaa	gaacgcgaga	gtgtgttttg	atccagagaa	tttcaaggag	300
ttcaagcttg	ttaagagaca	tcagcttagt	cacaatgttg	ccaagtctgt	ttttgaactc	360
ccaactttcta	ctctctgtgt	gggtcttccc	attggaccaac	acatcagttg	caggggaaag	420
gatggctcaag	gagaggaagt	tattaagcca	tacaccccga	ctacgttaga	ctctgacgtt	480
ggacgttttc	aacttgtcat	taagatgtat	cgcgaaggac	ggatgtctca	tcatttcagg	540
gagatgcgtg	ttggagacca	tcttgccgta	aagggaacca	agggtaggtt	caagtatcaa	600
ccaggtcagt	ttagggcatt	tggaaatgctt	gctggaggtt	caggcatcac	tcctatgttc	660
caagtggcca	gagcaattct	agaaaaacca	acagacaaga	caaaggtgca	tctcattttac	720
gccaacgtca	catcacgaca	cattctcttg	aaggagaagt	tgagggtctc	tactaccaat	780
taccctgaac	aattttaaaat	ctctctatgt	ttgaaccagc	ctcgggaagt	atgggtaggt	840
gggtgtggat	ttgtatcaaa	ggaaatgatt	cagactcatt	gccctgcacc	tgcactctgat	900
atcagatccc	taagatcggt	accaccgcca	atgaacaagg	ccatggctgc	aaaccttgaa	960
gctctgggat	actctccgga	gatgcaattc	cagttctgat	ctgaatatct	ttcttttggt	1020
gctctgaaac	ggaactcata	ataatttagt	tacaatccca	actacgagag	ttgtgtcttta	1080
actgagttag	agttgtatct	ctgttgtgtg	tCtgtttagc	ccactgaaa	gttctcattg	1140
attggtttac	gaattgttta	Ygacattttg	gttcacatat	accggttttg	tgcaaacact	1200
ttgtgctgt						

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..281

(D) OTHER INFORMATION: / Ceres Seq. ID 1567739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

Met	Asp	Thr	Glu	Phe	Leu	Arg	Thr	Leu	Asp	Arg	Gln	Ile	Leu	Leu	Gly
1					5					10				15	
Val	Phe	Val	Ala	Phe	Val	Ala	Val	Gly	Ala	Gly	Ala	Ala	Tyr	Phe	Leu
					20					25				30	
Thr	Ser	Ser	Lys	Lys	Arg	Arg	Val	Cys	Leu	Asp	Pro	Glu	Asn	Phe	Lys
					35					40				45	
Glu	Phe	Lys	Leu	Val	Lys	Arg	His	Gln	Leu	Ser	His	Asn	Val	Ala	Lys
					50					55				60	
Phe	Val	Phe	Glu	Leu	Pro	Thr	Ser	Thr	Ser	Val	Leu	Gly	Leu	Pro	Ile
65					70					75				80	
Gly	Gln	His	Ile	Ser	Cys	Arg	Gly	Lys	Asp	Gly	Gln	Gly	Glu	Asp	Val
					85					90				95	
Ile	Lys	Pro	Tyr	Thr	Pro	Thr	Thr	Leu	Asp	Ser	Asp	Val	Gly	Arg	Phe
					100					105				110	
Glu	Leu	Val	Ile	Lys	Met	Tyr	Pro	Gln	Gly	Arg	Met	Ser	His	His	Phe
					115					120				125	
Arg	Glu	Met	Arg	Val	Gly	Asp	His	Leu	Ala	Val	Lys	Gly	Pro	Lys	Gly
					130					135				140	
Arg	Phe	Lys	Tyr	Gln	Pro	Gly	Gln	Phe	Arg	Ala	Phe	Gly	Met	Leu	Ala
145					150					155				160	
Gly	Gly	Ser	Gly	Ile	Thr	Pro	Met	Phe	Gln	Val	Ala	Arg	Ala	Ile	Leu
					165					170				175	
Glu	Asn	Pro	Thr	Asp	Lys	Thr	Lys	Val	His	Leu	Ile	Tyr	Ala	Asn	Val
					180					185				190	
Thr	Tyr	Asp	Asp	Ile	Leu	Leu	Lys	Glu	Glu	Leu	Glu	Gly	Leu	Thr	Thr
					195					200				205	
Asn	Tyr	Pro	Glu	Gln	Phe	Lys	Ile	Phe	Tyr	Val	Leu	Asn	Gln	Pro	Pro
					210					215				220	

Glu Val Trp Asp Gly Gly Val Gly Phe Val Ser Lys Glu Met Ile Gln
225 230 235 240
Thr His Cys Pro Ala Pro Ala Ser Asp Ile Gln Ile Leu Arg Cys Gly
245 250 255
Pro Pro Pro Met Asn Lys Ala Met Ala Ala Asn Leu Glu Ala Leu Gly
260 265 270
Tyr Ser Pro Glu Met Gln Phe Gln Phe
275 280

(2) INFORMATION FOR SEQ ID NO:710:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1567740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

Met Tyr Pro Gln Gly Arg Met Ser His His Phe Arg Glu Met Arg Val
1 5 10 15
Gly Asp His Leu Ala Val Lys Gly Pro Lys Gly Arg Phe Lys Tyr Gln
20 25 30
Pro Gly Gln Phe Arg Ala Phe Gly Met Leu Ala Gly Gly Ser Gly Ile
35 40 45
Thr Pro Met Phe Gln Val Ala Arg Ala Ile Leu Glu Asn Pro Thr Asp
50 55 60
Lys Thr Lys Val His Leu Ile Tyr Ala Asn Val Thr Tyr Asp Asp Ile
65 70 75 80
Leu Leu Lys Glu Glu Leu Glu Gly Leu Thr Thr Asn Tyr Pro Glu Gln
85 90 95
Phe Lys Ile Phe Tyr Val Leu Asn Gln Pro Pro Glu Val Trp Asp Gly
100 105 110
Gly Val Gly Phe Val Ser Lys Glu Met Ile Gln Thr His Cys Pro Ala
115 120 125
Pro Ala Ser Asp Ile Gln Ile Leu Arg Cys Gly Pro Pro Pro Met Asn
130 135 140
Lys Ala Met Ala Ala Asn Leu Glu Ala Leu Gly Tyr Ser Pro Glu Met
145 150 155 160
Gln Phe Gln Phe

(2) INFORMATION FOR SEQ ID NO:711:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1567741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

Met Ser His His Phe Arg Glu Met Arg Val Gly Asp His Leu Ala Val
1 5 10 15
Lys Gly Pro Lys Gly Arg Phe Lys Tyr Gln Pro Gly Gln Phe Arg Ala
20 25 30
Phe Gly Met Leu Ala Gly Gly Ser Gly Ile Thr Pro Met Phe Gln Val
35 40 45
Ala Arg Ala Ile Leu Glu Asn Pro Thr Asp Lys Thr Lys Val His Leu

50	55	60
Ile Tyr Ala Asn Val Thr Tyr Asp Asp Ile Leu Lys Glu Glu Leu		
65	70	75
Glu Gly Leu Thr Thr Asn Tyr Pro Glu Gln Phe Lys Ile Phe Tyr Val		80
	85	90
Leu Asn Gln Pro Pro Glu Val Trp Asp Gly Gly Val Gly Phe Val Ser		95
	100	105
Lys Glu Met Ile Gln Thr His Cys Pro Ala Pro Ala Ser Asp Ile Gln		110
	115	120
Ile Leu Arg Cys Gly Pro Pro Pro Met Asn Lys Ala Met Ala Ala Asn		125
	130	135
Leu Glu Ala Leu Gly Tyr Ser Pro Glu Met Gln Phe Gln Phe		140
145	150	155

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1203

(D) OTHER INFORMATION: / Ceres Seq. ID 1567750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

ataaaaaaaa	aaacaaaaat	ataatgtgga	cttctaaaaa	cataagcttc	actttcttcca	60
tcacacaaat	acttctcgcg	tcttgcaacg	catccgcaaa	ggccaaaaac	caaccgctgt	120
tcccagcgat	tctaactctt	ggtgattcaa	cagtcgacac	aggcaacaat	aactaccctt	180
cacacaaat	cttcagagct	aaacatgttc	cttacgggat	tgatctccca	aaccactcac	240
ctaacgggaag	attctcaaac	ggaaaaattt	tctccgacat	aatcgcaacc	aaactcaaca	300
ctaaacaggtt	tggtctctcc	ttcttacaac	caaatctcac	cgaccagaag	attgtaacccg	360
gagtcgtgttt	tgcatcacga	ggtgccgggt	acgatgacca	aaccagtctc	acgacacaag	420
cgattcgtgt	ctcgggaaca	ccaaatatgt	tcaagagtta	ctttgctcgt	cttaagagta	480
tcgtaggaga	caagaaagcc	atgaagatca	taaacaaatgc	tttggtggtt	gtgagtcgag	540
ggcctaata	tttcaatctg	aattattacg	agggtccccc	atggcgctcg	atgtatcccta	600
gcatttctga	ttaccaagat	tttgctctta	ataagcttaa	caatttcgtg	atggagcttt	660
acagcctagg	ttgccggaaa	attttggtcg	gaggtttacc	gccaatggga	tgtttaccca	720
ttcaaatgac	tgctcaattc	cgcaacgtcc	taaggttttc	cttggaacaa	gagacacagag	780
actctgtttt	atacaactcag	aaacttcaga	agctctttac	tcagacacaa	gcactctctta	840
caggaagcaa	gatcctttac	tctgatgtct	atgaccttat	gatggagatg	ctccaaaacc	900
ctagcaataa	cgggttttaa	gagacgcaga	gaggtatgtg	tggaacaggg	ttcttgagga	960
cgagcttcat	gtgtaatgct	tattcttcca	tggttgagaa	tcgctcgagg	ttctgtttct	1020
ttgactcgat	tcatccatct	gaagctacct	acaattacat	tggtaatgtt	cttgatata	1080
agattcgtgg	gtggccttaa	gcttaagtta	tcaagatttg	caaagattga	acaaaattat	1140
ctgttYtcat	aatgtgacta	tttggtggac	Tcgtttgtta	atcaactatt	aactttggct	1200

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..367

(D) OTHER INFORMATION: / Ceres Seq. ID 1567751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

Lys Asn Lys Asn Lys Asn Ile Met Trp Thr Ser Lys Thr Ile Ser Phe		
1	5	10
Thr Phe Phe Ile Thr Thr Ile Leu Leu Ala Ser Cys Asn Ala Ser Ala		15

	20		25		30
Lys Ala Lys Thr Gln Pro Leu Phe Pro Ala Ile Leu Ile Phe Gly Asp	35	40	45	50	55
Ser Thr Val Asp Thr Gly Asn Asn Tyr Pro Ser Gln Thr Ile Phe	60	65	70	75	80
Arg Ala Lys His Val Pro Tyr Gly Ile Asp Leu Pro Asn His Ser Pro	85	90	95	100	105
Asn Gly Arg Phe Ser Asn Gly Lys Ile Phe Ser Asp Ile Ile Ala Thr	110	115	120	125	130
Lys Leu Asn Ile Lys Gln Phe Val Pro Phe Leu Gln Pro Asn Leu	135	140	145	150	155
Thr Asp Gln Glu Ile Val Thr Gly Val Cys Phe Ala Ser Ala Gly Ala	160	165	170	175	180
Gly Tyr Asp Asp Gln Thr Ser Leu Thr Thr Gln Ala Ile Arg Val Ser	185	190	195	200	205
Glu Gln Pro Asn Met Phe Lys Ser Tyr Ile Ala Arg Leu Lys Ser Ile	210	215	220	225	230
Val Gly Asp Lys Lys Ala Met Lys Ile Ile Asn Asn Ala Leu Val Val	235	240	245	250	255
Val Ser Ala Gly Pro Asn Asp Phe Ile Leu Asn Tyr Tyr Glu Val Pro	260	265	270	275	280
Thr Trp Arg Arg Met Tyr Pro Ser Ile Ser Asp Tyr Gln Asp Phe Val	285	290	295	300	305
Leu Asn Lys Leu Asn Asn Phe Val Met Glu Leu Tyr Ser Leu Gly Cys	310	315	320	325	330
Arg Lys Ile Leu Val Gly Gly Leu Pro Pro Met Gly Cys Leu Pro Ile	335	340	345	350	355
Gln Met Thr Ala Gln Phe Arg Asn Val Leu Arg Phe Cys Leu Glu Gln	360	365			

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..360
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

Met Trp Thr Ser Lys Thr Ile Ser Phe Thr Phe Phe Ile Thr Thr Ile	5	10	15
Leu Leu Ala Ser Cys Asn Ala Ser Ala Lys Ala Lys Thr Gln Pro Leu	20	25	30
Phe Pro Ala Ile Leu Ile Phe Gly Asp Ser Thr Val Asp Thr Gly Asn	35	40	45

Asn Asn Tyr Pro Ser Gln Thr Ile Phe Arg Ala Lys His Val Pro Tyr
50 55 60
Gly Ile Asp Leu Pro Asn His Ser Pro Asn Gly Arg Phe Ser Asn Gly
65 70 75 80
Lys Ile Phe Ser Asp Ile Ile Ala Thr Lys Leu Asn Ile Lys Gln Phe
85 90 95
Val Pro Pro Phe Leu Gln Pro Asn Leu Thr Asp Gln Glu Ile Val Thr
100 105 110
Gly Val Cys Phe Ala Ser Ala Gly Ala Gly Tyr Asp Asp Gln Thr Ser
115 120 125
Leu Thr Thr Gln Ala Ile Arg Val Ser Glu Gln Pro Asn Met Phe Lys
130 135 140
Ser Tyr Ile Ala Arg Leu Lys Ser Ile Val Gly Asp Lys Lys Ala Met
145 150 155 160
Lys Ile Ile Asn Asn Ala Leu Val Val Val Ser Ala Gly Pro Asn Asp
165 170 175
Phe Ile Leu Asn Tyr Tyr Glu Val Pro Thr Trp Arg Arg Met Tyr Pro
180 185 190
Ser Ile Ser Asp Tyr Gln Asp Phe Val Leu Asn Lys Leu Asn Asn Phe
195 200 205
Val Met Glu Leu Tyr Ser Leu Gly Cys Arg Lys Ile Leu Val Gly Gly
210 215 220
Leu Pro Pro Met Gly Cys Leu Pro Ile Gln Met Thr Ala Gln Phe Arg
225 230 235 240
Asn Val Leu Arg Phe Cys Leu Glu Gln Glu Asn Arg Asp Ser Val Leu
245 250 255
Tyr Asn Gln Lys Leu Gln Lys Leu Leu Pro Gln Thr Gln Ala Ser Leu
260 265 270
Thr Gly Ser Lys Ile Leu Tyr Ser Asp Val Tyr Asp Pro Met Met Glu
275 280 285
Met Leu Gln Asn Pro Ser Lys Tyr Gly Phe Lys Glu Thr Thr Arg Gly
290 295 300
Cys Cys Gly Thr Gly Phe Leu Glu Thr Ser Phe Met Cys Asn Ala Tyr
305 310 315 320
Ser Ser Met Cys Glu Asn Arg Ser Glu Phe Leu Phe Phe Asp Ser Ile
325 330 335
His Pro Ser Glu Ala Thr Tyr Asn Tyr Ile Gly Asn Val Leu Asp Thr
340 345 350
Lys Ile Arg Gly Trp Leu Lys Ala
355 360

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1567753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

Met Phe Lys Ser Tyr Ile Ala Arg Leu Lys Ser Ile Val Gly Asp Lys
1 5 10 15
Lys Ala Met Lys Ile Ile Asn Asn Ala Leu Val Val Val Ser Ala Gly
20 25 30
Pro Asn Asp Phe Ile Leu Asn Tyr Tyr Glu Val Pro Thr Trp Arg Arg
35 40 45
Met Tyr Pro Ser Ile Ser Asp Tyr Gln Asp Phe Val Leu Asn Lys Leu
50 55 60
Asn Asn Phe Val Met Glu Leu Tyr Ser Leu Gly Cys Arg Lys Ile Leu

65	70	75	80
Val Gly Gly Leu Pro	Pro Met Gly Cys	Leu Pro Ile Gln Met	Thr Ala
	85	90	95
Gln Phe Arg Asn Val Leu Arg Phe Cys	Leu Glu Gln Glu Asn Arg Asp		
	100	105	110
Ser Val Leu Tyr Asn Gln Lys Leu Gln Lys Leu Leu Pro	Gln Thr Gln		
	115	120	125
Ala Ser Leu Thr Gly Ser Lys Ile Leu Tyr Ser Asp Val Tyr Asp Pro			
	130	135	140
Met Met Glu Met Leu Gln Asn Pro Ser Lys Tyr Gly Phe Lys Glu Thr			
	145	150	155
Thr Arg Gly Cys Cys Gly Thr Gly Phe Leu Glu Thr Ser Phe Met Cys			
	165	170	175
Asn Ala Tyr Ser Ser Met Cys Glu Asn Arg Ser Glu Phe Leu Phe Phe			
	180	185	190
Asp Ser Ile His Pro Ser Glu Ala Thr Tyr Asn Tyr Ile Gly Asn Val			
	195	200	205
Leu Asp Thr Lys Ile Arg Gly Trp Leu Lys Ala			
	210	215	

(2) INFORMATION FOR SEQ ID NO:716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..678
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

aatcgattc	tccgatcgaa	tagccgacgg	agaaatgacc	aagttcagga	agctcggcgg	60
cccgacaggt	caccgtatgt	ccatgctcag	gactatgggt	tctcaattgg	tgcaacacga	120
gcgaattgag	accactgtta	caaaggctat	agaagttcgt	cgtcttgctg	ataatgat	180
tcaactcgga	aaagagggtt	cactagctgc	agcaagaaga	gctgctgggt	ttgttagagg	240
agatgatgta	cttcacaaga	ttttacaga	attggckcat	cgatacaaa	atagagctgg	300
tggtatacaca	agaatgcttc	gtactcgcat	tcgtgttggt	gatgctgccc	caatggccta	360
tatcgagttt	atcgatagag	agaacgagct	aaggcaatca	aaaccagcta	ctctcaacc	420
tcacactcga	gtgccacttg	atccatgggc	tagatcccg	ctcaccaggc	agtatgctcc	480
accaaaggag	gCaaaaaact	tctgattctg	acctataaat	agaagaagat	ctctctcgct	540
ctctcacacc	agaagatcat	gttttttttc	ccctggccca	tggtgtttct	ccctcaaccc	600
atagctttgt	atgtctggca	cettattcat	cactgcat	cacaatgtgt	ttaaaccagt	660
ttaaatgtag	tttctctg					

(2) INFORMATION FOR SEQ ID NO:717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

Ile Ala Phe Ser Asp Arg Ile Ala Asp Gly Glu Met Thr Lys Phe Arg	
1	5
Lys Leu Gly Arg Pro Ala Gly His Arg Met Ser Met Leu Arg Thr Met	
	20
Val Ser Gln Leu Val Gln His Glu Arg Ile Glu Thr Thr Val Thr Lys	
	35
	40
	45

Ala Ile Glu Val Arg Arg Leu Ala Asp Asn Met Ile Gln Leu Gly Lys
50 55 60
Glu Gly Ser Leu Ala Ala Ala Arg Arg Ala Ala Gly Phe Val Arg Gly
65 70 75 80
Asp Asp Val Leu His Lys Ile Phe Thr Glu Leu Xaa His Arg Tyr Lys
85 90 95
Asp Arg Ala Gly Tyr Thr Arg Met Leu Arg Thr Arg Ile Arg Val
100 105 110
Gly Asp Ala Ala Pro Met Ala Tyr Ile Glu Phe Ile Asp Arg Glu Asn
115 120 125
Glu Leu Arg Gln Ser Lys Pro Ala Thr Pro Gln Pro Pro Arg Val
130 135 140
Pro Leu Asp Pro Trp Ala Arg Ser Arg Leu Thr Arg Gln Tyr Ala Pro
145 150 155 160
Pro Lys Glu Ala Lys Asn Phe
165

(2) INFORMATION FOR SEQ ID NO:718:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1567764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

Met Thr Lys Phe Arg Lys Leu Gly Arg Pro Ala Gly His Arg Met Ser
1 5 10 15
Met Leu Arg Thr Met Val Ser Gln Leu Val Gln His Glu Arg Ile Glu
20 25 30
Thr Thr Val Thr Lys Ala Ile Glu Val Arg Arg Leu Ala Asp Asn Met
35 40 45
Ile Gln Leu Gly Lys Glu Gly Ser Leu Ala Ala Ala Arg Arg Ala Ala
50 55 60
Gly Phe Val Arg Gly Asp Val Leu His Lys Ile Phe Thr Glu Leu
65 70 75 80
Xaa His Arg Tyr Lys Asp Arg Ala Gly Gly Tyr Thr Arg Met Leu Arg
85 90 95
Thr Arg Ile Arg Val Gly Asp Ala Ala Pro Met Ala Tyr Ile Glu Phe
100 105 110
Ile Asp Arg Glu Asn Glu Leu Arg Gln Ser Lys Pro Ala Thr Pro Gln
115 120 125
Pro Pro Arg Val Pro Leu Asp Pro Trp Ala Arg Ser Arg Leu Thr
130 135 140
Arg Gln Tyr Ala Pro Pro Lys Glu Ala Lys Asn Phe
145 150 155

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1567765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

Met Ser Met Leu Arg Thr Met Val Ser Gln Leu Val Gln His Glu Arg

```

1           5           10           15
Ile Glu Thr Thr Val Thr Lys Ala Ile Glu Val Arg Arg Leu Ala Asp
      20           25           30
Asn Met Ile Gln Leu Gly Lys Glu Gly Ser Leu Ala Ala Arg Arg
      35           40           45
Ala Ala Gly Phe Val Arg Gly Asp Asp Val Leu His Lys Ile Phe Thr
      50           55           60
Glu Leu Xaa His Arg Tyr Lys Asp Arg Ala Gly Gly Tyr Thr Arg Met
      65           70           75           80
Leu Arg Thr Arg Ile Arg Val Gly Asp Ala Ala Pro Met Ala Tyr Ile
      85           90           95
Glu Phe Ile Asp Arg Glu Asn Glu Leu Arg Gln Ser Lys Pro Ala Thr
      100          105          110
Pro Gln Pro Pro Arg Val Pro Leu Asp Pro Trp Ala Arg Ser Arg
      115          120          125
Leu Thr Arg Gln Tyr Ala Pro Pro Lys Glu Ala Lys Asn Phe
      130          135          140

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(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1251 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1251

(D) OTHER INFORMATION: / Ceres Seq. ID 1567773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

```

acgcaggcaa agtgtctgta atttaattcta tagaagaaac agagctctct gttttgtttt      60
aatcttggtc tgcttccctt accggttttg cgctagaaac acgcccggagg cggamcaatc      120
cacagcaaaa gcaactcaaa taatacacgt cagcaattcc acgtggcatg attctctctg      180
ctttgtagat gtccaaatag gtatgccagt cagcggcgta tcagagctca aaagatacct      240
ccacggatc ggttacctca aggatggctc cgaatatatt tccgacgtgt tcgatgggtc      300
tgtggaatcg gcaatctctc tgtatcaaga aaatctcggg ttaccaataa ccggaagact      360
cgacacgagt acagttactc tcattgtcgt accgcgatgt ggcgttagtg atacgcacat      420
gaccatcaac aacgatttcc tccacacaac ggcgcattat acgtatttca acggtaaacc      480
gaaatggaac cgtgatacgc taacctacgc tatctccaaa actcaaaaac tcgattactt      540
gacgtcagaa gacgtcaaaa ccgttttccg gcgagctttt tcacagtggg caagcgtgat      600
tccggtgagt ttcgaggaag tcgacgattt caccgacggc gattttaaaga tcggtattca      660
cgctggtagc caccggtgac ggcttccggt tgacgggtga ottggaactt tagcacacgc      720
ttttgcccgc gagaacggga gggttcacct cgacgcggcg gagacgtgga tcgtcgacga      780
tgacttgaaa ggaattctca aggtggccgt tgacttggag tctgtggcga ctacagagat      840
cggtcaactt ttgggattag gacatagctc gcaggagtcg gcggttatgt atccgagctc      900
ccgacccgag accaaagaaa ttgatcttac ggttgatgac gtggcagggt tacttaagct      960
atatggtcgc aatcctaaac tacggttggg ttcaactaac cagtcggaag attctattaa      1020
aaacggcacc gttatcacata gattcttgtc ggggaatttt atcggtttat ttctgttggt      1080
tgttgggttc attcttttcc tataggttta taggcataaa aaatactggt ttatttcatt      1140
tatttttaat taaatgtaca tatatttttc aactatgtaa atgtaaatat atagtgaac      1200
aaaaaaagat gtacatatat agttaggctt ataattaggt ttatgtgtct g

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(2) INFORMATION FOR SEQ ID NO:721:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..367

(D) OTHER INFORMATION: / Ceres Seq. ID 1567774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

Arg	Arg	Gln	Met	Ser	Arg	Asn	Leu	Ile	Tyr	Arg	Arg	Asn	Arg	Ala	Leu
1			5						10				15		
Cys	Phe	Val	Leu	Ile	Leu	Phe	Cys	Phe	Pro	Tyr	Arg	Phe	Gly	Ala	Arg
			20				25						30		
Asn	Thr	Pro	Glu	Ala	Xaa	Gln	Ser	Thr	Ala	Lys	Ala	Thr	Gln	Ile	Ile
			35				40					45			
His	Val	Ser	Asn	Ser	Thr	Trp	His	Asp	Phe	Ser	Arg	Leu	Val	Asp	Val
			50			55					60				
Gln	Ile	Gly	Ser	His	Val	Ser	Gly	Val	Ser	Glu	Leu	Lys	Arg	Tyr	Leu
			65		70		75						80		
His	Arg	Phe	Gly	Tyr	Val	Lys	Asp	Gly	Ser	Glu	Ile	Phe	Ser	Asp	Val
			85					90					95		
Phe	Asp	Gly	Pro	Leu	Glu	Ser	Ala	Ile	Ser	Leu	Tyr	Gln	Glu	Asn	Leu
			100				105						110		
Gly	Leu	Pro	Ile	Thr	Gly	Arg	Leu	Asp	Thr	Ser	Thr	Val	Thr	Leu	Met
			115			120						125			
Ser	Leu	Pro	Arg	Cys	Gly	Val	Xaa	Asp	Thr	His	Met	Thr	Ile	Asn	Asn
			130			135					140				
Asp	Phe	Leu	His	Thr	Thr	Ala	His	Tyr	Thr	Tyr	Phe	Asn	Gly	Lys	Pro
			145			150			155					160	
Lys	Trp	Asn	Arg	Asp	Thr	Leu	Thr	Tyr	Ala	Ile	Ser	Lys	Thr	His	Lys
			165					170					175		
Leu	Asp	Tyr	Leu	Thr	Ser	Glu	Asp	Val	Lys	Thr	Val	Phe	Arg	Arg	Ala
			180					185					190		
Phe	Ser	Gln	Trp	Ser	Ser	Val	Ile	Pro	Val	Ser	Phe	Glu	Glu	Val	Asp
			195			200						205			
Asp	Phe	Thr	Thr	Ala	Asp	Leu	Lys	Ile	Gly	Phe	Tyr	Ala	Gly	Asp	His
			210			215					220				
Gly	Asp	Gly	Leu	Pro	Phe	Asp	Gly	Val	Leu	Gly	Thr	Leu	Ala	His	Ala
			225			230				235				240	
Phe	Ala	Pro	Glu	Asn	Gly	Arg	Leu	His	Leu	Asp	Ala	Ala	Glu	Thr	Trp
			245					250					255		
Ile	Val	Asp	Asp	Leu	Lys	Gly	Ser	Ser	Glu	Val	Ala	Val	Asp	Leu	
			260			265						270			
Glu	Ser	Val	Ala	Thr	His	Glu	Ile	Gly	His	Leu	Leu	Gly	Leu	Gly	His
			275			280						285			
Ser	Ser	Gln	Glu	Ser	Ala	Val	Met	Tyr	Pro	Ser	Leu	Arg	Pro	Arg	Thr
			290			295					300				
Lys	Lys	Val	Asp	Leu	Thr	Val	Asp	Asp	Val	Ala	Gly	Val	Leu	Lys	Leu
			305			310				315				320	
Tyr	Gly	Pro	Asn	Pro	Lys	Leu	Arg	Leu	Asp	Ser	Leu	Thr	Gln	Ser	Glu
			325					330					335		
Asp	Ser	Ile	Lys	Asn	Gly	Thr	Val	Ser	His	Arg	Phe	Leu	Ser	Gly	Asn
			340					345					350		
Phe	Ile	Gly	Tyr	Val	Leu	Leu	Val	Val	Gly	Leu	Ile	Leu	Phe	Leu	
			355			360						365			

(2) INFORMATION FOR SEQ ID NO:722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..364
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

Met	Ser	Arg	Asn	Leu	Ile	Tyr	Arg	Arg	Asn	Arg	Ala	Leu	Cys	Phe	Val
1			5					10					15		

Leu Ile Leu Phe Cys Phe Pro Tyr Arg Phe Gly Ala Arg Asn Thr Pro
20 25 30
Glu Ala Xaa Gln Ser Thr Ala Lys Ala Thr Gln Ile Ile His Val Ser
35 40 45
Asn Ser Thr Trp His Asp Phe Ser Arg Leu Val Asp Val Gln Ile Gly
50 55 60
Ser His Val Ser Gly Val Ser Glu Leu Lys Arg Tyr Leu His Arg Phe
65 70 75 80
Gly Tyr Val Lys Asp Gly Ser Glu Ile Phe Ser Asp Val Phe Asp Gly
85 90 95
Pro Leu Glu Ser Ala Ile Ser Leu Tyr Gln Glu Asn Leu Gly Leu Pro
100 105 110
Ile Thr Gly Arg Leu Asp Thr Ser Thr Val Thr Leu Met Ser Leu Pro
115 120 125
Arg Cys Gly Val Xaa Asp Thr His Met Thr Ile Asn Asn Asp Phe Leu
130 135 140
His Thr Thr Ala His Tyr Thr Tyr Phe Asn Gly Lys Pro Lys Trp Asn
145 150 155 160
Arg Asp Thr Leu Thr Tyr Ala Ile Ser Lys Thr His Lys Leu Asp Tyr
165 170 175
Leu Thr Ser Glu Asp Val Lys Thr Val Phe Arg Arg Ala Phe Ser Gln
180 185 190
Trp Ser Ser Val Ile Pro Val Ser Phe Glu Glu Val Asp Asp Phe Thr
195 200 205
Thr Ala Asp Leu Lys Ile Gly Phe Tyr Ala Gly Asp His Gly Asp Gly
210 215 220
Leu Pro Phe Asp Gly Val Leu Gly Thr Leu Ala His Ala Phe Ala Pro
225 230 235 240
Glu Asn Gly Arg Leu His Leu Asp Ala Ala Glu Thr Trp Ile Val Asp
245 250 255
Asp Asp Leu Lys Gly Ser Ser Glu Val Ala Val Asp Leu Glu Ser Val
260 265 270
Ala Thr His Glu Ile Gly His Leu Leu Gly Leu Gly His Ser Ser Gln
275 280 285
Glu Ser Ala Val Met Tyr Pro Ser Leu Arg Pro Arg Thr Lys Lys Val
290 295 300
Asp Leu Thr Val Asp Asp Val Ala Gly Val Leu Lys Leu Tyr Gly Pro
305 310 315 320
Asn Pro Lys Leu Arg Leu Asp Ser Leu Thr Gln Ser Glu Asp Ser Ile
325 330 335
Lys Asn Gly Thr Val Ser His Arg Phe Leu Ser Gly Asn Phe Ile Gly
340 345 350
Tyr Val Leu Leu Val Val Gly Leu Ile Leu Phe Leu
355 360

(2) INFORMATION FOR SEQ ID NO:723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..240
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

Met Ser Leu Pro Arg Cys Gly Val Xaa Asp Thr His Met Thr Ile Asn
1 5 10 15
Asn Asp Phe Leu His Thr Thr Ala His Tyr Thr Tyr Phe Asn Gly Lys
20 25 30
Pro Lys Trp Asn Arg Asp Thr Leu Thr Tyr Ala Ile Ser Lys Thr His

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..904
(D) OTHER INFORMATION: / Ceres Seq. ID 1567777

agtggagaaa	gaatcttct	tggcgaaattg	cttcgatctct	caattcgact	tctctatatata	60
agaagaacca	gtctctctgt	tggcgaaattg	tcatcatcat	catcattata	atcaaaacga	120
tgtgattctg	cgaaacogct	tctcaattct	catcggaatt	tgtgtctctc	tccaatctct	180
acaaacggag	ctaaactcttc	tagatcggag	caattcaatgg	ctgtctcttc	cgaaactcaa	240
tctctttaac	tcttaacgct	caaggatgct	aagggaagaac	agtttgatct	aagcatctac	300
aaagggaag	tctctctgat	tgtgaacgtt	gctcttcaat	tggctgttgc	taatctgaat	360
tatactgagc	tgtccgaGct	gatgatgaag	tacaaaggcc	atgctttcga	gattcttcgg	420
tttccgtgta	acCagttttg	gaatacaag	ctcgtgtacta	atgaagaagt	tgctcaagtt	480
gcttgctact	ctttcaaggc	cgatctaccc	atctttgaca	aggtttgagt	taacggtgac	540
aaagctgccc	cagttctacaa	gtttctgaaa	tcaagcaaa	gcgggctctt	tggagacggc	600
attagatgga	acttcgcgaa	tctcttggtt	gacaaaagat	gaaattgtgt	gcgacgcttt	660
gcaccaacca	ctctccctct	cagcatctgag	aaggatttga	agaagttgtt	ggaggttact	720
ctgttaagca	ggcgaagttg	cataaattaga	caataaaag	ctcattatg	tgttatatcc	780
aatactctgt	agtaagactga	gtctgtagt	gtgtgtgcct	tgtggacgc	tacaatatat	840
aatacgtttt	ttagcggcca	aactatgtaa	taatcgtaaa	tctaataatc	agattttccct	900

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..241

(D) OTHER INFORMATION: / Ceres Seq. ID 1567778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

Ser Glu Lys Arg Ile Phe Phe Trp Gln Met Leu Arg Ser Ser Ile Arg
1 5 10 15
Leu Leu Tyr Ile Arg Arg Thr Ser Pro Leu Leu Arg Ser Leu Ser Ser
20 25 30
Ser Ser Ser Leu Ser Ser Lys Arg Phe Asp Ser Ala Lys Pro Ile Phe
35 40 45
Asn Ser His Arg Thr Phe Cys Leu Pro Pro Ile Ser Thr Thr Gly Ala
50 55 60
Lys Leu Ser Arg Ser Glu His Ser Met Ala Ala Ser Ser Glu Pro Lys
65 70 75 80
Ser Leu Tyr Asp Phe Thr Val Lys Asp Ala Lys Gly Asn Asp Val Asp
85 90 95
Leu Ser Ile Tyr Lys Gly Lys Val Leu Leu Ile Val Asn Val Ala Ser
100 105 110
Gln Cys Gly Leu Thr Asn Ser Asn Tyr Thr Glu Leu Ala Gln Leu Tyr
115 120 125
Glu Lys Tyr Lys Gly His Gly Phe Glu Ile Leu Ala Phe Pro Cys Asn
130 135 140
Gln Phe Gly Asn Gln Glu Pro Gly Thr Asn Glu Ile Val Gln Phe
145 150 155 160
Ala Cys Thr Arg Phe Lys Ala Glu Tyr Pro Ile Phe Asp Lys Val Asp
165 170 175
Val Asn Gly Asp Lys Ala Ala Pro Val Tyr Lys Phe Leu Lys Ser Ser
180 185 190
Lys Gly Gly Leu Phe Gly Asp Gly Ile Lys Trp Asn Phe Ala Lys Phe
195 200 205
Leu Val Asp Lys Asp Gly Asn Val Val Asp Arg Phe Ala Pro Thr Thr
210 215 220
Ser Pro Leu Ser Ile Glu Lys Asp Leu Lys Lys Leu Leu Gly Val Thr
225 230 235 240
Ala

(2) INFORMATION FOR SEQ ID NO:726:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..232

(D) OTHER INFORMATION: / Ceres Seq. ID 1567779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

Met Leu Arg Ser Ser Ile Arg Leu Leu Tyr Ile Arg Arg Thr Ser Pro
1 5 10 15
Leu Leu Arg Ser Leu Ser Ser Ser Ser Ser Leu Ser Ser Lys Arg Phe
20 25 30
Asp Ser Ala Lys Pro Ile Phe Asn Ser His Arg Thr Phe Cys Leu Pro
35 40 45
Pro Ile Ser Thr Thr Gly Ala Lys Leu Ser Arg Ser Glu His Ser Met
50 55 60
Ala Ala Ser Ser Glu Pro Lys Ser Leu Tyr Asp Phe Thr Val Lys Asp
65 70 75 80
Ala Lys Gly Asn Asp Val Asp Leu Ser Ile Tyr Lys Gly Lys Val Leu

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1418
(D) OTHER INFORMATION: / Ceres Seq. ID 1567785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

atccattgat	gagtatataa	ttttgtttgt	gggtattgct	ttgtttgcat	tgctaagtgc	60
tttactcttt	ctggaagaaa	gcttttgaag	atcagcctaa	aagtgatctc	tcataactgc	120
ttaaaagatt	gttgaacctc	gaagatgtct	ttggccgaga	taaacaagaa	tgaagtgcag	180
attgttattg	gggctcttaa	tgctgacctt	acacagtttt	tgaccagctg	gaggcctttc	240
ttctccgat	tcctctgat	tgttgtcaaa	gatcctgagc	tcaaggagga	actcaacata	300
ccagaagcct	ttgacgtaga	tgctctactct	aagactgaca	tggaaaaagg	tgtgggcgca	360
tcacattcca	ccatgtttct	tggtctattct	tgcatatatt	tcggttatct	cgatatacaa	420
aagaagtaca	ttgtctctat	tgatgatgat	ttgttccctg	ctaaagatcc	gaagggttcc	480
ctagtggatg	ctgttactca	gcacgtgatc	aaccttgaaa	accacgccac	gcctctcttc	540
ttcaacaccc	tttatgatcc	ttactgcgag	ggagcggatt	ttgtccgtgg	ataccctttc	600
agcctcagaa	gtggtgtccc	ttgtgctgca	tcttggtggc	tttggtctaa	tctagctgat	660
cttgatgctc	caacacaagc	ttctcaagaca	gagaaaagga	acactgcata	tggttgatgcg	720
gttatgactg	ttccggccaa	ggctatgcta	cccataagcg	gaatcaacat	tgcttttaac	780
cgcgagtggg	tggtccagc	tttggtgcct	gcactcagat	tggtctggga	agggaaaagt	840
agatgggaaa	caacttgaaga	tggttggtgt	gggatgtgtc	tgaaacatat	ctctgatcat	900
ttgggttatg	gtgtgaaaac	cgactgcctc	tatgtgtgga	gaaacgagag	aggagatgca	960
gtggagagtt	tgaggaaagca	aatgggaagg	aatgaagctg	atggagaaaa	gtgttccatt	1020
tttcgattca	gtgaaattgc	ccgagactgc	gcttaaaagt	gaagatttgg	tgattgagct	1080
tgctaaagcg	gtgaaagagc	agtttagttc	agatgatcct	gcctttacgc	aaagctgctga	1140
tgctatgttt	aagtgggtcc	agctctggaa	ttctgttaat	tctagcgctt	gaagttgaa	1200
aatctcttga	ggttagggtc	ctttatcact	tctaagcata	ttatcatgtc	tcagagattt	1260
accacaagtc	ttttctttct	tttagtaca	tcatgtttat	ttttcttttt	tatctaaatt	1320
ataagcatgt	gttttttga	cactcaataa	tgtaacctga	tgaaccccat	ctgctttgac	1380
tcgatgatat	taatatctat	tgcttagctt	ttttacttt			

(2) INFORMATION FOR SEQ ID NO:729:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..303
(D) OTHER INFORMATION: / Ceres Seq. ID 1567786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

Met	Ser	Leu	Ala	Glu	Ile	Asn	Lys	Asn	Glu	Val	Ile	Gly
1				5					10		15	
Ala	Leu	Asn	Ala	Asp	Leu	Thr	Gln	Phe	Leu	Thr	Ser	Trp
			20				25				30	Phe
Phe	Ser	Gly	Phe	His	Leu	Ile	Val	Val	Lys	Asp	Pro	Glu
			35				40				45	Leu
Glu	Leu	Asn	Ile	Pro	Glu	Gly	Phe	Asp	Val	Asp	Val	Tyr
			50			55					60	Ser
Asp	Met	Glu	Lys	Val	Val	Gly	Ala	Ser	Asn	Ser	Thr	Met
			65			70			75			Phe
Tyr	Ser	Cys	Arg	Tyr	Phe	Gly	Tyr	Leu	Val	Ser	Lys	Lys
			85					90			95	Tyr
Val	Ser	Ile	Asp	Asp	Asp	Cys	Val	Pro	Ala	Lys	Asp	Pro
			100					105			110	Lys
Leu	Val	Asp	Ala	Val	Thr	Gln	His	Val	Ile	Asn	Leu	Glu
			115				120				125	Asn
Thr	Pro	Leu	Phe	Phe	Asn	Thr	Leu	Tyr	Asp	Pro	Tyr	Cys
			130			135				140		Gly
Asp	Phe	Val	Arg	Gly	Tyr	Pro	Phe	Ser	Leu	Arg	Ser	Gly
			145			150			155		160	Val
Ala	Ala	Ser	Cys	Gly	Leu	Trp	Leu	Asn	Leu	Ala	Asp	Leu
											Asp	Ala

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(2) INFORMATION FOR SEQ ID NO:730:

(A) LENGTH: 238 amino acids

(A) LENGTH: 238 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..238

(D) OTHER INFORMATION: / Ceres Seq. ID 1567787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

(2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..227
(D) OTHER INFORMATION: / Ceres Seq. ID 1567788
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:
Met Phe Ser Gly Tyr Ser Cys Arg Tyr Phe Gly Tyr Leu Val Ser Lys
1 5 10 15
Lys Lys Tyr Ile Val Ser Ile Asp Asp Asp Cys Val Pro Ala Lys Asp
20 25 30
Pro Lys Gly Phe Leu Val Asp Ala Val Thr Gln His Val Ile Asn Leu
35 40 45
Glu Asn Pro Ala Thr Pro Leu Phe Phe Asn Thr Leu Tyr Asp Pro Tyr
50 55 60
Cys Glu Gly Ala Asp Phe Val Arg Gly Tyr Pro Phe Ser Leu Arg Ser
65 70 75 80
Gly Val Pro Cys Ala Ala Ser Cys Gly Leu Trp Leu Asn Leu Ala Asp
85 90 95
Leu Asp Ala Pro Thr Gln Ala Leu Lys Thr Glu Lys Arg Asn Thr Ala
100 105 110
Tyr Val Asp Ala Val Met Thr Val Pro Ala Lys Ala Met Leu Pro Ile
115 120 125
Ser Gly Ile Asn Ile Ala Phe Asn Arg Glu Leu Val Gly Pro Ala Leu
130 135 140
Val Pro Ala Leu Arg Leu Ala Gly Glu Gly Lys Val Arg Trp Glu Thr
145 150 155 160
Leu Glu Asp Val Trp Cys Gly Met Cys Leu Lys His Ile Ser Asp His
165 170 175
Leu Gly Tyr Gly Val Lys Thr Gly Leu Pro Tyr Val Trp Arg Asn Glu
180 185 190
Arg Gly Asp Ala Val Glu Ser Leu Arg Lys Gln Met Gly Arg Asn Glu
195 200 205
Ala Asp Gly Glu Lys Cys Ser Ile Phe Arg Phe Ile Glu Ile Ala Arg
210 215 220
Asp Cys Ala
225

(2) INFORMATION FOR SEQ ID NO:732:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1304 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1304
(D) OTHER INFORMATION: / Ceres Seq. ID 1567789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

atctttcttc	tctctctatc	tctctctttt	gaacctataa	aactctttct	ttacaaggat	60
tgatcttttt	gtatttttga	ttttgacatt	tgttttgtgt	tcgatctctg	ttttgatgcg	120
atttctctgt	ttttaaagcc	atttgataga	tgttttcogg	taaagctcag	cgagagaaga	180
agaagaacaa	caatggagtt	tacagatttc	tcaaagacga	gttttttacta	cccgctcgta	240
caaaagcggtt	gggatttcgg	agattttacg	gcggcgagga	ggcattcttt	agggttcgat	300
gagttattaa	gtttctcagca	gcattcaagac	tttgctactg	tttctctcta	ttctctcatt	360
ctccaaacgt	ctccaaccgca	acgcacaaacg	acgaactcgg	cgaaagctgt	ttcaagatga	420
attcaagctc	caccgtcaga	gcaattagt	acgtcaaaag	tggagtcctt	gtgttcgat	480
catttgttga	taaaccCacc	ggcgactcct	aactcgtcat	cgatttcgtc	tgcttcaagc	540

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gaggctctaa atgaagagaa accgaaaaca gaagacaatg aagaagaagg aggtgaagat    600
caacaagaga agagtcatac taagaaacag ttgaagacaa agaagaataa tcagaagaga    660
cagagagagg caagagtgcg attcatgaca aagagtgaag ttgatcatc cgaagatggt    720
tatcgctggc gaaaatatgg tcaaaaagct gtcaaaaaca gtccttttcc caggagtgtac    780
taccgttgca caacggcttc atgtaacgtg aagaagagag tggagagatc attcagagat    840
ccaagcactg tggttacaac ctacgaaggt caacacactc acattagtcc actcagctct    900
cgctctattt ccactggagg ttctttcgga tcgtcaggag ctgcttcagag tctcggtaat    960
ggttgctttg ggtttcctat tgatggctcc acgttaatct ctctcagtt ccaacagctt   1020
gtccaatacc atcaccaca gacgcaacaa gaactcatgt cttgttttgg aggagtcac    1080
gagtacctta atagccaagc taatgagtat ggtgatgata atcgtgtgaa gaagagtgcg   1140
gttttggtta aagataatgg actttctgca gatgtgttgc cgtatcatat gttgaaggaa   1200
gagtagtagt atatatatg tcttatagtt ttYaactcag tttttttttg tataattgtc   1260
taaaagaaac ggatcttttg tctgatgaa gaagatgttt tctc

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(2) INFORMATION FOR SEQ ID NO:733:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..337

(D) OTHER INFORMATION: / Ceres Seq. ID 1567790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

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Met Gln Phe Thr Asp Phe Ser Lys Thr Ser Phe Tyr Tyr Pro Ser Ser
1      5      10      15
Gln Ser Val Trp Asp Phe Gly Asp Leu Ala Ala Glu Arg His Ser
20      25      30
Leu Gly Phe Met Glu Leu Leu Ser Ser Gln Gln His Gln Asp Phe Ala
35      40      45
Thr Val Ser Pro His Ser Phe Leu Leu Gln Thr Ser Gln Pro Gln Thr
50      55      60
Gln Thr Gln Pro Ser Ala Lys Leu Ser Ser Ser Ile Ile Gln Ala Pro
65      70      75
Pro Ser Glu Gln Leu Val Thr Ser Lys Val Glu Ser Leu Cys Ser Asp
85      90      95
His Leu Leu Ile Asn Pro Pro Ala Thr Pro Asn Ser Ser Ser Ile Ser
100      105      110
Ser Ala Ser Ser Glu Ala Leu Asn Glu Glu Lys Pro Lys Thr Glu Asp
115      120      125
Asn Gln Glu Glu Gly Gly Glu Asp Gln Gln Glu Lys Ser His Thr Lys
130      135      140
Lys Gln Leu Lys Ala Lys Lys Asn Asn Gln Lys Arg Gln Arg Glu Ala
145      150      155
Arg Val Ala Phe Met Thr Lys Ser Glu Val Asp His Leu Glu Asp Gly
165      170      175
Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ala Val Lys Asn Ser Pro Phe
180      185      190
Pro Arg Ser Tyr Tyr Arg Cys Thr Thr Ala Ser Cys Asn Val Lys Lys
195      200      205
Arg Val Glu Arg Ser Phe Arg Asp Pro Ser Thr Val Val Thr Thr Tyr
210      215      220
Glu Gly Gln His Thr His Ile Ser Pro Leu Thr Ser Arg Pro Ile Ser
225      230      235
Thr Gly Gly Phe Phe Gly Ser Ser Gly Ala Ala Ser Ser Leu Gly Asn
245      250      255
Gly Cys Phe Gly Phe Pro Ile Asp Gly Ser Thr Leu Ile Ser Pro Gln
260      265      270
Phe Gln Gln Leu Val Gln Tyr His His Gln Gln Gln Gln Glu Leu
275      280      285

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Met Ser Cys Phe Gly Gly Val Asn Glu Tyr Leu Asn Ser His Ala Asn
290 295 300
Glu Tyr Gly Asp Asn Arg Val Lys Lys Ser Arg Val Leu Val Lys
305 310 315 320
Asp Asn Gly Leu Leu Gln Asp Val Val Pro Tyr His Met Leu Lys Glu
325 330 335
Glu

(2) INFORMATION FOR SEQ ID NO:734:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..302

(D) OTHER INFORMATION: / Ceres Seq. ID 1567791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

Met Glu Leu Leu Ser Ser Gln Gln His Gln Asp Phe Ala Thr Val Ser
1 5 10 15
Pro His Ser Phe Leu Leu Gln Thr Ser Gln Pro Gln Thr Gln Gln
20 25 30
Pro Ser Ala Lys Leu Ser Ser Ser Ile Ile Gln Ala Pro Pro Ser Glu
35 40 45
Gln Leu Val Thr Ser Lys Val Glu Ser Leu Cys Ser Asp His Leu Leu
50 55 60
Ile Asn Pro Pro Ala Thr Pro Asn Ser Ser Ser Ile Ser Ser Ala Ser
65 70 75 80
Ser Glu Ala Leu Asn Glu Glu Lys Pro Lys Thr Glu Asp Asn Glu Glu
85 90 95
Glu Gly Gly Glu Asp Gln Gln Glu Lys Ser His Thr Lys Lys Gln Leu
100 105 110
Lys Ala Lys Lys Asn Asn Gln Lys Arg Gln Arg Glu Ala Arg Val Ala
115 120 125
Phe Met Thr Lys Ser Glu Val Asp His Leu Glu Asp Gly Tyr Arg Trp
130 135 140
Arg Lys Tyr Gly Gln Lys Ala Val Lys Asn Ser Pro Phe Pro Arg Ser
145 150 155 160
Tyr Tyr Arg Cys Thr Thr Ala Ser Cys Asn Val Lys Lys Arg Val Glu
165 170 175
Arg Ser Phe Arg Asp Pro Ser Thr Val Val Thr Thr Tyr Glu Gly Gln
180 185 190
His Thr His Ile Ser Pro Leu Thr Ser Arg Pro Ile Ser Thr Gly Gly
195 200 205
Phe Phe Gly Ser Ser Gly Ala Ala Ser Ser Leu Gly Asn Gly Cys Phe
210 215 220
Gly Phe Pro Ile Asp Gly Ser Thr Leu Ile Ser Pro Gln Phe Gln Gln
225 230 235 240
Leu Val Gln Tyr His His Gln Gln Gln Gln Gln Glu Leu Met Ser Cys
245 250 255
Phe Gly Gly Val Asn Glu Tyr Leu Asn Ser His Ala Asn Glu Tyr Gly
260 265 270
Asp Asp Asn Arg Val Lys Lys Ser Arg Val Leu Val Lys Asp Asn Gly
275 280 285
Leu Leu Gln Asp Val Val Pro Tyr His Met Leu Lys Glu Glu
290 295 300

(2) INFORMATION FOR SEQ ID NO:735:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..173
(D) OTHER INFORMATION: / Ceres Seq. ID 1567792
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:
Met Thr Lys Ser Glu Val Asp His Leu Glu Asp Gly Tyr Arg Trp Arg
1 5 10 15
Lys Tyr Gly Gln Lys Ala Val Lys Asn Ser Pro Phe Pro Arg Ser Tyr
20 25 30
Tyr Arg Cys Thr Thr Ala Ser Cys Asn Val Lys Lys Arg Val Glu Arg
35 40 45
Ser Phe Arg Asp Pro Ser Thr Val Val Thr Thr Tyr Glu Gly Gln His
50 55 60
Thr His Ile Ser Pro Leu Thr Ser Arg Pro Ile Ser Thr Gly Gly Phe
65 70 75 80
Phe Gly Ser Ser Gly Ala Ala Ser Ser Leu Gly Asn Gly Cys Phe Gly
85 90 95
Phe Pro Ile Asp Gly Ser Thr Leu Ile Ser Pro Gln Phe Gln Gln Leu
100 105 110
Val Gln Tyr His His Gln Gln Gln Gln Glu Leu Met Ser Cys Phe
115 120 125
Gly Gly Val Asn Glu Tyr Leu Asn Ser His Ala Asn Glu Tyr Gly Asp
130 135 140
Asp Asn Arg Val Lys Lys Ser Arg Val Leu Val Lys Asp Asn Gly Leu
145 150 155 160
Leu Gln Asp Val Val Pro Tyr His Met Leu Lys Glu Glu
165 170

(2) INFORMATION FOR SEQ ID NO:736:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 853 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..853
(D) OTHER INFORMATION: / Ceres Seq. ID 1567797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

agaatttgag attgcctctg caaagagtaa aatggcgaat cctaaagtct tcttcgacat 60
cttgattggg aagatgaagg cagggcgtgt tctaattggag ttatttgcag atgtgactcc 120
gagaacagct aataatttcc gtgctttgtg cactggggag aatggatttg gaaagcagg 180
gaaggcttta cactacaagg gctcagcctt tcaccgtata atcccagggt tcatgtgtca 240
aggtggagat ttactctcgt ggaatggaac tggaggagaa tctattttac ggtctaaatt 300
tgaagatgag aaactcaagt tgaagcacac tgggtccagg attttgtcta tggctaactc 360
tgggtcccaac actagtggtt ctacgttctt catctgcaca gagaagactt cgtgcttga 420
tgggaacatc gtgttttttc ggaaagtgtt tgatggatac aatgtgggtca aggcaatgga 480
ggatgttgGg ctctgacatg ggaatccctt ctgaacgagt tgtgattgaa gattgtgggt 540
agctcaagaa cccaagtcca taagtcttta aaacattggg tgggttgatc ttgacaggtt 600
attctatcat atgctgtgaa gcagagacag catcttagcg ttaaggtaaa tctagtctgt 660
gatgcactac ttgtgttttg actatatcat atgaacctta ggaagtggtc catccttgta 720
agttgttttc ttaaaaactc tgtgtgagac taggtgggat gataataatg gttagtcttc 780
ttatgaagac atttggtttt gtactcttct tattttgggt tagttaatat gaatgaacca 840
aactcttctt agg

(2) INFORMATION FOR SEQ ID NO:737:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..164
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567798
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

Glu	Phe	Glu	Ile	Ala	Ser	Ala	Lys	Ser	Lys	Met	Ala	Asn	Pro	Lys	Val
1			5						10					15	
Phe	Phe	Asp	Ile	Leu	Ile	Gly	Lys	Met	Lys	Ala	Gly	Arg	Val	Val	Met
		20					25						30		
Glu	Leu	Phe	Ala	Asp	Val	Thr	Pro	Arg	Thr	Ala	Asn	Asn	Phe	Arg	Ala
		35				40					45				
Leu	Cys	Thr	Gly	Glu	Asn	Gly	Ile	Gly	Lys	Ala	Gly	Lys	Ala	Leu	His
		50			55					60					
Tyr	Lys	Gly	Ser	Ala	Phe	His	Arg	Ile	Ile	Pro	Gly	Phe	Met	Cys	Gln
65				70					75					80	
Gly	Gly	Asp	Phe	Thr	Arg	Gly	Asn	Gly	Thr	Gly	Gly	Glu	Ser	Ile	Tyr
			85						90				95		
Gly	Ser	Lys	Phe	Glu	Asp	Glu	Asn	Phe	Lys	Leu	Lys	His	Thr	Gly	Pro
		100					105					110			
Gly	Ile	Leu	Ser	Met	Ala	Asn	Ser	Gly	Pro	Asn	Thr	Ser	Gly	Ser	Gln
		115				120					125				
Phe	Phe	Ile	Cys	Thr	Glu	Lys	Thr	Ser	Trp	Leu	Asp	Gly	Lys	His	Val
		130				135					140				
Val	Phe	Gly	Lys	Val	Val	Asp	Gly	Tyr	Asn	Val	Val	Lys	Ala	Met	Glu
145				150					155					160	
Asp	Val	Gly	Leu												

(2) INFORMATION FOR SEQ ID NO:738:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..154
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567799
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

Met	Ala	Asn	Pro	Lys	Val	Phe	Phe	Asp	Ile	Leu	Ile	Gly	Lys	Met	Lys
1			5						10				15		
Ala	Gly	Arg	Val	Val	Met	Glu	Leu	Phe	Ala	Asp	Val	Thr	Pro	Arg	Thr
		20				25						30			
Ala	Asn	Asn	Phe	Arg	Ala	Leu	Cys	Thr	Gly	Glu	Asn	Gly	Ile	Gly	Lys
		35				40				45					
Ala	Gly	Lys	Ala	Leu	His	Tyr	Lys	Gly	Ser	Ala	Phe	His	Arg	Ile	Ile
		50			55					60					
Pro	Gly	Phe	Met	Cys	Gln	Gly	Gly	Asp	Phe	Thr	Arg	Gly	Asn	Gly	Thr
65				70					75				80		
Gly	Gly	Glu	Ser	Ile	Tyr	Gly	Ser	Lys	Phe	Glu	Asp	Glu	Asn	Phe	Lys
		85				90						95			
Leu	Lys	His	Thr	Gly	Pro	Gly	Ile	Leu	Ser	Met	Ala	Asn	Ser	Gly	Pro
		100				105					110				
Asn	Thr	Ser	Gly	Ser	Gln	Phe	Phe	Ile	Cys	Thr	Glu	Lys	Thr	Ser	Trp
		115			120						125				
Leu	Asp	Gly	Lys	His	Val	Val	Phe	Gly	Lys	Val	Val	Asp	Gly	Tyr	Asn
130				135							140				

Val Val Lys Ala Met Glu Asp Val Gly Leu
145 150

(2) INFORMATION FOR SEQ ID NO:739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

Met Lys Ala Gly Arg Val Val Met Glu Leu Phe Ala Asp Val Thr Pro
1 5 10 15
Arg Thr Ala Asn Asn Phe Arg Ala Leu Cys Thr Gly Glu Asn Gly Ile
20 25 30
Gly Lys Ala Gly Lys Ala Leu His Tyr Lys Gly Ser Ala Phe His Arg
35 40 45
Ile Ile Pro Gly Phe Met Cys Gln Gly Gly Asp Phe Thr Arg Gly Asn
50 55 60
Gly Thr Gly Gly Glu Ser Ile Tyr Gly Ser Lys Phe Glu Asp Glu Asn
65 70 75 80
Phe Lys Leu Lys His Thr Gly Pro Gly Ile Leu Ser Met Ala Asn Ser
85 90 95
Gly Pro Asn Thr Ser Gly Ser Gln Phe Phe Ile Cys Thr Glu Lys Thr
100 105 110
Ser Trp Leu Asp Gly Lys His Val Val Phe Gly Lys Val Val Asp Gly
115 120 125
Tyr Asn Val Val Lys Ala Met Glu Asp Val Gly Leu
130 135 140

(2) INFORMATION FOR SEQ ID NO:740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1033
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

ctcaatttct tttttttctt cagaaatttc ctccgatttc aaaattttcc ggtgaaatcg 60
aaaaaaaaag cgagatcttc ttctctaagt cgcgacgacct taagcagaga tcaatatgtc 120
taactggcga aGctcgccga gcaagccgag cggtacgaag agatggttca attcatggaa 180
cagctcgtaa gtggagctac accggccggt gagctgaccg tagaagagag gaactttctc 240
tcggtcgcggt ataaaaacgt gattggatct ctctgctgcg catggagaaat cgtgtctttc 300
attgagcaaa aggaagagag caggaaagaac gaagaacacg tgcgcttgt taaggattac 360
agatctaaag ttgagactga gctttcttcg atctgttctg ggattctcag gttacttgat 420
tcgactctga ttctcttcag taactgccagt gactctaagg ttttttaact gaagatgaaa 480
ggagattatc atcgttatatt ggctgagttt aaatctggtg atgagaggaa aactgcgtct 540
gaagatacta tgatcgctta caaagctgct caggacgttg cagttgtctga tctagcaact 600
aacatccaga tcaggtcttg ttggctctt aactcttcag tgttttacta cgagattctc 660
aacctcttcg agaaagcttg tagcatggcg aaacaggctt ttgaagaagc cattgctgag 720
ctggacacat tgggagagga gacatacaag gacagctact tcatcatgca gtgtctaagg 780
gacaactcaa cctctttgac ctccgatgat caggagcaga tggatgagc ctgaaggtct 840
aatggaaqaa aagacggtta tgtaatgtac atcgcaacct aacgcaaaaa ctgagttcaa 900
cctcctttgc tgtaaaaact gTtcgaaaag aaaagtttgt ttttttatga cagatttatg 960
gcacagcttt ggtgttatct gctgctctgt atcaactctg tttttgtttg gtaattttatc 1020

ctcatctttg etc

(2) INFORMATION FOR SEQ ID NO:741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..277
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

Leu Asn Phe Phe Phe Ser Ser Arg Asn Phe Leu Arg Phe Gln Asn Phe
1 5 10 15
Pro Val Lys Ser Lys Lys Lys Ala Arg Ser Ser Ser Leu Met Ala Thr
20 25 30
Thr Leu Ser Arg Asp Gln Tyr Val Tyr Met Ala Lys Leu Ala Glu Gln
35 40 45
Ala Glu Arg Tyr Glu Glu Met Val Gln Phe Met Glu Gln Leu Val Ser
50 55 60
Gly Ala Thr Pro Ala Gly Glu Leu Thr Val Glu Glu Arg Asn Leu Leu
65 70 75 80
Ser Val Ala Tyr Lys Asn Val Ile Gly Ser Leu Arg Ala Ala Trp Arg
85 90 95
Ile Val Ser Ser Ile Glu Gln Lys Glu Glu Ser Arg Lys Asn Glu Glu
100 105 110
His Val Ser Leu Val Lys Asp Tyr Arg Ser Lys Val Glu Thr Glu Leu
115 120 125
Ser Ser Ile Cys Ser Gly Ile Leu Arg Leu Leu Asp Ser His Leu Ile
130 135 140
Pro Ser Ala Thr Ala Ser Glu Ser Lys Val Phe Tyr Leu Lys Met Lys
145 150 155 160
Gly Asp Tyr His Arg Tyr Leu Ala Glu Phe Lys Ser Gly Asp Glu Arg
165 170 175
Lys Thr Ala Ala Glu Asp Thr Met Ile Ala Tyr Lys Ala Ala Gln Asp
180 185 190
Val Ala Val Ala Asp Leu Ala Pro Thr His Pro Ile Arg Leu Gly Leu
195 200 205
Ala Leu Asn Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn Ser Ser Glu
210 215 220
Lys Ala Cys Ser Met Ala Lys Gln Ala Phe Glu Glu Ala Ile Ala Glu
225 230 235 240
Leu Asp Thr Leu Gly Glu Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met
245 250 255
Gln Leu Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp Met Gln Glu
260 265 270
Gln Met Asp Glu Ala
275

(2) INFORMATION FOR SEQ ID NO:742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..248
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:


```

Met Ala Thr Thr Leu Ser Arg Asp Gln Tyr Val Tyr Met Ala Lys Leu
1      5      10
Ala Glu Gln Ala Glu Arg Tyr Glu Glu Met Val Gln Phe Met Glu Gln
20     25     30
Leu Val Ser Gly Ala Thr Pro Ala Gly Glu Leu Thr Val Glu Glu Arg
35     40     45
Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly Ser Leu Arg Ala
50     55     60
Ala Trp Arg Ile Val Ser Ser Ile Glu Gln Lys Glu Glu Ser Arg Lys
65     70     75     80
Asn Glu Glu His Val Ser Leu Val Lys Asp Tyr Arg Ser Lys Val Glu
85     90     95
Thr Glu Leu Ser Ser Ile Cys Ser Gly Ile Leu Arg Leu Leu Asp Ser
100    105    110
His Leu Ile Pro Ser Ala Thr Ala Ser Glu Ser Lys Val Phe Tyr Leu
115    120    125
Lys Met Lys Gly Asp Tyr His Arg Tyr Leu Ala Glu Phe Lys Ser Gly
130    135    140
Asp Glu Arg Lys Thr Ala Ala Glu Asp Thr Met Ile Ala Tyr Lys Ala
145    150    155    160
Ala Gln Asp Val Ala Val Ala Asp Leu Ala Pro Thr His Pro Ile Arg
165    170    175
Leu Gly Leu Ala Leu Asn Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn
180    185    190
Ser Ser Glu Lys Ala Cys Ser Met Ala Lys Gln Ala Phe Glu Glu Ala
195    200    205
Ile Ala Glu Leu Asp Thr Leu Gly Glu Glu Ser Tyr Lys Asp Ser Thr
210    215    220
Leu Ile Met Gln Leu Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp
225    230    235    240
Met Gln Glu Gln Met Asp Glu Ala
245

```

(2) INFORMATION FOR SEQ ID NO:743:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 236 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..236
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

```

Met Ala Lys Leu Ala Glu Gln Ala Glu Arg Tyr Glu Glu Met Val Gln
1      5      10      15
Phe Met Glu Gln Leu Val Ser Gly Ala Thr Pro Ala Gly Glu Leu Thr
20     25     30
Val Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly
35     40     45
Ser Leu Arg Ala Ala Trp Arg Ile Val Ser Ser Ile Glu Gln Lys Glu
50     55     60
Glu Ser Arg Lys Asn Glu Glu His Val Ser Leu Val Lys Asp Tyr Arg
65     70     75     80
Ser Lys Val Glu Thr Glu Leu Ser Ser Ile Cys Ser Gly Ile Leu Arg
85     90     95
Leu Leu Asp Ser His Leu Ile Pro Ser Ala Thr Ala Ser Glu Ser Lys
100    105    110
Val Phe Tyr Leu Lys Met Lys Gly Asp Tyr His Arg Tyr Leu Ala Glu
115    120    125
Phe Lys Ser Gly Asp Glu Arg Lys Thr Ala Ala Glu Asp Thr Met Ile

```

(C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..392

(D) OTHER INFORMATION: / Ceres Seq. ID 1567836

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

Phe	Leu	Asp	Lys	Gln	Arg	Ala	Arg	Asp	Gly	Ser	His	Ile	Ile	Thr	Arg	
1			5						10					15		
Ser	Ile	Phe	Ser	Arg	Lys	Arg	Lys	Cys	Asp	Tyr	Pro	Phe	Asp	Phe	Phe	
			20					25					30			
Ala	Glu	Glu	Asp	Glu	Arg	Glu	Lys	Lys	Arg	Lys	Arg	Phe	Glu	Ile	Met	
		35					40					45				
Ala	Asn	Val	Val	Gly	Gln	Leu	Lys	Arg	Gly	Ile	Ser	Arg	Gln	Phe	Ser	
	50					55					60					
Thr	Gly	Ser	Leu	Arg	Arg	Thr	Leu	Ser	Arg	Gln	Phe	Thr	Arg	Gln	Ala	
65				70					75					80		
Ser	His	Asp	Pro	Arg	Arg	Asn	Asn	Met	Arg	Phe	Ser	Phe	Gly	Arg	Gln	
			85					90						95		
Ser	Ser	Leu	Asp	Pro	Ile	Arg	Arg	Ser	Pro	Asp	Gly	Ser	Asn	Gly	Pro	
		100						105					110			
Gln	Leu	Ala	Val	Pro	Asp	Asn	Leu	Asp	Ala	Thr	Met	Gln	Leu	Leu	Phe	
	115						120					125				
Val	Ala	Cys	Arg	Gly	Asp	Val	Glu	Gly	Val	Gln	Asp	Leu	Leu	Asp	Glu	
	130					135					140					
Gly	Ile	Asp	Val	Asn	Ser	Ile	Asp	Leu	Asp	Gly	Arg	Thr	Ala	Leu	His	
	145			150						155				160		
Ile	Ala	Ala	Cys	Glu	Gly	His	Val	Asp	Val	Val	Lys	Leu	Leu	Leu	Thr	
			165					170						175		
Arg	Lys	Ala	Asn	Ile	Asp	Ala	Arg	Asp	Arg	Trp	Gly	Ser	Thr	Ala	Ala	
		180					185						190			
Ala	Asp	Ala	Lys	Tyr	Tyr	Gly	Asn	Met	Asp	Val	Phe	Asn	Ile	Leu	Lys	
	195						200					205				
Ala	Arg	Gly	Ala	Lys	Val	Pro	Lys	Thr	Lys	Arg	Thr	Pro	Met	Val	Val	
	210					215					220					
Ala	Asn	Pro	Arg	Glu	Val	Pro	Glu	Tyr	Glu	Leu	Asn	Pro	Gln	Glu	Leu	
225				230					235					240		
Gln	Val	Arg	Lys	Ala	Asp	Gly	Ile	Ser	Lys	Gly	Ile	Tyr	Gln	Val	Ala	
			245						250					255		
Lys	Trp	Asn	Gly	Thr	Lys	Val	Ser	Val	Lys	Ile	Leu	Asp	Lys	Asp	Leu	
		260					265					270				
Tyr	Lys	Asp	Ser	Asp	Thr	Ile	Asn	Ala	Phe	Lys	His	Glu	Leu	Thr	Leu	
	275						280					285				
Phe	Glu	Lys	Val	Arg	His	Pro	Asn	Val	Val	Gln	Phe	Val	Gly	Ala	Val	
	290					295					300					
Thr	Gln	Asn	Val	Pro	Met	Met	Ile	Val	Ser	Glu	Tyr	His	Pro	Lys	Gly	
305				310						315				320		
Asp	Leu	Gly	Ser	Tyr	Leu	Gln	Lys	Lys	Gly	Arg	Leu	Ser	Pro	Ala	Lys	
			325						330					335		
Val	Leu	Arg	Phe	Ala	Leu	Asp	Ile	Ala	Arg	Gly	Met	Asn	Tyr	Leu	His	
		340					345						350			
Glu	Cys	Lys	Pro	Glu	Pro	Val	Ile	His	Cys	Asp	Leu	Lys	Pro	Lys	Asn	
	355					360					365					
Ile	Met	Leu	Asp	Ser	Gly	Gly	His	Leu	Lys	Val	Ala	Gly	Ile	Trp	Phe	
	370					375					380					
Asp	Lys	Phe	Cys	Lys	Val	Ile	Ile									
385					390											

- (2) INFORMATION FOR SEQ ID NO:746:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..345
(D) OTHER INFORMATION: / Ceres Seq. ID 1567837
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:
Met Ala Asn Val Val Gly Gln Leu Lys Arg Gly Ile Ser Arg Gln Phe
1 5 10 15
Ser Thr Gly Ser Leu Arg Arg Thr Leu Ser Arg Gln Phe Thr Arg Gln
20 25 30
Ala Ser His Asp Pro Arg Arg Asn Asn Met Arg Phe Ser Phe Gly Arg
35 40 45
Gln Ser Ser Leu Asp Pro Ile Arg Arg Ser Pro Asp Gly Ser Asn Gly
50 55 60
Pro Gln Leu Ala Val Pro Asp Asn Leu Asp Ala Thr Met Gln Leu Leu
65 70 75 80
Phe Val Ala Cys Arg Gly Asp Val Glu Gly Val Gln Asp Leu Leu Asp
85 90 95
Glu Gly Ile Asp Val Asn Ser Ile Asp Leu Asp Gly Arg Thr Ala Leu
100 105 110
His Ile Ala Ala Cys Glu Gly His Val Asp Val Val Lys Leu Leu Leu
115 120 125
Thr Arg Lys Ala Asn Ile Asp Ala Arg Asp Arg Trp Gly Ser Thr Ala
130 135 140
Ala Ala Asp Ala Lys Tyr Tyr Gly Asn Met Asp Val Phe Asn Ile Leu
145 150 155 160
Lys Ala Arg Gly Ala Lys Val Pro Lys Thr Lys Arg Thr Pro Met Val
165 170 175
Val Ala Asn Pro Arg Glu Val Pro Glu Tyr Glu Leu Asn Pro Gln Glu
180 185 190
Leu Gln Val Arg Lys Ala Asp Gly Ile Ser Lys Gly Ile Tyr Gln Val
195 200 205
Ala Lys Trp Asn Gly Thr Lys Val Ser Val Lys Ile Leu Asp Lys Asp
210 215 220
Leu Tyr Lys Asp Ser Asp Thr Ile Asn Ala Phe Lys His Glu Leu Thr
225 230 235 240
Leu Phe Glu Lys Val Arg His Pro Asn Val Val Gln Phe Val Gly Ala
245 250 255
Val Thr Gln Asn Val Pro Met Met Ile Val Ser Glu Tyr His Pro Lys
260 265 270
Gly Asp Leu Gly Ser Tyr Leu Gln Lys Lys Gly Arg Leu Ser Pro Ala
275 280 285
Lys Val Leu Arg Phe Ala Leu Asp Ile Ala Arg Gly Met Asn Tyr Leu
290 295 300
His Glu Cys Lys Pro Glu Pro Val Ile His Cys Asp Leu Lys Pro Lys
305 310 315 320
Asn Ile Met Leu Asp Ser Gly Gly His Leu Lys Val Ala Gly Ile Trp
325 330 335
Phe Asp Lys Phe Cys Lys Val Ile Ile
340 345

(2) INFORMATION FOR SEQ ID NO:747:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide

(B) LOCATION: 1..304

(D) OTHER INFORMATION: / Ceres Seq. ID 1567838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

```
Met Arg Phe Ser Phe Gly Arg Gln Ser Ser Leu Asp Pro Ile Arg Arg
1      5      10      15
Ser Pro Asp Gly Ser Asn Gly Pro Gln Leu Ala Val Pro Asp Asn Leu
20      25      30
Asp Ala Thr Met Gln Leu Leu Phe Val Ala Cys Arg Gly Asp Val Glu
35      40      45
Gly Val Gln Asp Leu Leu Asp Glu Gly Ile Asp Val Asn Ser Ile Asp
50      55      60
Leu Asp Gly Arg Thr Ala Leu His Ile Ala Ala Cys Glu Gly His Val
65      70      75      80
Asp Val Val Lys Leu Leu Thr Arg Lys Ala Asn Ile Asp Ala Arg
85      90      95
Asp Arg Trp Gly Ser Thr Ala Ala Asp Ala Lys Tyr Tyr Gly Asn
100     105     110
Met Asp Val Phe Asn Ile Leu Lys Ala Arg Gly Ala Lys Val Pro Lys
115     120     125
Thr Lys Arg Thr Pro Met Val Val Ala Asn Pro Arg Glu Val Pro Glu
130     135     140
Tyr Glu Leu Asn Pro Gln Glu Leu Gln Val Arg Lys Ala Asp Gly Ile
145     150     155     160
Ser Lys Gly Ile Tyr Gln Val Ala Lys Trp Asn Gly Thr Lys Val Ser
165     170     175
Val Lys Ile Leu Asp Lys Asp Leu Tyr Lys Asp Ser Asp Thr Ile Asn
180     185     190
Ala Phe Lys His Glu Leu Thr Leu Phe Glu Lys Val Arg His Pro Asn
195     200     205
Val Val Gln Phe Val Gly Ala Val Thr Gln Asn Val Pro Met Met Ile
210     215     220
Val Ser Glu Tyr His Pro Lys Gly Asp Leu Gly Ser Tyr Leu Gln Lys
225     230     235     240
Lys Gly Arg Leu Ser Pro Ala Lys Val Leu Arg Phe Ala Leu Asp Ile
245     250     255
Ala Arg Gly Met Asn Tyr Leu His Glu Cys Lys Pro Glu Pro Val Ile
260     265     270
His Cys Asp Leu Lys Pro Lys Asn Ile Met Leu Asp Ser Gly Gly His
275     280     285
Leu Lys Val Ala Gly Ile Trp Phe Asp Lys Phe Cys Lys Val Ile Ile
290     295     300
```

(2) INFORMATION FOR SEQ ID NO:748:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1884 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1884

(D) OTHER INFORMATION: / Ceres Seq. ID 1567843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

```
acagcttctg atctcaactag tgttcgtcat cttgttctga ttgaagtttg ggaagtgggtg 60
atggtaatat gagcagcagc gcgtgtagcc atcggcggtt tgcgaaagc tcgtctcgtc 120
acataacctc ctctctctcg tctcttctca gtgtcgccag atgagtatgg acgcacaaag 180
cgttttctga aagcttagga gttctggtct attacgaact caaggtctaa ttggaggcaa 240
gtggcttgac tcgtatgaca ataagacaat caaggttaac aatccagcaa ccggtgaaat 300
tatagctgat gttgcattga tgggaacaaa agagacaaat gatgctattg cttcttctta 360
```

tgaagcattt	acctcttgga	gcagattgac	tgctggagag	aggagtaaa	ttttcggag	420
atggtagtac	ctctctgatt	cacacaagga	agaacttgga	caactataaa	ctttggagca	480
aggaaaaacca	ctcaaggaa	ccatcggaga	ggtagcatat	ggggcaagtt	ttatttagta	540
ctatggcgaag	gaggcaaaa	gtgtatatgg	tgtatataat	cctccgaatc	tgtctgctgc	600
ccgactgtgt	gttctaaaaa	agcctgtcgg	tattgttgg	gcaattacc	cttggaaatt	660
ccccttagcc	atgattactc	ggaaggctgg	ccctgctctt	gcttctggat	gcacgggtgt	720
tgtaaaacca	tctgaactta	cgcccttaac	agcacttgct	gcggctgaac	ttgcaacttca	780
agctggagtt	cctccggggg	cacttaattg	ggtcatggga	aatgctccctg	aatttgggga	840
tgctttgctt	acgagctcac	aggtgagaaa	aatcacgttc	acgggatcaa	cagcagttgg	900
gaagaaagttg	atggcagctg	ctgcacctac	cgtaagaaga	gtttctctag	aacttggcgg	960
caacgcacc	tctatagtat	ttgatgatgc	agacctggat	gtagctgtaa	aaggaaagct	1020
tgcagcgaaa	tttaggaata	gtggtcagac	atgtgtttgt	gcgaacagag	tactttgtca	1080
agatggtatc	tatgataaat	ttgctgaggg	ctttctgaa	gcgggttcaa	aattagaagt	1140
aggagatggg	tttaggggat	ggacaaccca	gggtccactt	ataaatgatg	cagcagttga	1200
aaaaggttag	acatttgtac	aaagtgctgt	ttctaaggga	gcaaaaatca	tcattgggtg	1260
caaaagggac	agtcctaggga	tgactttcta	tgagcctact	gttatccggc	atgtttcggg	1320
taacatgatc	atgtctaaag	aggagatttt	tggacctgta	gttcccttta	ttcgggttcaa	1380
aaccgaggag	gcgcgtatca	gaattgtctaa	tgacacaatt	gcaggacttg	ctgcttatat	1440
attcacaaac	agtgctcaaa	gatcttggcg	tgattttgaa	gcacttgaat	atggaactgt	1500
aggggtgaac	gaaggactca	tatcaacaga	ggtggctcca	ttcgggggag	tgaagcagtc	1560
tggtcttggga	aggggaagat	ccaagtatgg	tatggacgaa	taccttgaga	tcaaaatcgt	1620
atgcttctgga	gatattgaata	gacactgatt	tggtttgttt	gaaaagcttt	agaaaattgt	1680
agtttttttc	ctccactcgt	atccttcttaa	taaaagctta	ctgtggaaca	taataaggtat	1740
tcggaggata	cttcttaaga	aataagatt	tggtctacga	ccaattgtta	gcattgattt	1800
tagataataa	tttgggggtt	ccattttatt	tatcttgttt	tacgttattt	ttttctttgt	1860
tttactgttaa	ttttgttaat	tcgg				

(2) INFORMATION FOR SEQ ID NO:749:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 495 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..495

(D) OTHER INFORMATION: / Ceres Seq. ID 1567844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

Met	Ser	Met	Asp	Ala	Gln	Ser	Val	Ser	Glu	Lys	Leu	Arg	Ser	Ser	Gly
1				5						10				15	
Leu	Leu	Arg	Thr	Gln	Gly	Leu	Ile	Gly	Gly	Lys	Trp	Leu	Asp	Ser	Tyr
			20					25					30		
Asp	Asn	Lys	Thr	Ile	Lys	Val	Asn	Asn	Pro	Ala	Thr	Gly	Glu	Ile	Ile
		35					40					45			
Ala	Asp	Val	Ala	Cys	Met	Gly	Thr	Lys	Glu	Thr	Asn	Asp	Ala	Ile	Ala
		50				55					60				
Ser	Ser	Tyr	Glu	Ala	Phe	Thr	Ser	Trp	Ser	Arg	Leu	Thr	Ala	Gly	Glu
		65			70				75					80	
Arg	Ser	Lys	Val	Leu	Arg	Arg	Trp	Tyr	Asp	Leu	Leu	Ile	Ala	His	Lys
		85						90						95	
Glu	Glu	Leu	Gly	Gln	Leu	Ile	Thr	Leu	Glu	Gln	Gly	Lys	Pro	Leu	Lys
		100						105					110		
Glu	Ala	Ile	Gly	Glu	Val	Ala	Tyr	Gly	Ala	Ser	Phe	Ile	Glu	Tyr	Tyr
		115				120					125				
Ala	Glu	Glu	Ala	Lys	Arg	Val	Tyr	Gly	Asp	Ile	Ile	Pro	Pro	Asn	Leu
		130				135					140				
Ser	Asp	Arg	Arg	Leu	Leu	Val	Leu	Lys	Gln	Pro	Val	Gly	Ile	Val	Gly
		145			150				155					160	
Ala	Ile	Thr	Pro	Trp	Asn	Phe	Pro	Leu	Ala	Met	Ile	Thr	Arg	Lys	Val
		165						170						175	
Gly	Pro	Ala	Leu	Ala	Ser	Gly	Cys	Thr	Val	Val	Val	Lys	Pro	Ser	Glu

(X1) SEQUENCE															
Met	Asp	Ala	Gln	Ser	Val	Ser	Glu	Lys	Leu	Arg	Ser	Ser	Gly	Leu	Leu
1			5						10					15	
Arg	Thr	Gln	Gly	Leu	Ile	Gly	Gly	Lys	Trp	Leu	Asp	Ser	Thr	Asp	Asn
		20						25					30		
Lys	Thr	Ile	Lys	Val	Asn	Asn	Pro	Ala	Thr	Gly	Glu	Ile	Ile	Ala	Asp
		35					40					45			
Val	Ala	Cys	Met	Gly	Thr	Lys	Glu	Thr	Asn	Asp	Ala	Ile	Ala	Ser	Ser
	50					55				60					
Tyr	Glu	Ala	Phe	Thr	Ser	Trp	Ser	Arg	Leu	Thr	Ala	Gly	Glu	Arg	Ser
65				70					75				80		

Lys Val Leu Arg Arg Trp Tyr Asp Leu Leu Ile Ala His Lys Glu Glu
85 90 95
Leu Gly Gln Leu Ile Thr Leu Glu Gln Gly Lys Pro Leu Lys Glu Ala
100 105 110
Ile Gly Glu Val Ala Tyr Gly Ala Ser Phe Ile Glu Tyr Tyr Ala Glu
115 120 125
Glu Ala Lys Arg Val Tyr Gly Asp Ile Ile Pro Pro Asn Leu Ser Asp
130 135 140
Arg Arg Leu Leu Val Leu Lys Gln Pro Val Gly Ile Val Gly Ala Ile
145 150 155 160
Thr Pro Trp Asn Phe Pro Leu Ala Met Ile Thr Arg Lys Val Gly Pro
165 170 175
Ala Leu Ala Ser Gly Cys Thr Val Val Val Lys Pro Ser Glu Leu Thr
180 185 190
Pro Leu Thr Ala Leu Ala Ala Glu Leu Ala Leu Gln Ala Gly Val
195 200 205
Pro Pro Gly Ala Leu Asn Val Val Met Gly Asn Ala Pro Glu Ile Gly
210 215 220
Asp Ala Leu Leu Thr Ser Pro Gln Val Arg Lys Ile Thr Phe Thr Gly
225 230 235 240
Ser Thr Ala Val Gly Lys Lys Leu Met Ala Ala Ala Pro Thr Val
245 250 255
Lys Lys Val Ser Leu Glu Leu Gly Gly Asn Ala Pro Ser Ile Val Phe
260 265 270
Asp Asp Ala Asp Leu Asp Val Ala Val Lys Gly Thr Leu Ala Ala Lys
275 280 285
Phe Arg Asn Ser Gly Gln Thr Cys Val Cys Ala Asn Arg Val Leu Val
290 295 300
Gln Asp Gly Ile Tyr Asp Lys Phe Ala Glu Ala Phe Ser Glu Ala Val
305 310 315 320
Gln Lys Leu Glu Val Gly Asp Gly Phe Arg Asp Gly Thr Thr Gln Gly
325 330 335
Pro Leu Ile Asn Asp Ala Ala Val Gln Lys Val Glu Thr Phe Val Gln
340 345 350
Asp Ala Val Ser Lys Gly Ala Lys Ile Ile Ile Gly Gly Lys Arg His
355 360 365
Ser Leu Gly Met Thr Phe Tyr Glu Pro Thr Val Ile Arg Asp Val Ser
370 375 380
Asp Asn Met Ile Met Ser Lys Glu Glu Ile Phe Gly Pro Val Ala Pro
385 390 395 400
Leu Ile Arg Phe Lys Thr Glu Glu Asp Ala Ile Arg Ile Ala Asn Asp
405 410 415
Thr Ile Ala Gly Leu Ala Ala Tyr Ile Phe Thr Asn Ser Val Gln Arg
420 425 430
Ser Trp Arg Val Phe Glu Ala Leu Glu Tyr Gly Leu Val Gly Val Asn
435 440 445
Glu Gly Leu Ile Ser Thr Glu Val Ala Pro Phe Gly Gly Val Lys Gln
450 455 460
Ser Gly Leu Gly Arg Glu Gly Ser Lys Tyr Gly Met Asp Glu Tyr Leu
465 470 475 480
Glu Ile Lys Tyr Val Cys Leu Gly Asp Met Asn Arg His
485 490

(2) INFORMATION FOR SEQ ID NO:751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..442

(D) OTHER INFORMATION: / Ceres Seq. ID 1567846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

Met Gly Thr Lys Glu Thr Asn Asp Ala Ile Ala Ser Ser Tyr Glu Ala
1 5 10 15
Phe Thr Ser Trp Ser Arg Leu Thr Ala Gly Glu Arg Ser Lys Val Leu
20 25 30
Arg Arg Trp Tyr Asp Leu Leu Ile Ala His Lys Glu Glu Leu Gly Gln
35 40 45
Leu Ile Thr Leu Glu Gln Gly Lys Pro Leu Lys Glu Ala Ile Gly Glu
50 55 60
Val Ala Tyr Gly Ala Ser Phe Ile Glu Tyr Tyr Ala Glu Glu Ala Lys
65 70 75 80
Arg Val Tyr Gly Asp Ile Ile Pro Pro Asn Leu Ser Asp Arg Arg Leu
85 90 95
Leu Val Leu Lys Gln Pro Val Gly Ile Val Gly Ala Ile Thr Pro Trp
100 105 110
Asn Phe Pro Leu Ala Met Ile Thr Arg Lys Val Gly Pro Ala Leu Ala
115 120 125
Ser Gly Cys Thr Val Val Val Lys Pro Ser Glu Leu Thr Pro Leu Thr
130 135 140
Ala Leu Ala Ala Ala Glu Leu Ala Leu Gln Ala Gly Val Pro Pro Gly
145 150 155 160
Ala Leu Asn Val Val Met Gly Asn Ala Pro Glu Ile Gly Asp Ala Leu
165 170 175
Leu Thr Ser Pro Gln Val Arg Lys Ile Thr Phe Thr Gly Ser Thr Ala
180 185 190
Val Gly Lys Lys Leu Met Ala Ala Ala Pro Thr Val Lys Lys Val
195 200 205
Ser Leu Glu Leu Gly Gly Asn Ala Pro Ser Ile Val Phe Asp Asp Ala
210 215 220
Asp Leu Asp Val Ala Val Lys Gly Thr Leu Ala Ala Lys Phe Arg Asn
225 230 235 240
Ser Gly Gln Thr Cys Val Cys Ala Asn Arg Val Leu Val Gln Asp Gly
245 250 255
Ile Tyr Asp Lys Phe Ala Glu Ala Phe Ser Glu Ala Val Gln Lys Leu
260 265 270
Glu Val Gly Asp Gly Phe Arg Asp Gly Thr Thr Gln Gly Pro Leu Ile
275 280 285
Asn Asp Ala Ala Val Gln Lys Val Glu Thr Phe Val Gln Asp Ala Val
290 295 300
Ser Lys Gly Ala Lys Ile Ile Ile Gly Gly Lys Arg His Ser Leu Gly
305 310 315 320
Met Thr Phe Tyr Glu Pro Thr Val Ile Arg Asp Val Ser Asp Asn Met
325 330 335
Ile Met Ser Lys Glu Glu Ile Phe Gly Pro Val Ala Pro Leu Ile Arg
340 345 350
Phe Lys Thr Glu Glu Asp Ala Ile Arg Ile Ala Asn Asp Thr Ile Ala
355 360 365
Gly Leu Ala Ala Tyr Ile Phe Thr Asn Ser Val Gln Arg Ser Trp Arg
370 375 380
Val Phe Glu Ala Leu Glu Tyr Gly Leu Val Gly Val Asn Glu Gly Leu
385 390 395 400
Ile Ser Thr Glu Val Ala Pro Phe Gly Gly Val Lys Gln Ser Gly Leu
405 410 415
Gly Arg Glu Gly Ser Lys Tyr Gly Met Asp Glu Tyr Leu Glu Ile Lys
420 425 430
Tyr Val Cys Leu Gly Asp Met Asn Arg His
435 440

(2) INFORMATION FOR SEQ ID NO:752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1386
(D) OTHER INFORMATION: / Ceres Seq. ID 1567877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

aaacctttct	cttctctgct	aacgagaaaa	caaaagctat	cgtcttttct	actactacta	60
ctgctattat	tacattgaat	ccctttgtgt	cttctcttct	agctgctact	ttgttcgagt	120
gctttcttac	atgcgcgtcg	agattgttga	caggaaaaag	aagtctctgt	gaacacGaga	180
Ntgtagctga	gattctaaag	caatggagag	agtacaatga	gcagattgag	gcagaactct	240
gtatcgatgg	tgggtgtcca	aaatcaatcc	gaaagccctc	tccaaaaagg	tcgaggaagg	300
gttgtatgaa	aggtaaaggt	ggacctgaaa	acgggatttg	tgactataga	gaagttagac	360
agaggagatg	gggtaaaatg	gttgcgtgag	tcogtgagcc	agacggaggt	gctagggtgt	420
ggctcggtac	tttctccagt	tcatatgaag	ctgcattggc	ttatgacgag	gcggccaaag	480
ctatatatgg	tcagttctgc	agactcaatc	ttcccgagat	cacaaatcgc	tctttctoga	540
ctgctgccac	tgccactgtg	tcaggctcgg	ttactgcatt	ttctgatgaa	tctgaagttt	600
gtgcacgtga	ggatacaaat	gcaagttcag	gttttggtca	ggtgaaacta	gaggattgta	660
gcgatgaata	tgttctctta	gatagttctc	agtgatttaa	agaggagctg	aaaggaaaaag	720
aggaagttag	ggaagaacat	aacttggctg	ttggttttgg	aattggacag	gactcgaaaa	780
gggagacttt	ggatgcttgg	ttgatgggaa	atggcaatga	acaagaacca	ttggaagtgt	840
gtgtggatga	aacgtttgat	attaatgagc	tattgggtat	attaaacgac	aaacatgtgt	900
ctgtccaaga	gacaatgcag	tatcaagtgg	atagacaccc	aaatttcagt	taccaaacgc	960
agtttccaaa	ttctaacctg	ctcgggagcc	tcaacctcat	ggagattgct	caaccaggag	1020
ttgattatgg	atgtccctta	gtgcagccca	gtgatatgga	gaactatgag	attgatttag	1080
accatccgag	gttcaatgat	cttgacatac	aggacttgga	ttttggagga	gacaaagatg	1140
ttcatggatc	tacataagat	ttcaaattto	gttgactgtg	cctaagtttg	tgtattctgt	1200
ccgagacgggt	gtagctgtta	ctagctagaa	gctgcctctc	tttgaagcta	ctgatacttt	1260
ctgatattaa	tggttgtgag	acgtagtaca	tgtagttagg	taatgtagga	caagttcaaa	1320
tatgattcct	tctttctttt	tcttgtgaat	acatatgaca	tatgaagaag	ttcaaacgtt	1380
gggtcc						

(2) INFORMATION FOR SEQ ID NO:753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..384
(D) OTHER INFORMATION: / Ceres Seq. ID 1567878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

Thr	Phe	Leu	Phe	Ser	Ala	Asn	Glu	Lys	Thr	Lys	Ala	Ile	Val	Phe	Ala
1			5						10					15	
Thr	Thr	Thr	Thr	Thr	Ala	Ile	Ile	Thr	Leu	Asn	Pro	Leu	Cys	Ser	Ser
					20				25					30	
Ser	Ala	Ala	Ala	Thr	Leu	Phe	Glu	Cys	Phe	Leu	Thr	Cys	Arg	Arg	Leu
					35				40					45	
Leu	Thr	Gly	Lys	Gly	Ser	Leu	Val	Glu	His	Glu	Xaa	Val	Ala	Glu	Ile
					50				55					60	
Leu	Arg	Gln	Trp	Arg	Glu	Tyr	Asn	Glu	Gln	Ile	Glu	Ala	Glu	Ser	Cys
					65				70					75	
Ile	Asp	Gly	Gly	Gly	Pro	Lys	Ser	Ile	Arg	Lys	Pro	Pro	Pro	Lys	Gly
					85				90					95	
Ser	Arg	Lys	Gly	Cys	Met	Lys	Gly	Lys	Gly	Gly	Pro	Glu	Asn	Gly	Ile
					100				105					110	
Cys	Asp	Tyr	Arg	Glu	Val	Arg	Gln	Arg	Arg	Trp	Gly	Lys	Trp	Val	Ala

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      115              120              125
Glu Ile Arg Glu Pro Asp Gly Gly Ala Arg Leu Trp Leu Gly Thr Phe
130              135              140
Ser Ser Ser Tyr Glu Ala Ala Leu Ala Tyr Asp Glu Ala Ala Lys Ala
145              150              155              160
Ile Tyr Gly Gln Ser Ala Arg Leu Asn Leu Pro Glu Ile Thr Asn Arg
      165              170              175
Ser Ser Ser Thr Ala Ala Thr Ala Thr Val Ser Gly Ser Val Thr Ala
      180              185              190
Phe Ser Asp Glu Ser Glu Val Cys Ala Arg Glu Asp Thr Asn Ala Ser
      195              200              205
Ser Gly Phe Gly Gln Val Lys Leu Glu Asp Cys Ser Asp Glu Tyr Val
      210              215              220
Leu Leu Asp Ser Ser Gln Cys Ile Lys Glu Glu Leu Lys Gly Lys Glu
      225              230              235              240
Glu Val Arg Glu Glu His Asn Leu Ala Val Gly Phe Gly Ile Gly Gln
      245              250              255
Asp Ser Lys Arg Glu Thr Leu Asp Ala Trp Leu Met Gly Asn Gly Asn
      260              265              270
Glu Gln Glu Pro Leu Glu Phe Gly Val Asp Glu Thr Phe Asp Ile Asn
      275              280              285
Glu Leu Leu Gly Ile Leu Asn Asp Asn Asn Val Ser Gly Gln Glu Thr
      290              295              300
Met Gln Tyr Gln Val Asp Arg His Pro Asn Phe Ser Tyr Gln Thr Gln
      305              310              315              320
Phe Pro Asn Ser Asn Leu Leu Gly Ser Leu Asn Pro Met Glu Ile Ala
      325              330              335
Gln Pro Gly Val Asp Tyr Gly Cys Pro Tyr Val Gln Pro Ser Asp Met
      340              345              350
Glu Asn Tyr Gly Ile Asp Leu Asp His Arg Arg Phe Asn Asp Leu Asp
      355              360              365
Ile Gln Asp Leu Asp Phe Gly Gly Asp Lys Asp Val His Gly Ser Thr
      370              375              380

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(2) INFORMATION FOR SEQ ID NO:754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..283
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

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Met Lys Gly Lys Gly Gly Pro Glu Asn Gly Ile Cys Asp Tyr Arg Glu
1      5      10      15
Val Arg Gln Arg Arg Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro
      20      25      30
Asp Gly Gly Ala Arg Leu Trp Leu Gly Thr Phe Ser Ser Ser Tyr Glu
      35      40      45
Ala Ala Leu Ala Tyr Asp Glu Ala Ala Lys Ala Ile Tyr Gly Gln Ser
      50      55      60
Ala Arg Leu Asn Leu Pro Glu Ile Thr Asn Arg Ser Ser Ser Thr Ala
      65      70      75      80
Ala Thr Ala Thr Val Ser Gly Ser Val Thr Ala Phe Ser Asp Glu Ser
      85      90      95
Glu Val Cys Ala Arg Glu Asp Thr Asn Ala Ser Ser Gly Phe Gly Gln
      100      105      110

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Val Lys Leu Glu Asp Cys Ser Asp Glu Tyr Val Leu Leu Asp Ser Ser
115 120 125
Gln Cys Ile Lys Glu Glu Leu Lys Gly Lys Glu Glu Val Arg Glu Glu
130 135 140
His Asn Leu Ala Val Gly Phe Gly Ile Gly Gln Asp Ser Lys Arg Glu
145 150 155 160
Thr Leu Asp Ala Trp Leu Met Gly Asn Gly Asn Glu Gln Glu Pro Leu
165 170 175
Glu Phe Gly Val Asp Glu Thr Phe Asp Ile Asn Glu Leu Leu Gly Ile
180 185 190
Leu Asn Asp Asn Asn Val Ser Gly Gln Glu Thr Met Gln Tyr Gln Val
195 200 205
Asp Arg His Pro Asn Phe Ser Tyr Gln Thr Gln Phe Pro Asn Ser Asn
210 215 220
Leu Leu Gly Ser Leu Asn Pro Met Glu Ile Ala Gln Pro Gly Val Asp
225 230 235 240
Tyr Gly Cys Pro Tyr Val Gln Pro Ser Asp Met Glu Asn Tyr Gly Ile
245 250 255
Asp Leu Asp His Arg Arg Phe Asn Asp Leu Asp Ile Gln Asp Leu Asp
260 265 270
Phe Gly Gly Asp Lys Asp Val His Gly Ser Thr
275 280

(2) INFORMATION FOR SEQ ID NO:755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..572
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

aaaatagctg atcattttgg aggggaagcct cacttgggtt acatgctgat ccgcgacaaa	60
ttggcagagc ttccaggagga gaagaacaaa gtccacaagg aacgggtcga agaaaggaga	120
tcaaaggaga ggagtagaga gcgagaatca agtaaaagaca gagacggagg agatagccgt	180
gaccgaggaa gagatgttga ccgcagGagt agagatcgtg acaggcacca tgaccaccga	240
gaacatgaca gaaactataa ccagtcacgt ggctatgact caagaagccg gcgcagttca	300
cggtcccggt ctagggaaag accgagggat catgatcgcc gcagacgcca tgaccgctac	360
taagaccctg ccaagagctgg ttgcacctgg tttaaagagt ttctacagat gcgttttagga	420
ttctatttgg agttacaac acctttcttt ttctttgctc aagtgtttta aggatttttg	480
agattgtaac ttactttaag ttgttaAgag gagcttcttc agatatcttt aatttgtttt	540
ttatgttgtt gacatcaaa acttgcgagt ag	

(2) INFORMATION FOR SEQ ID NO:756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

Lys Ile Ala Asp His Phe Gly Gly Lys Leu His Leu Gly Tyr Met Leu	
1 5 10 15	
Ile Arg Asp Lys Leu Ala Glu Leu Gln Glu Lys Asn Lys Val His	
20 25 30	
Lys Glu Arg Val Glu Glu Arg Arg Ser Lys Glu Arg Ser Arg Glu Arg	

35 40 45
Glu Ser Ser Lys Asp Arg Asp Gly Gly Asp Ser Arg Asp Arg Gly Arg
50 55 60
Asp Val Asp Arg Arg Ser Arg Asp Arg Asp Arg His His Asp His Arg
65 70 75
Glu His Asp Arg Asn Tyr Asn Gln Ser Arg Gly Tyr Asp Ser Arg Ser
85 90 95
Arg Arg Ser Ser Arg Ser Arg Ser Arg Glu Arg Pro Arg Asp His Asp
100 105 110
Arg Arg Arg Arg His Asp Arg Tyr
115 120

(2) INFORMATION FOR SEQ ID NO:757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

Met Leu Ile Arg Asp Lys Leu Ala Glu Leu Gln Glu Glu Lys Asn Lys
1 5 10 15
Val His Lys Glu Arg Val Glu Glu Arg Arg Ser Lys Glu Arg Ser Arg
20 25 30
Glu Arg Glu Ser Ser Lys Asp Arg Asp Gly Gly Asp Ser Arg Asp Arg
35 40 45
Gly Arg Asp Val Asp Arg Arg Ser Arg Asp Arg Asp Arg His His Asp
50 55 60
His Arg Glu His Asp Arg Asn Tyr Asn Gln Ser Arg Gly Tyr Asp Ser
65 70 75 80
Arg Ser Arg Arg Ser Ser Arg Ser Arg Ser Arg Glu Arg Pro Arg Asp
85 90 95
His Asp Arg Arg Arg Arg His Asp Arg Tyr
100 105

(2) INFORMATION FOR SEQ ID NO:758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

Met Leu Thr Ala Gly Val Glu Ile Val Thr Gly Thr Met Thr Thr Glu
1 5 10 15
Asn Met Thr Glu Thr Ile Thr Ser His Val Ala Met Thr Gln Glu Ala
20 25 30
Gly Ala Val His Gly Pro Gly Leu Gly Lys Asp Arg Gly Ile Met Ile
35 40 45
Ala Ala Asp Ala Met Thr Ala Thr Lys Thr Leu Pro Lys Met Val Ala
50 55 60
Pro Gly Leu Arg Gly Ser Tyr Arg Cys Val
65 70

(2) INFORMATION FOR SEQ ID NO:759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1148
(D) OTHER INFORMATION: / Ceres Seq. ID 1567896
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

caaaggtttt	caatgaatc	catgacaagt	aaactcaagt	acgggtctgt	tccccctt	60
aatcattttg	ctgaggaagc	aacaactctt	gacttgcaaa	gcgtcttcgg	gaggttcaact	120
ttcgatacaa	ttttcattcg	tataactggt	tctgattccta	gatctctctc	cattgaaatg	180
ctcgaagcag	aatttgcata	agctctcgac	gatgttggag	aagggtattct	ttataggcat	240
tttaaaccaa	ggttctgtg	gaagctgcaa	aactggatag	gattcggaca	agagaagaag	300
ctcactgaag	ctaattgaca	ttttgaccgc	gtgtgtgcc	aatacatatc	agccaagaga	360
gaagagatta	aaagatcaca	agggacttcc	aatggaggaa	gtcaggatct	tttaacttcc	420
ttcataaagc	tagacacgac	caagtacaag	ctcttgaatc	cgagtgcaga	taagtctctt	480
agagacaaca	tcttagcttt	cattctagcg	ggaagagaca	caacagccac	cgctctctct	540
gtggtctctt	ggcttctctc	tgaataatcca	catgtggtag	ccaagtattca	tcaagagatc	600
aaatcaacaa	ctgatctatc	aagaacagga	aatagccaa	agaatgtaga	caagtgtgtg	660
tatttacatg	gtgcgtgtg	tgaagcaatg	agactctacc	caccagtctc	Cttcgagcgc	720
aagtctccaa	tcaaatcaga	tgtgcttcca	agtggccata	aagttgatgc	aaactctaa	780
attattatct	gtctttatgc	attggggagg	atgcccagcg	tttggggaga	agatgcattc	840
cagttcgaag	cagagagatg	gatttcggag	aatggaggca	taaaacatga	gcctctcttc	900
aagtttttgt	cggttcaatg	cggttcaatg	actgtctag	gtaaacatct	agctattgact	960
caaatgaaga	tagtgccagt	ggagatatta	cgaaactacg	acattaaagt	ttctcaagga	1020
cagaagattg	tgcacgctct	tggttttata	ttgtcaatga	aacatggctc	tcaaatcact	1080
gttactaaga	gatgttctgc	ttgaatttat	tcattgtatta	aataaaaaaa	tcattttggt	1140
ttggtttt						

(2) INFORMATION FOR SEQ ID NO:760:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..367
(D) OTHER INFORMATION: / Ceres Seq. ID 1567897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

Gln	Arg	Phe	Ser	Met	Ser	Thr	Met	Thr	Ser	Lys	Leu	Lys	Tyr	Gly	Leu
1			5							10				15	
Val	Pro	Leu	Leu	Asn	His	Phe	Ala	Glu	Gly	Thr	Thr	Leu	Asp	Leu	
			20					25				30			
Gln	Ser	Val	Phe	Gly	Arg	Phe	Thr	Phe	Asp	Thr	Ile	Phe	Ile	Leu	Ile
			35				40				45				
Thr	Gly	Ser	Asp	Pro	Arg	Ser	Leu	Ser	Ile	Glu	Met	Pro	Glu	Asp	Glu
			50				55				60				
Phe	Ala	Lys	Ala	Leu	Asp	Asp	Val	Gly	Glu	Gly	Ile	Leu	Tyr	Arg	His
65				70					75					80	
Phe	Lys	Pro	Arg	Phe	Leu	Trp	Lys	Leu	Gln	Asn	Trp	Ile	Gly	Phe	Gly
			85					90				95			
Gln	Glu	Lys	Lys	Leu	Thr	Glu	Ala	Asn	Ala	Thr	Phe	Asp	Arg	Val	Cys
			100				105					110			
Ala	Lys	Tyr	Ile	Ser	Ala	Lys	Arg	Glu	Glu	Ile	Lys	Arg	Ser	Gln	Gly
			115				120					125			
Thr	Ser	Asn	Gly	Gly	Ser	Gln	Asp	Leu	Leu	Thr	Ser	Phe	Ile	Lys	Leu
			130				135				140				
Asp	Thr	Thr	Lys	Tyr	Lys	Leu	Leu	Asn	Pro	Ser	Asp	Asp	Lys	Phe	Leu

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145          150          155          160
Arg Asp Asn Ile Leu Ala Phe Ile Leu Ala Gly Arg Asp Thr Thr Ala
          165          170          175
Thr Ala Leu Ser Trp Phe Phe Trp Leu Leu Ser Glu Asn Pro His Val
          180          185          190
Val Ala Lys Ile His Gln Glu Ile Asn Ile Asn Thr Asp Leu Ser Arg
          195          200          205
Thr Gly Asn Ser Gln Glu Asn Val Asp Lys Leu Val Tyr Leu His Gly
          210          215          220
Ala Leu Cys Glu Ala Met Arg Leu Tyr Pro Pro Val Ser Phe Gly Arg
225          230          235          240
Lys Ser Pro Ile Lys Ser Asp Val Leu Pro Ser Gly His Lys Val Asp
          245          250          255
Ala Asn Ser Lys Ile Ile Ile Cys Leu Tyr Ala Leu Gly Arg Met Arg
          260          265          270
Ala Val Trp Gly Glu Asp Ala Ser Gln Phe Lys Pro Glu Arg Trp Ile
          275          280          285
Ser Glu Asn Gly Gly Ile Lys His Glu Pro Ser Phe Lys Phe Leu Ser
          290          295          300
Phe Asn Ala Gly Pro Arg Thr Cys Leu Gly Lys His Leu Ala Met Thr
305          310          315          320
Gln Met Lys Ile Val Ala Val Glu Ile Leu Arg Asn Tyr Asp Ile Lys
          325          330          335
Val Leu Gln Gly Gln Lys Ile Val Pro Ala Leu Gly Phe Ile Leu Ser
          340          345          350
Met Lys His Gly Leu Gln Ile Thr Val Thr Lys Arg Cys Ser Ala
          355          360          365

```

(2) INFORMATION FOR SEQ ID NO:761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..363
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

```

Met Ser Thr Met Thr Ser Lys Leu Lys Tyr Gly Leu Val Pro Leu Leu
1          5          10          15
Asn His Phe Ala Glu Glu Gly Thr Thr Leu Asp Leu Gln Ser Val Phe
          20          25          30
Gly Arg Phe Thr Phe Asp Thr Ile Phe Ile Leu Ile Thr Gly Ser Asp
          35          40          45
Pro Arg Ser Leu Ser Ile Glu Met Pro Glu Asp Glu Phe Ala Lys Ala
          50          55          60
Leu Asp Asp Val Gly Glu Gly Ile Leu Tyr Arg His Phe Lys Pro Arg
65          70          75          80
Phe Leu Trp Lys Leu Gln Asn Trp Ile Gly Phe Gly Gln Glu Lys Lys
          85          90          95
Leu Thr Glu Ala Asn Ala Thr Phe Asp Arg Val Cys Ala Lys Tyr Ile
          100          105          110
Ser Ala Lys Arg Glu Glu Ile Lys Arg Ser Gln Gly Thr Ser Asn Gly
          115          120          125
Gly Ser Gln Asp Leu Leu Thr Ser Phe Ile Lys Leu Asp Thr Thr Lys
          130          135          140
Tyr Lys Leu Leu Asn Pro Ser Asp Asp Lys Phe Leu Arg Asp Asn Ile
145          150          155          160
Leu Ala Phe Ile Leu Ala Gly Arg Asp Thr Thr Ala Thr Ala Leu Ser
          165          170          175

```

Trp Phe Phe Trp Leu Leu Ser Glu Asn Pro His Val Val Ala Lys Ile
180 185 190
His Gln Glu Ile Asn Ile Asn Thr Asp Leu Ser Arg Thr Gly Asn Ser
195 200 205
Gln Glu Asn Val Asp Lys Leu Val Tyr Leu His Gly Ala Leu Cys Glu
210 215 220
Ala Met Arg Leu Tyr Pro Pro Val Ser Phe Gly Arg Lys Ser Pro Ile
225 230 235 240
Lys Ser Asp Val Leu Pro Ser Gly His Lys Val Asp Ala Asn Ser Lys
245 250 255
Ile Ile Ile Cys Leu Tyr Ala Leu Gly Arg Met Arg Ala Val Trp Gly
260 265 270
Glu Asp Ala Ser Gln Phe Lys Pro Glu Arg Trp Ile Ser Glu Asn Gly
275 280 285
Gly Ile Lys His Glu Pro Ser Phe Lys Phe Leu Ser Phe Asn Ala Gly
290 295 300
Pro Arg Thr Cys Leu Gly Lys His Leu Ala Met Thr Gln Met Lys Ile
305 310 315 320
Val Ala Val Glu Ile Leu Arg Asn Tyr Asp Ile Lys Val Leu Gln Gly
325 330 335
Gln Lys Ile Val Pro Ala Leu Gly Phe Ile Leu Ser Met Lys His Gly
340 345 350
Leu Gln Ile Thr Val Thr Lys Arg Cys Ser Ala
355 360

(2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..360

(D) OTHER INFORMATION: / Ceres Seq. ID 1567899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

Met Thr Ser Lys Leu Lys Tyr Gly Leu Val Pro Leu Leu Asn His Phe
1 5 10 15
Ala Glu Glu Gly Thr Thr Leu Asp Leu Gln Ser Val Phe Gly Arg Phe
20 25 30
Thr Phe Asp Thr Ile Phe Ile Leu Ile Thr Gly Ser Asp Pro Arg Ser
35 40 45
Leu Ser Ile Glu Met Pro Glu Asp Glu Phe Ala Lys Ala Leu Asp Asp
50 55 60
Val Gly Glu Gly Ile Leu Tyr Arg His Phe Lys Pro Arg Phe Leu Trp
65 70 75 80
Lys Leu Gln Asn Trp Ile Gly Phe Gly Gln Glu Lys Lys Leu Thr Glu
85 90 95
Ala Asn Ala Thr Phe Asp Arg Val Cys Ala Lys Tyr Ile Ser Ala Lys
100 105 110
Arg Glu Glu Ile Lys Arg Ser Gln Gly Thr Ser Asn Gly Gly Ser Gln
115 120 125
Asp Leu Leu Thr Ser Phe Ile Lys Leu Asp Thr Thr Lys Tyr Lys Leu
130 135 140
Leu Asn Pro Ser Asp Asp Lys Phe Leu Arg Asp Asn Ile Leu Ala Phe
145 150 155 160
Ile Leu Ala Gly Arg Asp Thr Thr Ala Thr Ala Leu Ser Trp Phe Phe
165 170 175
Trp Leu Leu Ser Glu Asn Pro His Val Val Ala Lys Ile His Gln Glu
180 185 190
Ile Asn Ile Asn Thr Asp Leu Ser Arg Thr Gly Asn Ser Gln Glu Asn


```

195              200              205
Val Asp Lys Leu Val Tyr Leu His Gly Ala Leu Cys Glu Ala Met Arg
210              215
Leu Tyr Pro Pro Val Ser Phe Gly Arg Lys Ser Pro Ile Lys Ser Asp
225              230              235              240
Val Leu Pro Ser Gly His Lys Val Asp Ala Asn Ser Lys Ile Ile Ile
245              250              255
Cys Leu Tyr Ala Leu Gly Arg Met Arg Ala Val Trp Gly Glu Asp Ala
260              265              270
Ser Gln Phe Lys Pro Glu Arg Trp Ile Ser Glu Asn Gly Gly Ile Lys
275              280              285
His Glu Pro Ser Phe Lys Phe Leu Ser Phe Asn Ala Gly Pro Arg Thr
290              295              300
Cys Leu Gly Lys His Leu Ala Met Thr Gln Met Lys Ile Val Ala Val
305              310              315              320
Glu Ile Leu Arg Asn Tyr Asp Ile Lys Val Leu Gln Gly Gln Lys Ile
325              330              335
Val Pro Ala Leu Gly Phe Ile Leu Ser Met Lys His Gly Leu Gln Ile
340              345              350
Thr Val Thr Lys Arg Cys Ser Ala
355              360

```

(2) INFORMATION FOR SEQ ID NO:763:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

```

ggcttgctgc agaagttggg attcgttctt ttataatttg ccttgaaaac gaaaacgaaa      60
ataaaaaagcg gagagagaga tggctagata cgcgtcgagca attactgtct tctcccccca      120
cggtcacctc ttccaagtgc aatacgcctt tgaagccgtc cgcaagggta acgcgcgcgt      180
cgggtgtccg ggtacgcaca ccgtgttcct cgccgtcgag aagaagtcca ccccgaagct      240
tcaggattct agatcagcca gaaaaattgt gagccttgac aatcacattg ccttggcatg      300
cgcggggctc aaggctgatg ccgcagtcct gattaacaaa gcaaggatcg agtgcaaaag      360
ccacaggctt acacttgagg accctgtcac tgttgagtac atcactgcgt acattgtctg      420
ccttcaacag aagtataacc aaagtgtgtg tgcagaccc ttctggtctt ctactcttat      480
cgttggtctt gacccttact ctgcctctcc ttccctatat cagactgac ttctgtggac      540
tttctctgct tggaaagcta atgctaccgg cagaaactcc aactctatta gggaattctc      600
cgagaagaac tacaaagaat cctctggcca agaaaactatt aaactcgcta tccgtgctct      660
gcttgaggta gttgagagtg gcggaagaaa cattgaggtt gccgtaatga cacgggagga      720
aactGgGtGt cgccagctag aagaagctga aattgatgca atcgttgcca agatcgaaag      780
tgaaggcgcg cgacagaaca gccacagaag gccctccaaa ggaaactcta taaaacaata      840
actgtttctg ttcttcaatc tgaactttacc ttcttctgct ctctgttttc tcaactctgt      900
tttgactcga gccactcttt ttgcaaaaaga agaactgtac cccatcgttt tgttaacttg      960
aaaatgctcc aaaaaaaaac tgaagaaaag gtttaaaatt cgcttgatct tgcatacaacc      1020
aaggataaat ttctgtgtgc tcatgtttag atagagaagt gactctccat tttctattta      1080
taagtaagca gaacaattag tggt

```

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..253

(D) OTHER INFORMATION: / Ceres Seq. ID 1567905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

```
Met Ala Arg Tyr Asp Arg Ala Ile Thr Val Phe Ser Pro Asp Gly His
1      5      10      15
Leu Phe Gln Val Glu Tyr Ala Leu Glu Ala Val Arg Lys Gly Asn Ala
20     25     30
Ala Val Gly Val Arg Gly Thr Asp Thr Val Val Leu Ala Val Glu Lys
35     40     45
Lys Ser Thr Pro Lys Leu Gln Asp Ser Arg Ser Ala Arg Lys Ile Val
50     55     60
Ser Leu Asp Asn His Ile Ala Leu Ala Cys Ala Gly Leu Lys Ala Asp
65     70     75     80
Ala Arg Val Leu Ile Asn Lys Ala Arg Ile Glu Cys Gln Ser His Arg
85     90     95
Leu Thr Leu Glu Asp Pro Val Thr Val Glu Tyr Ile Thr Arg Tyr Ile
100    105    110
Ala Gly Leu Gln Gln Lys Tyr Thr Gln Ser Gly Gly Val Arg Pro Phe
115    120    125
Gly Leu Ser Thr Leu Ile Val Gly Phe Asp Pro Tyr Ser Arg Leu Pro
130    135    140
Ser Leu Tyr Gln Thr Asp Pro Ser Gly Thr Phe Ser Ala Trp Lys Ala
145    150    155    160
Asn Ala Thr Gly Arg Asn Ser Asn Ser Ile Arg Glu Phe Leu Glu Lys
165    170    175
Asn Tyr Lys Glu Ser Ser Gly Gln Glu Thr Ile Lys Leu Ala Ile Arg
180    185    190
Ala Leu Leu Glu Val Val Glu Ser Gly Gly Lys Asn Ile Glu Val Ala
195    200    205
Val Met Thr Arg Glu Glu Thr Gly Leu Arg Gln Leu Glu Glu Ala Glu
210    215    220
Ile Asp Ala Ile Val Ala Lys Ile Glu Ala Glu Gly Arg Arg Ser
225    230    235    240
Ser Gln Glu Arg Pro Ser Lys Gly Asn Leu Ile Lys Gln
245    250
```

(2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1956 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1956

(D) OTHER INFORMATION: / Ceres Seq. ID 1567929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

```
ctctcatttt Gctactcttc ttcaaaagca cactcaatat ttcgagatcc tctcggtcttg 60
ttcgtctctc gtgaacgac ccactctattg ttctctgctg gtctcagatt cgactcaactt 120
ggatattctc gatactgaag aagcctcctt ctctcttttc cgctcttccc gatgccgac 180
gataagatct caaagatgta tgctagttaa gagaaggagg aacgtgcgag gatggcatca 240
tttgttggtg caatggctat cagtgatctg gtttaagtota ctttagggcc aaagggcatg 300
gataaaatct tacaactctac tggtagaggt catgcggtca ctgttactaa cgatggtgct 360
actattctca agtcacttca catagacaac cctgcagcta aagttcttgt tgacatctcg 420
aaagtccaag atgatgaggt tggatgatgga actactctgt ttgtttcttt ggccggcgag 480
cttctgaggg aagcagaaaa gctcttggtt tctaagattc accctatgac catcatagca 540
ggttacagaa tggctctcga atgtgctcgt aatgctttac tgaagagagt cattgataac 600
aaggacaagt cagagaagtt taggtcagac ttgttgaa ga ttgcgatgac tacttttatg 660
tccaaaatc tctcacagga caaggaacat ttgcagaaaa tggccgtgga tgcgtcttttc 720
aggctaaagg gaagcagaaa ctgggaagct attcagatca tcaaaaaaac tggagggtct 780
ctgaaggatt cgttttttga tgaagggttt attcttgaca agaaaatagg aattggcgag 840
```

cctaagcgca	tagaagaatgc	aaatatcttta	gtagctaata	ctgctatgga	taccgataaa	900
gtgaagattt	acgggtgcaag	tgctcgtgtg	gattccatga	ccaaggtgtg	tgagattgaa	960
ggggctttaga	aggaaaaaaat	gaagacaaag	gtgaagaaga	tcataaggcca	cggaatacaac	1020
tgcttttgta	acagggcagtt	gatctacaat	ttccctgagg	aactctttgc	tgatgtcgtg	1080
atacttgcta	ttgagcatgc	tgacttttag	ggaatagagc	gtctttggtt	ggttactgtg	1140
ggtgaaattg	cttcgacctt	tgacaaccca	gagctctgta	agcttgggca	ttgcaagcct	1200
atagaaagaaa	tcattgattgg	tgaagacaag	ttgattcatt	tcctgtgttg	tgaaatgggc	1260
caggcttggt	caattgtcct	aagaggggccc	agtcaccatg	tcctagatga	cggtgaaaga	1320
tcactccatg	atgccttatg	tgtactctct	caaacagtga	atgatactag	agttttgctt	1380
ggaggtggtt	ggccagagat	ggtgatggca	aaggaaagtag	atgagcttgc	aaggaaaact	1440
gctggcaaaa	aatctcatgc	caattgaagct	ttctcactgt	ctctagtgtg	tataccgaca	1500
acaactcgctg	acaacgcgtg	tttagacagt	gccgaattgg	ttgctoaagt	ctgtgcagag	1560
caccacactg	aagggtgtgaa	cgctgggagc	gacgtcatca	ctggagctgt	aggagatgat	1620
gaagagagag	gaattctatga	agcattcaaa	gtgaagcaag	cggttctgct	ttcagccaca	1680
gaagcatctg	agatgatatt	gcgagtggtg	gaatcatta	catgtgctcc	taggaggaga	1740
gaagacagga	tgtgaaaaac	tcaacacaaa	acatgaagc	tggtggggagc	ctagagattc	1800
catgattgtg	ttttcgattt	ggatcagaat	acaacttttc	taatatgttt	aatgttttgc	1860
tcctccttag	aactcatctt	tttgttttgt	ttccttttaa	tcttgttttg	agtttgaatt	1920
ttagctgttg	aaaaaagtgt	tagctccaaa	gttttt			

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 527 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..527

(D) OTHER INFORMATION: / Ceres Seq. ID 1567930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

Met	Pro	Ile	Asp	Lys	Ile	Phe	Lys	Asp	Asp	Ala	Ser	Glu	Glu	Lys	Gly
1			5					10						15	
Glu	Arg	Ala	Arg	Met	Ala	Ser	Phe	Val	Gly	Ala	Met	Ala	Ile	Ser	Asp
			20					25					30		
Leu	Val	Lys	Ser	Thr	Leu	Gly	Pro	Lys	Gly	Met	Asp	Lys	Ile	Leu	Gln
			35				40					45			
Ser	Thr	Gly	Arg	Gly	His	Ala	Val	Thr	Val	Thr	Asn	Asp	Gly	Ala	Thr
			50				55				60				
Ile	Leu	Lys	Ser	Leu	His	Ile	Asp	Asn	Pro	Ala	Ala	Lys	Val	Leu	Val
65					70				75					80	
Asp	Ile	Ser	Lys	Val	Gln	Asp	Asp	Glu	Val	Gly	Asp	Gly	Thr	Thr	Ser
				85					90				95		
Val	Val	Val	Leu	Ala	Gly	Glu	Leu	Leu	Arg	Glu	Ala	Glu	Lys	Leu	Val
			100					105					110		
Ala	Ser	Lys	Ile	His	Pro	Met	Thr	Ile	Ile	Ala	Gly	Tyr	Arg	Met	Ala
			115				120					125			
Ser	Glu	Cys	Ala	Arg	Asn	Ala	Leu	Leu	Lys	Arg	Val	Ile	Asp	Asn	Lys
			130				135				140				
Asp	Asn	Ala	Glu	Lys	Phe	Arg	Ser	Asp	Leu	Leu	Lys	Ile	Ala	Met	Thr
145					150				155					160	
Thr	Leu	Cys	Ser	Lys	Ile	Leu	Ser	Gln	Asp	Lys	Glu	His	Phe	Ala	Glu
			165						170				175		
Met	Ala	Val	Asp	Ala	Val	Phe	Arg	Leu	Lys	Gly	Ser	Thr	Asn	Leu	Glu
			180					185					190		
Ala	Ile	Gln	Ile	Ile	Lys	Lys	Pro	Gly	Gly	Ser	Leu	Lys	Asp	Ser	Phe
			195				200					205			
Leu	Asp	Glu	Gly	Phe	Ile	Leu	Asp	Lys	Lys	Ile	Gly	Ile	Gly	Gln	Pro
210							215				220				
Lys	Arg	Ile	Glu	Asn	Ala	Asn	Ile	Leu	Val	Ala	Asn	Thr	Ala	Met	Asp
225					230					235				240	

```

Thr Asp Lys Val Lys Ile Tyr Gly Ala Arg Val Arg Val Asp Ser Met
                245                250                255
Thr Lys Val Ala Glu Ile Glu Gly Ala Glu Lys Glu Lys Met Lys Asp
                260                265                270
Lys Val Lys Lys Lys Ile Ile Gly His Gly Ile Asn Cys Phe Val Asn Arg
                275                280                285
Gln Leu Ile Tyr Asn Phe Pro Glu Glu Leu Phe Ala Asp Ala Gly Ile
                290                295                300
Leu Ala Ile Glu His Ala Asp Phe Glu Gly Ile Glu Arg Leu Gly Leu
305                310                315                320
Val Thr Gly Gly Glu Ile Ala Ser Thr Phe Asp Asn Pro Glu Ser Val
                325                330                335
Lys Leu Gly His Cys Lys Leu Ile Glu Glu Ile Met Ile Gly Glu Asp
                340                345                350
Lys Leu Ile His Phe Ser Gly Cys Glu Met Gly Gln Ala Cys Ser Ile
                355                360                365
Val Leu Arg Gly Ala Ser His His Val Leu Asp Glu Ala Glu Arg Ser
370                375                380
Leu His Asp Ala Leu Cys Val Leu Ser Gln Thr Val Asn Asp Thr Arg
385                390                395                400
Val Leu Leu Gly Gly Trp Pro Glu Met Val Met Ala Lys Glu Val
                405                410                415
Asp Glu Leu Ala Arg Lys Thr Ala Gly Lys Lys Ser His Ala Ile Glu
                420                425                430
Ala Phe Ser Arg Ala Leu Val Ala Ile Pro Thr Thr Ile Ala Asp Asn
                435                440                445
Ala Gly Leu Asp Ser Ala Glu Leu Val Ala Gln Leu Arg Ala Glu His
450                455                460
His Thr Glu Gly Cys Asn Ala Gly Ile Asp Val Ile Thr Gly Ala Val
465                470                475                480
Gly Asp Met Glu Glu Arg Gly Ile Tyr Glu Ala Phe Lys Val Lys Gln
                485                490                495
Ala Val Leu Leu Ser Ala Thr Glu Ala Ser Glu Met Ile Leu Arg Val
500                505                510
Asp Glu Ile Ile Thr Cys Ala Pro Arg Arg Arg Glu Asp Arg Met
515                520                525

```

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..507
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

```

Met Ala Ser Phe Val Gly Ala Met Ala Ile Ser Asp Leu Val Lys Ser
1          5          10          15
Thr Leu Gly Pro Lys Gly Met Asp Lys Ile Leu Gln Ser Thr Gly Arg
          20          25          30
Gly His Ala Val Thr Val Thr Asn Asp Gly Ala Thr Ile Leu Lys Ser
          35          40          45
Leu His Ile Asp Asn Pro Ala Ala Lys Val Leu Val Asp Ile Ser Lys
          50          55          60
Val Gln Asp Asp Glu Val Gly Asp Gly Thr Thr Ser Val Val Val Leu
65          70          75          80
Ala Gly Glu Leu Leu Arg Glu Ala Glu Lys Leu Val Ala Ser Lys Ile
          85          90          95
His Pro Met Thr Ile Ile Ala Gly Tyr Arg Met Ala Ser Glu Cys Ala

```

100	105	110
Arg Asn Ala Leu Leu Lys Arg Val Ile Asp Asn Lys Asp Asn Ala Glu		
115	120	125
Lys Phe Arg Ser Asp Leu Leu Lys Ile Ala Met Thr Thr Leu Cys Ser		
130	135	140
Lys Ile Leu Ser Gln Asp Lys Glu His Phe Ala Glu Met Ala Val Asp		
145	150	155
Ala Val Phe Arg Leu Lys Gly Ser Thr Asn Leu Glu Ala Ile Gln Ile		
165	170	175
Ile Lys Lys Pro Gly Gly Ser Leu Lys Asp Ser Phe Leu Asp Glu Gly		
180	185	190
Phe Ile Leu Asp Lys Lys Ile Gly Ile Gly Gln Pro Lys Arg Ile Glu		
195	200	205
Asn Ala Asn Ile Leu Val Ala Asn Thr Ala Met Asp Thr Asp Lys Val		
210	215	220
Lys Ile Tyr Gly Ala Arg Val Arg Val Asp Ser Met Thr Lys Val Ala		
225	230	235
Glu Ile Glu Gly Ala Glu Lys Glu Lys Met Lys Asp Lys Val Lys Lys		
245	250	255
Ile Ile Gly His Gly Ile Asn Cys Phe Val Asn Arg Gln Leu Ile Tyr		
260	265	270
Asn Phe Pro Glu Glu Leu Phe Ala Asp Ala Gly Ile Leu Ala Ile Glu		
275	280	285
His Ala Asp Phe Glu Gly Ile Glu Arg Leu Gly Leu Val Thr Gly Gly		
290	295	300
Glu Ile Ala Ser Thr Phe Asp Asn Pro Glu Ser Val Lys Leu Gly His		
305	310	315
Cys Lys Leu Ile Glu Glu Ile Met Ile Gly Glu Asp Lys Leu Ile His		
325	330	335
Phe Ser Gly Cys Glu Met Gly Gln Ala Cys Ser Ile Val Leu Arg Gly		
340	345	350
Ala Ser His His Val Leu Asp Glu Ala Glu Arg Ser Leu His Asp Ala		
355	360	365
Leu Cys Val Leu Ser Gln Thr Val Asn Asp Thr Arg Val Leu Leu Gly		
370	375	380
Gly Gly Trp Pro Glu Met Val Met Ala Lys Glu Val Asp Glu Leu Ala		
385	390	395
Arg Lys Thr Ala Gly Lys Lys Ser His Ala Ile Glu Ala Phe Ser Arg		
405	410	415
Ala Leu Val Ala Ile Pro Thr Thr Ile Ala Asp Asn Ala Gly Leu Asp		
420	425	430
Ser Ala Glu Leu Val Ala Gln Leu Arg Ala Glu His His Thr Glu Gly		
435	440	445
Cys Asn Ala Gly Ile Asp Val Ile Thr Gly Ala Val Gly Asp Met Glu		
450	455	460
Glu Arg Gly Ile Tyr Glu Ala Phe Lys Val Lys Gln Ala Val Leu Leu		
465	470	475
Ser Ala Thr Glu Ala Ser Glu Met Ile Leu Arg Val Asp Glu Ile Ile		
485	490	495
Thr Cys Ala Pro Arg Arg Arg Glu Asp Arg Met		
500	505	

- (2) INFORMATION FOR SEQ ID NO:768:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 500 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
- (A) NAME/KEY: peptide
- (B) LOCATION: 1..500

(D) OTHER INFORMATION: / Ceres Seq. ID 1567932
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

Met Ala Ile Ser Asp Leu Val Lys Ser Thr Leu Gly Pro Lys Gly Met
1 5 10 15
Asp Lys Ile Leu Gln Ser Thr Gly Arg Gly His Ala Val Thr Val Thr
20 25 30
Asn Asp Gly Ala Thr Ile Leu Lys Ser Leu His Ile Asp Asn Pro Ala
35 40 45
Ala Lys Val Leu Val Asp Ile Ser Lys Val Gln Asp Asp Glu Val Gly
50 55 60
Asp Gly Thr Thr Ser Val Val Val Leu Ala Gly Glu Leu Leu Arg Glu
65 70 75 80
Ala Glu Lys Leu Val Ala Ser Lys Ile His Pro Met Thr Ile Ile Ala
85 90 95
Gly Tyr Arg Met Ala Ser Glu Cys Ala Arg Asn Ala Leu Leu Lys Arg
100 105 110
Val Ile Asp Asn Lys Asp Asn Ala Glu Lys Phe Arg Ser Asp Leu Leu
115 120 125
Lys Ile Ala Met Thr Thr Leu Cys Ser Lys Ile Leu Ser Gln Asp Lys
130 135 140
Glu His Phe Ala Glu Met Ala Val Asp Ala Val Phe Arg Leu Lys Gly
145 150 155 160
Ser Thr Asn Leu Glu Ala Ile Gln Ile Ile Lys Lys Pro Gly Gly Ser
165 170 175
Leu Lys Asp Ser Phe Leu Asp Glu Gly Phe Ile Leu Asp Lys Lys Ile
180 185 190
Gly Ile Gly Gln Pro Lys Arg Ile Glu Asn Ala Asn Ile Leu Val Ala
195 200 205
Asn Thr Ala Met Asp Thr Asp Lys Val Lys Ile Tyr Gly Ala Arg Val
210 215 220
Arg Val Asp Ser Met Thr Lys Val Ala Glu Ile Glu Gly Ala Glu Lys
225 230 235 240
Glu Lys Met Lys Asp Lys Val Lys Lys Ile Ile Gly His Gly Ile Asn
245 250 255
Cys Phe Val Asn Arg Gln Leu Ile Tyr Asn Phe Pro Glu Glu Leu Phe
260 265 270
Ala Asp Ala Gly Ile Leu Ala Ile Glu His Ala Asp Phe Glu Gly Ile
275 280 285
Glu Arg Leu Gly Leu Val Thr Gly Gly Glu Ile Ala Ser Thr Phe Asp
290 295 300
Asn Pro Glu Ser Val Lys Leu Gly His Cys Lys Leu Ile Glu Glu Ile
305 310 315 320
Met Ile Gly Glu Asp Lys Leu Ile His Phe Ser Gly Cys Glu Met Gly
325 330 335
Gln Ala Cys Ser Ile Val Leu Arg Gly Ala Ser His His Val Leu Asp
340 345 350
Glu Ala Glu Arg Ser Leu His Asp Ala Leu Cys Val Leu Ser Gln Thr
355 360 365
Val Asn Asp Thr Arg Val Leu Leu Gly Gly Gly Trp Pro Glu Met Val
370 375 380
Met Ala Lys Glu Val Asp Glu Leu Ala Arg Lys Thr Ala Gly Lys Lys
385 390 395 400
Ser His Ala Ile Glu Ala Phe Ser Arg Ala Leu Val Ala Ile Pro Thr
405 410 415
Thr Ile Ala Asp Asn Ala Gly Leu Asp Ser Ala Glu Leu Val Ala Gln
420 425 430
Leu Arg Ala Glu His His Thr Glu Gly Cys Asn Ala Gly Ile Asp Val
435 440 445
Ile Thr Gly Ala Val Gly Asp Met Glu Glu Arg Gly Ile Tyr Glu Ala
450 455 460
Phe Lys Val Lys Gln Ala Val Leu Leu Ser Ala Thr Glu Ala Ser Glu

465 470 475 480
Met Ile Leu Arg Val Asp Glu Ile Ile Thr Cys Ala Pro Arg Arg Arg
485 490 495
Glu Asp Arg Met
500

(2) INFORMATION FOR SEQ ID NO:769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1504
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

atcttcgcctt	gcttctctcct	caaaaaggtga	aaaatttagag	cgagagagat	agagagagat	60
ttcaaaaacga	aaatccagag	aaagggctctt	gccagtttag	ggcatccttg	tgggtgagag	120
agcgattgag	agatttcaaa	aggaggaaga	ggaagatcac	agtgtagagag	agatttagag	180
ggagagaaga	aagagagatt	ctttttgagt	gtgttagggg	ttcatttctc	ctcgagatct	240
acatttatct	cttctcatgg	aacggaagct	tgtgtttttg	ggaatcccgct	gggatattga	300
ttccgatggg	cttaaggatt	acatgtcaaa	atttgagagac	ttggaggatt	gtattgtcat	360
gaaggatcga	tcaatctggaa	gatctcgttg	atttggtatg	gtcacttttg	cttcagccga	420
agatgcaaa	aatgctttga	aaggtgaaca	cttttttagg	aacaggatct	tggaagttaa	480
agtggttaca	ccaaaggaag	agatgagaca	gcctgcacaa	aaagtgcaga	ggatcttcgt	540
tgctcgaact	ccttcacacg	tctctgaatc	agatttccga	agccattttg	agaggtatgg	600
ggaaaataca	gacttataca	tgctcaagga	ctacaactcg	aagcagaccc	gacgaatagg	660
gtttatcaca	ttctctagtg	ctgattcaat	ggaggatctg	atggaggaca	ctcatgatct	720
gggagggtaca	acagttgtcg	ttgatcgggc	aacacacaaa	gaggtgatgc	atccgcctag	780
gccaccgccca	gtggctagaa	tgtcgcgcgc	accgctggct	attgcaggtg	gattttggag	840
tccaggtgtgt	tatggagctt	atgatgtcta	catttctgca	gtacaagatg	acgcagcgct	900
tggtgcccct	actttgtatg	ataatccocg	cacgttttat	ggaagagggg	aaccaaccac	960
aaggggaata	ggaaacaaga	tctttgttgg	acggcttctc	caagaagcat	ccgttgatga	1020
tcttcgcgat	tattttggga	gatttggcca	tattcaagat	gcttatattc	caaaggaccc	1080
aaagagaagt	ggacatagag	gttttggatt	tgttaccttt	gctgaaaatg	gtgttgaca	1140
tcgtgtagcc	cgaagatctc	atgaaatctg	tggacaagag	gtagcaatag	attcacgaac	1200
gcctcttgat	gaagctggac	ctagcgcgtg	cgcaagtctc	atgttaagtt	cttctcgctc	1260
tgaatttttt	gggtgctatg	gaggtcctat	gcgcgcattt	ggtcgaatgt	atggaggcat	1320
gagcttggag	gattggggag	atggaatgcc	aaacgcgaag	ccatcaagac	cagaccggag	1380
gtaccggcca	tactaatgca	gcagaccaac	atttcattag	ctttggctgt	gtccttttat	1440
agaaacttca	ctttgtcaga	tctattttaa	ttgaagcttt	tgtttatgtt	ttaccctcgg	1500

(2) INFORMATION FOR SEQ ID NO:770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..379
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

Met	Glu	Arg	Lys	Leu	Val	Val	Leu	Gly	Ile	Pro	Trp	Asp	Ile	Asp	Ser
1					5				10					15	
Asp	Gly	Leu	Lys	Asp	Tyr	Met	Ser	Lys	Phe	Gly	Asp	Leu	Glu	Asp	Cys
			20					25				30			
Ile	Val	Met	Lys	Asp	Arg	Ser	Thr	Gly	Arg	Ser	Arg	Gly	Phe	Gly	Tyr
			35				40					45			

Val Thr Phe Ala Ser Ala Glu Asp Ala Lys Asn Ala Leu Lys Gly Glu
50 55 60
His Phe Leu Gly Asn Arg Ile Leu Glu Val Lys Val Ala Thr Pro Lys
65 70 75 80
Glu Glu Met Arg Gln Pro Ala Lys Lys Val Thr Arg Ile Phe Val Ala
85 90 95
Arg Ile Pro Ser Ser Val Ser Glu Ser Asp Phe Arg Ser His Phe Glu
100 105 110
Arg Tyr Gly Glu Ile Thr Asp Leu Tyr Met Pro Lys Asp Tyr Asn Ser
115 120 125
Lys Gln His Arg Arg Ile Gly Phe Ile Thr Phe Ser Ser Ala Asp Ser
130 135 140
Val Glu Asp Leu Met Glu Asp Thr His Asp Leu Gly Gly Thr Thr Val
145 150 155 160
Ala Val Asp Arg Ala Thr Pro Lys Glu Asp Asp His Pro Pro Arg Pro
165 170 175
Pro Pro Val Ala Arg Met Ser Arg Pro Pro Val Ala Ile Ala Gly Gly
180 185 190
Phe Gly Ala Pro Gly Gly Tyr Gly Ala Tyr Asp Ala Tyr Ile Ser Ala
195 200 205
Ala Thr Arg Tyr Ala Ala Leu Gly Ala Pro Thr Leu Tyr Asp Asn Pro
210 215 220
Ala Thr Phe Tyr Gly Arg Gly Glu Pro Thr Thr Arg Gly Ile Gly Asn
225 230 235 240
Lys Ile Phe Val Gly Arg Leu Pro Gln Glu Ala Ser Val Asp Asp Leu
245 250 255
Arg Asp Tyr Phe Gly Arg Phe Gly His Ile Gln Asp Ala Tyr Ile Pro
260 265 270
Lys Asp Pro Lys Arg Ser Gly His Arg Gly Phe Gly Phe Val Thr Phe
275 280 285
Ala Glu Asn Gly Val Ala Asp Arg Val Ala Arg Arg Ser His Glu Ile
290 295 300
Cys Gly Gln Glu Val Ala Ile Asp Ser Ala Thr Pro Leu Asp Glu Ala
305 310 315 320
Gly Pro Ser Ala Gly Ala Ser Ser Met Leu Ser Ser Ser Arg Pro Glu
325 330 335
Tyr Phe Gly Gly Tyr Gly Gly Pro Met Arg Ala Phe Gly Arg Met Tyr
340 345 350
Gly Gly Met Ser Leu Asp Asp Trp Gly Tyr Gly Met Pro Asn Ala Arg
355 360 365
Pro Ser Arg Pro Asp Arg Arg Tyr Arg Pro Tyr
370 375

(2) INFORMATION FOR SEQ ID NO:771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..357
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

Met Ser Lys Phe Gly Asp Leu Glu Asp Cys Ile Val Met Lys Asp Arg
1 5 10 15
Ser Thr Gly Arg Ser Arg Gly Phe Gly Tyr Val Thr Phe Ala Ser Ala
20 25 30
Glu Asp Ala Lys Asn Ala Leu Lys Gly Glu His Phe Leu Gly Asn Arg
35 40 45
Ile Leu Glu Val Lys Val Ala Thr Pro Lys Glu Glu Met Arg Gln Pro

50 55 60
Ala Lys Lys Val Thr Arg Ile Phe Val Ala Arg Ile Pro Ser Ser Val
65 70 75 80
Ser Glu Ser Asp Phe Arg Ser His Phe Glu Arg Tyr Gly Glu Ile Thr
85 90 95
Asp Leu Tyr Met Pro Lys Asp Tyr Asn Ser Lys Gln His Arg Arg Ile
100 105 110
Gly Phe Ile Thr Phe Ser Ser Ala Asp Ser Val Glu Asp Leu Met Glu
115 120 125
Asp Thr His Asp Leu Gly Gly Thr Thr Val Ala Val Asp Arg Ala Thr
130 135 140
Pro Lys Glu Asp Asp His Pro Pro Arg Pro Pro Val Ala Arg Met
145 150 155 160
Ser Arg Pro Pro Val Ala Ile Ala Gly Gly Phe Gly Ala Pro Gly Gly
165 170 175
Tyr Gly Ala Tyr Asp Ala Tyr Ile Ser Ala Ala Thr Arg Tyr Ala Ala
180 185 190
Leu Gly Ala Pro Thr Leu Tyr Asp Asn Pro Ala Thr Phe Tyr Gly Arg
195 200 205
Gly Glu Pro Thr Thr Arg Gly Ile Gly Asn Lys Ile Phe Val Gly Arg
210 215 220
Leu Pro Gln Glu Ala Ser Val Asp Asp Leu Arg Asp Tyr Phe Gly Arg
225 230 235 240
Phe Gly His Ile Gln Asp Ala Tyr Ile Pro Lys Asp Pro Lys Arg Ser
245 250 255
Gly His Arg Gly Phe Gly Phe Val Thr Phe Ala Glu Asn Gly Val Ala
260 265 270
Asp Arg Val Ala Arg Arg Ser His Glu Ile Cys Gly Gln Glu Val Ala
275 280 285
Ile Asp Ser Ala Thr Pro Leu Asp Glu Ala Gly Pro Ser Ala Gly Ala
290 295 300
Ser Ser Met Leu Ser Ser Ser Arg Pro Glu Tyr Phe Gly Gly Tyr Gly
305 310 315 320
Gly Pro Met Arg Ala Phe Gly Arg Met Tyr Gly Gly Met Ser Leu Asp
325 330 335
Asp Trp Gly Tyr Gly Met Pro Asn Ala Arg Pro Ser Arg Pro Asp Arg
340 345 350
Arg Tyr Arg Pro Tyr
355

(2) INFORMATION FOR SEQ ID NO:772:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..345

(D) OTHER INFORMATION: / Ceres Seq. ID 1567936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

Met Lys Asp Arg Ser Thr Gly Arg Ser Arg Gly Phe Gly Tyr Val Thr
1 5 10 15
Phe Ala Ser Ala Glu Asp Ala Lys Asn Ala Leu Lys Gly Glu His Phe
20 25 30
Leu Gly Asn Arg Ile Leu Glu Val Lys Val Ala Thr Pro Lys Glu Glu
35 40 45
Met Arg Gln Pro Ala Lys Lys Val Thr Arg Ile Phe Val Ala Arg Ile
50 55 60
Pro Ser Ser Val Ser Glu Ser Asp Phe Arg Ser His Phe Glu Arg Tyr
65 70 75 80

Gly Glu Ile Thr Asp Leu Tyr Met Pro Lys Asp Tyr Asn Ser Lys Gln
85 90 95
His Arg Arg Ile Gly Phe Ile Thr Phe Ser Ser Ala Asp Ser Val Glu
100 105 110
Asp Leu Met Glu Asp Thr His Asp Leu Gly Gly Thr Thr Val Ala Val
115 120 125
Asp Arg Ala Thr Pro Lys Glu Asp Asp His Pro Pro Arg Pro Pro Pro
130 135 140
Val Ala Arg Met Ser Arg Pro Pro Val Ala Ile Ala Gly Gly Phe Gly
145 150 155 160
Ala Pro Gly Gly Tyr Gly Ala Tyr Asp Ala Tyr Ile Ser Ala Ala Thr
165 170 175
Arg Tyr Ala Ala Leu Gly Ala Pro Thr Leu Tyr Asp Asn Pro Ala Thr
180 185 190
Phe Tyr Gly Arg Gly Glu Pro Thr Thr Arg Gly Ile Gly Asn Lys Ile
195 200 205
Phe Val Gly Arg Leu Pro Gln Glu Ala Ser Val Asp Asp Leu Arg Asp
210 215 220
Tyr Phe Gly Arg Phe Gly His Ile Gln Asp Ala Tyr Ile Pro Lys Asp
225 230 235 240
Pro Lys Arg Ser Gly His Arg Gly Phe Gly Phe Val Thr Phe Ala Glu
245 250 255
Asn Gly Val Ala Asp Arg Val Ala Arg Arg Ser His Glu Ile Cys Gly
260 265 270
Gln Glu Val Ala Ile Asp Ser Ala Thr Pro Leu Asp Glu Ala Gly Pro
275 280 285
Ser Ala Gly Ala Ser Ser Met Leu Ser Ser Ser Arg Pro Glu Tyr Phe
290 295 300
Gly Gly Tyr Gly Gly Pro Met Arg Ala Phe Gly Arg Met Tyr Gly Gly
305 310 315 320
Met Ser Leu Asp Asp Trp Gly Tyr Gly Met Pro Asn Ala Arg Pro Ser
325 330 335
Arg Pro Asp Arg Arg Tyr Arg Pro Tyr
340 345

(2) INFORMATION FOR SEQ ID NO:773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1140

(D) OTHER INFORMATION: / Ceres Seq. ID 1567941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

attttttcttg	agagatccaa	aaaaagtatc	agaaagaaga	agaagacgac	tccaaaaaWc	60
gatgccgtat	tacaccaaacg	acgacaatga	cgtcgacgat	ttcacggaat	acgatccgat	120
gccttatagt	ggaggtctacg	acatcacccgt	gacatacggc	cgttcaattc	caccgtccga	180
cgagacttgt	taccctctct	ctctctctct	cggcgacgccc	tttgatgatc	agcgacctaa	240
tttctctctc	aacaacgatt	cttctgctta	tgacgaccaa	gctcttaaaa	ccgagtcacg	300
tagctatgca	gcaccccgac	ccgttggtatc	tggatctgat	tttgcccgga	aacctaatc	360
tggatattgga	gggagaacgg	aggttgagta	tggccggaaa	actgaatcgg	agcatggatc	420
tggctatggt	gggagaattg	agagcgatta	cgtgaagcct	agctatggcg	gtcacgagga	480
tggatggtgac	gatggtcaca	aaaaacatag	tggtaaggat	tatgatgatg	gagatgagaa	540
gagtaagaag	aaggagaagg	agaagaagaa	ggataagaag	aaagatggta	ataactctga	600
agatgatgat	tttaagaaga	agaagaagaa	atagcagtae	aaggagcatt	atgatgatga	660
tgattatgat	gagaagaaga	agaagaagaa	agactataat	gatgatgatg	agaagaagaa	720
gaagaagcat	tataatgatg	atgatgatga	gaagaagaag	aagcattaca	atgatgatga	780
tgatgagaag	aagaagaaga	aggagatcat	tgatgatgat	gataagaaga	agaagaagca	840
ctatgataat	gatgatgatg	agaagaagaa	gaagaaggat	catcgtgatg	atgatgatga	900

gaagaagaag aagaagdata accaccacaa gggacatgac taaaaaaggt ttatgatttg	960
ggattttgcat tottatgact aaataagtaa caacaactta agcacacttc tgctctctac	1020
gtttatgtca atgtttgttt tgtttttgcg tctgtgtttt gctgctaact tcaatgagat	1080
cttcataagt catatgtaat atgttttagtg tacgtgtgttt ctagtgatgt cgtttggtct	1140

(2) INFORMATION FOR SEQ ID NO:774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..210
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

Phe	Phe	Leu	Arg	Asp	Pro	Lys	Lys	Val	Ser	Glu	Arg	Arg	Arg	Arg	Arg	Arg	Arg
1				5					10							15	
Leu	Gln	Lys	Xaa	Met	Pro	Tyr	Tyr	Thr	Asn	Asp	Asp	Asn	Asp	Asp	Val	Asp	
			20					25							30		
Asp	Phe	Thr	Glu	Tyr	Asp	Pro	Met	Pro	Tyr	Ser	Gly	Gly	Tyr	Asp	Ile		
			35					40					45				
Thr	Val	Thr	Tyr	Gly	Arg	Ser	Ile	Pro	Pro	Ser	Asp	Glu	Thr	Cys	Tyr		
			50				55					60					
Pro	Leu	Ser	Ser	Leu	Ser	Gly	Asp	Ala	Phe	Glu	Tyr	Gln	Arg	Pro	Asn		
				70					75					80			
Phe	Ser	Ser	Asn	Asn	Asp	Ser	Ser	Ala	Tyr	Asp	Asp	Gln	Ala	Leu	Lys		
				85					90					95			
Thr	Glu	Tyr	Ser	Ser	Tyr	Ala	Arg	Pro	Gly	Pro	Val	Gly	Ser	Gly	Ser		
				100				105					110				
Asp	Phe	Gly	Arg	Lys	Pro	Asn	Ser	Gly	Tyr	Gly	Gly	Arg	Thr	Glu	Val		
			115					120				125					
Glu	Tyr	Gly	Arg	Lys	Thr	Glu	Ser	Glu	His	Gly	Ser	Gly	Tyr	Gly	Gly		
			130					135				140					
Arg	Ile	Glu	Ser	Asp	Tyr	Val	Lys	Pro	Ser	Tyr	Gly	Gly	His	Glu	Asp		
				145			150				155			160			
Asp	Gly	Asp	Asp	Gly	His	Lys	Lys	His	Ser	Gly	Lys	Asp	Tyr	Asp	Asp		
				165					170					175			
Gly	Asp	Glu	Lys	Ser	Lys	Lys	Lys	Glu	Lys	Glu	Lys	Lys	Lys	Asp	Lys		
			180					185					190				
Lys	Lys	Asp	Gly	Asn	Asn	Ser	Glu	Asp	Asp	Glu	Phe	Lys	Lys	Lys	Lys		
			195				200					205					
Lys	Lys																
																	210

(2) INFORMATION FOR SEQ ID NO:775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..190
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

Met	Pro	Tyr	Tyr	Thr	Asn	Asp	Asp	Asn	Asp	Val	Asp	Asp	Phe	Thr	Glu		
1				5					10					15			
Tyr	Asp	Pro	Met	Pro	Tyr	Ser	Gly	Gly	Tyr	Asp	Ile	Thr	Val	Thr	Tyr		
			20					25					30				

(2) INFORMATION FOR SEQ ID NO:776:

(A) LENGTH: 171 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: \mathbb{R}^n

MOLECULE TYPE: peptide

(ix) FEATURE:

(1A) FEATURE.
(A) NAME.

(A) NAME/REF.: peptide
(B) LOCATION: 1 171

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:776:

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:776:
Pro Tyr Ser Gly Gly Tyr Asp Ile Thr Val T

(2) INFORMATION FOR SEQ ID NO:777:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1257 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1257

(D) OTHER INFORMATION: / Ceres Seq. ID 1567945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

agtataaaga	cgacaaagta	aacaaaaaaa	aaaagagttc	tcttacaatt	ttcctaaatt	60
cttgattttg	agattttcact	ttttccgatt	tgaacaaatg	atgataaact	gcggtggagc	120
caaggcgggc	aaatcgctgt	taatggcggc	tggaccaagt	ttgttctcga	cggtccgtac	180
ggtttcgtct	cacgaggtct	tatcagcaag	ccatatattg	aagcctgggt	ttacatctgc	240
ttggatatgg	actagagctc	cgacagattg	aggtatgaga	ttcgctagca	cgatcactct	300
gggagagaaa	actccgatga	aggaggagga	cgcgaaatcg	aagaaaaacg	agaacgaatc	360
caccggtgga	gacgcgcgcg	gaggtataaa	caaggagagt	aaaggaaatc	cgagctattg	420
gggtgttgaa	cctaataaga	ttactaaga	agatggttct	gaatggaagt	ggaactgttt	480
caggccatgg	gagacgtata	aagctgatat	agatagattc	gaagaagcat	catgttccaa	540
cgaggtttct	tgatagaata	gcttattgga	ctgttaaatc	tttctgttgg	cctaccgatt	600
tgttctttcca	gaggagatat	ggatgtcgag	ctatgatgct	tgaacctgta	gcagcagcat	660
ctcgtaaggt	tggaggaatg	ttactacact	gcaaatcgct	tcgacgtttt	gagcaaaagt	720
gaggatggat	taaggctctt	cttgagggaag	cagagaatga	gagaatgcac	cttatgacat	780
tcctggaagt	cgcgaaacgc	aaatgggtacg	agagagcgct	cgtgatcact	gtgcaaggag	840
tcttcttcaa	cgcttatttc	cttggttact	taatctctcc	caagtgttgc	catcgatagg	900
ttgggtacct	tgaagaagaa	gcgatccatt	cttatactga	gtttctcaag	gaacttgaca	960
aaggtaacat	tgagaatggt	cctgctccgg	ctattgctat	tgattactgg	aggcttctcg	1020
ctgatgcgac	Acttctgat	gttctgatgg	ttgttcgtgc	tgacgagcgt	catcacctgt	1080
atgtaaacca	ttttgcatct	gatattcact	accaaggtcg	tgaactaaag	gaagctccag	1140
ctccaattgg	gtatcattga	ttcgattaaa	agaagagcgt	tttctcaagt	ttaaaacttt	1200
gttctaaaga	atttaagttc	tttgacttgt	atatacataa	tcacctctgc	ttaagct	

(2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1567946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

Met	Met	Leu	Glu	Thr	Val	Ala	Ala	Val	Pro	Gly	Met	Val	Gly	Gly	Met
1				5				10					15		
Leu	Leu	His	Cys	Lys	Ser	Leu	Arg	Arg	Glu	Gln	Ser	Gly	Gly	Trp	
				20				25				30			
Ile	Lys	Ala	Leu	Leu	Glu	Glu	Ala	Glu	Asn	Glu	Arg	Met	His	Leu	Met
				35				40				45			
Thr	Phe	Met	Glu	Val	Ala	Lys	Pro	Lys	Trp	Tyr	Glu	Arg	Ala	Leu	Val
				50				55				60			
Ile	Thr	Val	Gln	Gly	Val	Phe	Phe	Asn	Ala	Tyr	Phe	Leu	Gly	Tyr	Leu
65				70				75				80			
Ile	Ser	Pro	Lys	Phe	Ala	His	Arg	Met	Val	Gly	Tyr	Leu	Glu	Glu	Glu
				85				90				95			
Ala	Ile	His	Ser	Tyr	Thr	Glu	Phe	Leu	Lys	Glu	Leu	Asp	Lys	Gly	Asn
				100				105				110			
Ile	Glu	Asn	Val	Pro	Ala	Pro	Ala	Ile	Ala	Ile	Asp	Tyr	Trp	Arg	Leu
				115				120				125			
Pro	Ala	Asp	Ala	Thr	Leu	Arg	Asp	Val	Val	Met	Val	Val	Arg	Ala	Asp
				130				135				140			
Glu	Ala	His	His	Arg	Asp	Val	Asn	His	Phe	Ala	Ser	Asp	Ile	His	Tyr
145				150				155				160			
Gln	Gly	Arg	Glu	Leu	Lys	Glu	Ala	Pro	Ala	Pro	Ile	Gly	Tyr	His	
				165				170				175			

(2) INFORMATION FOR SEQ ID NO:779:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..174
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567947
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:
Met Leu Glu Thr Val Ala Ala Val Pro Gly Met Val Gly Gly Met Leu
1 5 10 15
Leu His Cys Lys Ser Leu Arg Arg Phe Glu Gln Ser Gly Gly Trp Ile
 20 25 30
Lys Ala Leu Leu Glu Glu Ala Glu Asn Glu Arg Met His Leu Met Thr
 35 40 45
Phe Met Glu Val Ala Lys Pro Lys Trp Tyr Glu Arg Ala Leu Val Ile
50 55 60
Thr Val Gln Gly Val Phe Phe Asn Ala Tyr Phe Leu Gly Tyr Leu Ile
65 70 75 80
Ser Pro Lys Phe Ala His Arg Met Val Gly Tyr Leu Glu Glu Ala
 85 90 95
Ile His Ser Tyr Thr Glu Phe Leu Lys Glu Leu Asp Lys Gly Asn Ile
 100 105 110
Glu Asn Val Pro Ala Pro Ala Ile Ala Ile Asp Tyr Trp Arg Leu Pro
 115 120 125
Ala Asp Ala Thr Leu Arg Asp Val Val Met Val Val Arg Ala Asp Glu
130 135 140
Ala His His Arg Asp Val Asn His Phe Ala Ser Asp Ile His Tyr Gln
145 150 155 160
Gly Arg Glu Leu Lys Glu Ala Pro Ala Pro Ile Gly Tyr His
 165 170
(2) INFORMATION FOR SEQ ID NO:780:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..164
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567948
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:
Met Val Gly Gly Met Leu Leu His Cys Lys Ser Leu Arg Arg Phe Glu
1 5 10 15
Gln Ser Gly Gly Trp Ile Lys Ala Leu Leu Glu Glu Ala Glu Asn Glu
 20 25 30
Arg Met His Leu Met Thr Phe Met Glu Val Ala Lys Pro Lys Trp Tyr
35 40 45
Glu Arg Ala Leu Val Ile Thr Val Gln Gly Val Phe Phe Asn Ala Tyr
50 55 60
Phe Leu Gly Tyr Leu Ile Ser Pro Lys Phe Ala His Arg Met Val Gly
65 70 75 80
Tyr Leu Glu Glu Glu Ala Ile His Ser Tyr Thr Glu Phe Leu Lys Glu
 85 90 95
Leu Asp Lys Gly Asn Ile Glu Asn Val Pro Ala Pro Ala Ile Ala Ile
 100 105 110
Asp Tyr Trp Arg Leu Pro Ala Asp Ala Thr Leu Arg Asp Val Val Met
115 120 125

Val Val Arg Ala Asp Glu Ala His His Arg Asp Val Asn His Phe Ala
130 135 140
Ser Asp Ile His Tyr Gln Gly Arg Glu Leu Lys Glu Ala Pro Ala Pro
145 150 155 160
Ile Gly Tyr His

(2) INFORMATION FOR SEQ ID NO:781:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1969 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1969

(D) OTHER INFORMATION: / Ceres Seq. ID 1567957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

aacagctggc	catgtctatgc	atgtgttcat	caatggccaa	ttatctggat	ctgcgtatgg	60
tagtttagac	tctctaaac	taacttttcg	gaaaggtgtg	aatctaaagag	ctggtttcaa	120
caaaattgcg	atactaaaga	tcgctgttgg	tctccgaat	ctgggtccac	attttgagac	180
atggaatgct	ggagtttttg	gtccagtttc	attgaatggt	ctcaatggcg	gacgaaaaga	240
tctatcatgg	cagaaatgga	cttataaggt	tggtcttaaa	ggagagtctc	tgagtcttca	300
ttoacttagt	gggagctcac	cggttgagtg	ggcagaaggt	gcatttgttg	cacagaaaaca	360
accacttact	tggtacaaga	cgactttctc	tgctccagct	ggaaattcgc	cattggcgtg	420
agacatggga	agcatgggga	aaggtcaaat	atggataaat	gggcagagct	tgggacgtca	480
ctggcctgca	tataaagcag	ttggttcttg	cagcgagtg	tcttatactg	gaacattcag	540
agaggacaag	tgcttaagaa	actgtggaga	ggcttctcaa	agatgggtacc	atgtcccaag	600
gtcgttgctc	aaacaaagtg	gcaatctatt	ggttgtcttt	gaggagtggg	gaggagaccc	660
gaacggaaac	tcgttggtca	gaagagaagt	ggacagtgtg	tgtgcagata	tctatgaatg	720
gcgaatcaag	ctggtgaact	accaattgca	tgcttctgga	aaagttaata	aaccattgca	780
tcccaaatg	catctgcaat	gcgggGccgc	gacaaaagat	caccaccgtg	aagtttgcta	840
gtttcgggac	acctgaaggg	acttgttgta	gttaccgtca	aggaagctgt	catgcccatc	900
actcotatga	cgctttcaac	aaactatgtg	ttgggcagaa	ctggtgttct	gtaactgtag	960
caccggagat	gtttggtgga	gatccgtgtc	caaatgtgtg	gaagaaactc	gcggtggaag	1020
ccgtttgtgc	ttaaatgaaa	gcagacgcag	cagcaatcaa	aagactgtaa	aggtgggtac	1080
ttacgcattc	ttacaggttt	ctgatgggat	tagtatgttt	tatgaagaca	acagaagaag	1140
ttggtatttt	tctagctcct	tattttatca	cggtggaagt	tgtacaaaag	gacgcaaac	1200
gcggttcaac	aatttcagag	gttggtgatt	atatgtaaat	aagcttggga	agggtttgtt	1260
attgttaacc	aagaagaag	atgaagaaga	agaagcacat	tgagactgga	gaacttaagt	1320
ccatgtgtag	attcttcttc	tttctcttct	ttttctttag	aaacacacac	aacctcaaga	1380
acttaaaaaa	taactctaca	gagatggctg	ttggaatcct	tgaggttagt	ctgatcagtg	1440
gcgaaggtct	caagcgtctc	gtatttcttg	gtaagataga	gaagatccaat	gagatccaat	1500
acaaagggca	aaccgcgcaa	agcagcgttg	ctaaagaaga	tggaggtaga	aatccgcacat	1560
ggaatgataa	attgaaatgg	agagcagagt	ttcctggctc	cgccgcgcgc	tacaaaactca	1620
tcgtcgaagt	catggatcat	gatactttct	ccctgcagca	tttcaattgc	gaagccacgg	1680
tacatgtgaa	agagctattg	gaaatgggag	tggagaaggg	aacgcggcga	ctaaaggccaa	1740
ccaagtacaa	catgtgtgac	tccgatctct	ccctttgttg	cgagcttctc	attggagttt	1800
cttaactctc	tttgcaagag	aggggaatgg	atggagaaca	gtttggagga	tggagacata	1860
gcgaagttga	ttagtttgg	ttcttaaaac	tgctgatttt	attcttctct	tctatcttta	1920
gtgtcaacat	cattaagata	ttcataagta	caaaaaatta	tttaaatgg		

(2) INFORMATION FOR SEQ ID NO:782:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..279

(D) OTHER INFORMATION: / Ceres Seq. ID 1567958

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

Thr Ala Gly His Ala Met His Val Phe Ile Asn Gly Gln Leu Ser Gly
1 5 10 15
Ser Ala Tyr Gly Ser Leu Asp Ser Pro Lys Leu Thr Phe Arg Lys Gly
20 25 30
Val Asn Leu Arg Ala Gly Phe Asn Lys Ile Ala Ile Leu Ser Ile Ala
35 40 45
Val Gly Leu Pro Asn Val Gly Pro His Phe Glu Thr Trp Asn Ala Gly
50 55 60
Val Leu Gly Pro Val Ser Leu Asn Gly Leu Asn Gly Gly Arg Lys Asp
65 70 75 80
Leu Ser Trp Gln Lys Trp Thr Tyr Lys Val Gly Leu Lys Gly Glu Ser
85 90 95
Leu Ser Leu His Ser Leu Ser Gly Ser Ser Ser Val Glu Trp Ala Glu
100 105 110
Gly Ala Phe Val Ala Gln Lys Gln Pro Leu Thr Trp Tyr Lys Thr Thr
115 120 125
Phe Ser Ala Pro Ala Gly Asn Ser Pro Leu Ala Val Asp Met Gly Ser
130 135 140
Met Gly Lys Gly Gln Ile Trp Ile Asn Gly Gln Ser Leu Gly Arg His
145 150 155 160
Trp Pro Ala Tyr Lys Ala Val Gly Ser Cys Ser Glu Cys Ser Tyr Thr
165 170 175
Gly Thr Phe Arg Glu Asp Lys Cys Leu Arg Asn Cys Gly Glu Ala Ser
180 185 190
Gln Arg Trp Tyr His Val Pro Arg Ser Trp Leu Lys Pro Ser Gly Asn
195 200 205
Leu Leu Val Val Phe Glu Glu Trp Gly Gly Asp Pro Asn Gly Ile Ser
210 215 220
Leu Val Arg Arg Glu Val Asp Ser Val Cys Ala Asp Ile Tyr Glu Trp
225 230 235 240
Gln Ser Thr Leu Val Asn Tyr Gln Leu His Ala Ser Gly Lys Val Asn
245 250 255
Lys Pro Leu His Pro Lys Val His Leu Gln Cys Gly Ala Arg Thr Lys
260 265 270
Asp His His Arg Glu Val Cys
275

(2) INFORMATION FOR SEQ ID NO:783:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..274

(D) OTHER INFORMATION: / Ceres Seq. ID 1567959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

Met His Val Phe Ile Asn Gly Gln Leu Ser Gly Ser Ala Tyr Gly Ser
1 5 10 15
Leu Asp Ser Pro Lys Leu Thr Phe Arg Lys Gly Val Asn Leu Arg Ala
20 25 30
Gly Phe Asn Lys Ile Ala Ile Leu Ser Ile Ala Val Gly Leu Pro Asn
35 40 45
Val Gly Pro His Phe Glu Thr Trp Asn Ala Gly Val Leu Gly Pro Val
50 55 60
Ser Leu Asn Gly Leu Asn Gly Gly Arg Lys Asp Leu Ser Trp Gln Lys
65 70 75 80
Trp Thr Tyr Lys Val Gly Leu Lys Gly Glu Ser Leu Ser Leu His Ser

Met	Lys	Lys	Lys	Lys	His	Ile	Glu	Thr	Gly	Glu	Ser	Lys	Ser	Met	Cys
1				5					10					15	
Arg	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Arg	Asn	Asn	Thr	Asn	Pro
			20					25					30		
Lys	Asn	Leu	Lys	Asn	Asn	Ser	Thr	Glu	Met	Ala	Val	Gly	Ile	Leu	Glu
		35					40					45			
Val	Ser	Leu	Ile	Ser	Gly	Lys	Gly	Leu	Lys	Arg	Ser	Asp	Phe	Leu	Gly
		50				55					60				
Lys	Ile	Asp	Pro	Tyr	Val	Glu	Ile	Gln	Tyr	Lys	Gly	Gln	Thr	Arg	Lys
65					70					75				80	
Ser	Ser	Val	Ala	Lys	Glu	Asp	Gly	Gly	Arg	Asn	Pro	Thr	Trp	Asn	Asp
				85					90					95	
Lys	Leu	Lys	Trp	Arg	Ala	Glu	Phe	Pro	Gly	Ser	Gly	Ala	Asp	Tyr	Lys
			100					105					110		
Leu	Ile	Val	Lys	Val	Met	Asp	His	Asp	Thr	Phe	Ser	Ser	Asp	Asp	Phe
		115						120					125		
Ile	Gly	Glu	Ala	Thr	Val	His	Val	Lys	Glu	Leu	Leu	Glu	Met	Gly	Val
		130				135						140			
Glu	Lys	Gly	Thr	Ala	Glu	Leu	Arg	Pro	Thr	Lys	Tyr	Asn	Ile	Val	Asp
145					150					155				160	
Ser	Asp	Leu	Ser	Phe	Val	Gly	Glu	Leu	Leu	Ile	Gly	Val	Ser	Tyr	Ser
				165					170					175	
Leu	Leu	Gln	Asp	Arg	Gly	Met	Asp	Gly	Glu	Gln	Phe	Gly	Gly	Trp	Lys
			180					185					190		

His Ser Gln Val Asp
195

(2) INFORMATION FOR SEQ ID NO:785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1858
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

cttcttaaac	tgttttttaa	ctctccatct	ctaaaaagac	catcaacgct	cttctcttta	60
ttgcagcaga	aacagaaacc	agttcaataa	agcttttttg	taagaaaaat	tgaaaggaaa	120
agataattga	aaactcgtag	agagaaaagt	gcacagaatc	tgaaattctg	acacttttta	180
ccacgaataa	tgattctctt	tgaaaaaca	tgactcaatg	ttttctttat	ctttttctct	240
gaattgaggt	tgttttgtac	ttaaagtatg	ctcctttatc	taccgttgac	tgattctact	300
cttttattct	caactttttc	ctgatttgct	cgtgtgttta	cttcaattcc	tcagtttctg	360
tgtgaaaagt	tgagtttcat	gtgatcaaaa	ttggggcctt	actactttta	agagaatgag	420
tgacaaaagc	gagtttgcgc	caagaagaag	ggatttggct	aatacgccag	tgatttttga	480
tcctccggag	aatccaatgt	tgggtccttc	tcogatgatg	gattcattca	gagaaactct	540
ttggcatgat	tgtggtttca	atgtccacac	agatgcagac	acttccctta	gaggttaata	600
taatatgtat	atcacctctt	aaatgggttg	gaatatggct	cagttccctg	cagattcagg	660
attcatttag	cgtgctgcga	agttttcttt	ttttggkatg	tggtgaaatg	atgatgaacc	720
aaacaacaat	atctcttgga	gttccagatt	caactggctt	gtttcttcaa	gatacacaga	780
ttcttagtgg	atccaaacta	gataatggct	ctcttactga	tgactctaag	ttagtgaag	840
agagatcgat	taataatgta	tcagagattt	ctcaatctag	tgaggagta	ggatcatgat	900
atgtctaaagt	tgggcaaaac	tcttccaagg	ggtttagtag	taagaagagg	aaaagacttg	960
ggaagggatt	tgaaagaaga	gaagataaaa	agcaaaaagg	tgagcaaatg	ccaacttcaa	1020
atgcgaacaa	gacaaacagt	gagaagcaac	cttctgatto	tttaaaagct	gggtatatct	1080
acatgagggc	acgaagaggg	caggctacta	atagtccacg	tcttgctgaa	agtgaaagaa	1140
gagaaaaaat	cagtgaaagg	atgaagtctt	tgcagaatct	tgtgccaggt	tgccacaagg	1200
tgactggtaa	ggcagttatg	ctcgatgaaa	tcattaacta	tgtgcaatca	cttcaatgcc	1260
aaatcgagtt	tttatcgatg	aaactttcgg	ctgtgaatcc	tgtgctcgat	tttaacctgt	1320
aaagcctctc	tgcaaaagat	gctcttcaat	catctgcacc	gacatttccc	cacaacatgt	1380
cgatgcttta	tctctctgta	tcgtatctct	ctcaaacagg	attcatgcaa	ccgaacattt	1440
ctccaatggt	gctatttgat	ggaggattaa	aacggcagga	aacacatgga	tatgaaagtg	1500
atcacacaaa	tctgttccac	aagaaccatg	aaacggcgac	tgcaactgat	catgaagata	1560
caacagctga	catgaaggtg	gagccgtaga	tgtttctttc	tcactttgtc	ctcagcttta	1620
gctgtcgata	tagtgccgcg	cggctcgaga	ttttattaac	ttcgaacaga	agagtgaaaa	1680
cgaaacagag	gaggaagcag	attttgtctt	tgaatatatt	acagctcccg	gagaaagagt	1740
cgagagtaag	aatcaacaat	gttgtgtaat	gaatagctac	tgctctgctc	ttttgtagct	1800
attgtctgct	tcttttttgt	acatataaat	ccatgcaagg	gaagaggaat	gttaattcc	

(2) INFORMATION FOR SEQ ID NO:786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..347
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

Met	Met	Val	Val	Ser	Met	Ser	Thr	Gln	Met	Gln	Thr	Leu	Pro	Leu	Glu
1		5						10				15			
Val	Ile	Ile	Ile	Leu	Ile	Tyr	Leu	Leu	Lys	Trp	Val	Gly	Ile	Trp	Leu
		20						25				30			

Ser Ser Leu Gln Ile Gln Asp Ser Leu Ser Val Leu Gln Ser Phe Leu
35 40 45
Phe Leu Xaa Cys Gly Glu Met Met Met Asn Gln Gln Ser Ser Leu
50 55 60
Gly Val Pro Asp Ser Thr Gly Leu Phe Leu Gln Asp Thr Gln Ile Pro
65 70 75 80
Ser Gly Ser Lys Leu Asp Asn Gly Pro Leu Thr Asp Ala Ser Lys Leu
85 90 95
Val Lys Glu Arg Ser Ile Asn Asn Val Ser Glu Asp Ser Gln Ser Ser
100 105 110
Gly Gly Asn Gly His Asp Asp Ala Lys Cys Gly Gln Thr Ser Ser Lys
115 120 125
Gly Phe Ser Ser Lys Lys Arg Lys Arg Ile Gly Lys Asp Cys Glu Glu
130 135 140
Glu Glu Asp Lys Lys Gln Lys Asp Glu Gln Ser Pro Thr Ser Asn Ala
145 150 155 160
Asn Lys Thr Asn Ser Glu Lys Gln Pro Ser Asp Ser Leu Lys Asp Gly
165 170 175
Tyr Ile His Met Arg Ala Arg Arg Gly Gln Ala Thr Asn Ser His Ser
180 185 190
Leu Ala Glu Arg Val Arg Arg Glu Lys Ile Ser Glu Arg Met Lys Phe
195 200 205
Leu Gln Asp Leu Val Pro Gly Cys Asp Lys Val Thr Gly Lys Ala Val
210 215 220
Met Leu Asp Glu Ile Ile Asn Tyr Val Gln Ser Leu Gln Cys Gln Ile
225 230 235 240
Glu Phe Leu Ser Met Lys Leu Ser Ala Val Asn Pro Val Leu Asp Phe
245 250 255
Asn Leu Glu Ser Leu Leu Ala Lys Asp Ala Leu Gln Ser Ser Ala Pro
260 265 270
Thr Phe Pro His Asn Met Ser Met Leu Tyr Pro Pro Val Ser Tyr Leu
275 280 285
Ser Gln Thr Gly Phe Met Gln Pro Asn Ile Ser Ser Met Leu Leu Leu
290 295 300
Ser Gly Gly Leu Lys Arg Gln Glu Thr His Gly Tyr Glu Ser Asp His
305 310 315 320
His Asn Leu Val His Lys Asn His Glu Thr Gly Thr Ala Pro Asp His
325 330 335
Glu Asp Thr Thr Ala Asp Met Lys Val Glu Pro
340 345

(2) INFORMATION FOR SEQ ID NO:787:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..346

(D) OTHER INFORMATION: / Ceres Seq. ID 1567966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

Met Val Val Ser Met Ser Thr Gln Met Gln Thr Leu Pro Leu Glu Val
1 5 10 15
Ile Ile Ile Leu Ile Tyr Leu Leu Lys Trp Val Gly Ile Trp Leu Ser
20 25 30
Ser Leu Gln Ile Gln Asp Ser Leu Ser Val Leu Gln Ser Phe Leu Phe
35 40 45
Leu Xaa Cys Gly Glu Met Met Met Asn Gln Gln Gln Ser Ser Leu Gly
50 55 60
Val Pro Asp Ser Thr Gly Leu Phe Leu Gln Asp Thr Gln Ile Pro Ser

65				70				75				80
Gly	Ser	Lys	Leu	Asp	Asn	Gly	Pro	Leu	Thr	Asp	Ala	Ser
				85					90			Lys
												95
Lys	Glu	Arg	Ser	Ile	Asn	Asn	Val	Ser	Glu	Asp	Ser	Gln
			100					105				110
Gly	Asn	Gly	His	Asp	Asp	Ala	Lys	Cys	Gly	Gln	Thr	Ser
			115				120					125
Phe	Ser	Ser	Lys	Lys	Arg	Lys	Arg	Ile	Gly	Lys	Asp	Cys
							135				140	Glu
												145
Glu	Asp	Lys	Lys	Gln	Lys	Asp	Glu	Gln	Ser	Pro	Thr	Ser
							150			155		160
Lys	Thr	Asn	Ser	Glu	Lys	Gln	Pro	Ser	Asp	Ser	Leu	Lys
				165					170			175
Ile	His	Met	Arg	Ala	Arg	Arg	Gly	Gln	Ala	Thr	Asn	Ser
			180				185					190
Ala	Glu	Arg	Val	Arg	Arg	Glu	Lys	Ile	Ser	Glu	Arg	Met
			195				200					205
Gln	Asp	Leu	Val	Pro	Gly	Cys	Asp	Lys	Val	Thr	Gly	Lys
							215					220
Leu	Asp	Glu	Ile	Ile	Asn	Tyr	Val	Gln	Ser	Leu	Gln	Cys
							230					235
Phe	Leu	Ser	Met	Lys	Leu	Ser	Ala	Val	Asn	Pro	Val	Leu
				245					250			255
Leu	Glu	Ser	Leu	Leu	Ala	Lys	Asp	Ala	Leu	Gln	Ser	Ser
				260				265				270
Phe	Pro	His	Asn	Met	Ser	Met	Leu	Tyr	Pro	Pro	Val	Ser
				275			280					285
Gln	Thr	Gly	Phe	Met	Gln	Pro	Asn	Ile	Ser	Ser	Met	Leu
							295				300	Leu
Gly	Gly	Leu	Lys	Arg	Gln	Glu	Thr	His	Gly	Tyr	Glu	Ser
							310					315
Asn	Leu	Val	His	Lys	Asn	His	Glu	Thr	Gly	Thr	Ala	Pro
				325					330			335
Asp	Thr	Thr	Ala	Asp	Met	Lys	Val	Glu	Pro			
				340				345				

(2) INFORMATION FOR SEQ ID NO:788:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..342

(D) OTHER INFORMATION: / Ceres Seq. ID 1567967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

Met	Ser	Thr	Gln	Met	Gln	Thr	Leu	Pro	Leu	Glu	Val	Ile	Ile	Ile	Leu
1				5				10						15	
Ile	Tyr	Leu	Leu	Lys	Trp	Val	Gly	Ile	Trp	Leu	Ser	Ser	Leu	Gln	Ile
			20					25					30		
Gln	Asp	Ser	Leu	Ser	Val	Leu	Gln	Ser	Phe	Leu	Phe	Leu	Xaa	Cys	Gly
			35				40					45			
Glu	Met	Met	Met	Asn	Gln	Gln	Gln	Ser	Ser	Leu	Gly	Val	Pro	Asp	Ser
			50				55				60				
Thr	Gly	Leu	Phe	Leu	Gln	Asp	Thr	Gln	Ile	Pro	Ser	Gly	Ser	Lys	Leu
			65			70			75					80	
Asp	Asn	Gly	Pro	Leu	Thr	Asp	Ala	Ser	Lys	Leu	Val	Lys	Glu	Arg	Ser
				85				90						95	
Ile	Asn	Asn	Val	Ser	Glu	Asp	Ser	Gln	Ser	Ser	Gly	Gly	Asn	Gly	His
			100					105						110	

Asp Asp Ala Lys Cys Gly Gln Thr Ser Ser Lys Gly Phe Ser Ser Lys
115 120 125
Lys Arg Lys Arg Ile Gly Lys Asp Cys Glu Glu Glu Glu Asp Lys Lys
130 135 140
Gln Lys Asp Glu Gln Ser Pro Thr Ser Asn Ala Asn Lys Thr Asn Ser
145 150 155 160
Glu Lys Gln Pro Ser Asp Ser Leu Lys Asp Gly Tyr Ile His Met Arg
165 170 175
Ala Arg Arg Gly Gln Ala Thr Asn Ser His Ser Leu Ala Glu Arg Val
180 185 190
Arg Arg Glu Lys Ile Ser Glu Arg Met Lys Phe Leu Gln Asp Leu Val
195 200 205
Pro Gly Cys Asp Lys Val Thr Gly Lys Ala Val Met Leu Asp Glu Ile
210 215 220
Ile Asn Tyr Val Gln Ser Leu Gln Cys Gln Ile Glu Phe Leu Ser Met
225 230 235 240
Lys Leu Ser Ala Val Asn Pro Val Leu Asp Phe Asn Leu Glu Ser Leu
245 250 255
Leu Ala Lys Asp Ala Leu Gln Ser Ser Ala Pro Thr Phe Pro His Asn
260 265 270
Met Ser Met Leu Tyr Pro Pro Val Ser Tyr Leu Ser Gln Thr Gly Phe
275 280 285
Met Gln Pro Asn Ile Ser Ser Met Leu Leu Leu Ser Gly Gly Leu Lys
290 295 300
Arg Gln Glu Thr His Gly Tyr Glu Ser Asp His His Asn Leu Val His
305 310 315 320
Lys Asn His Glu Thr Gly Thr Ala Pro Asp His Glu Asp Thr Thr Ala
325 330 335
Asp Met Lys Val Glu Pro
340

(2) INFORMATION FOR SEQ ID NO:789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..522

(D) OTHER INFORMATION: / Ceres Seq. ID 1567975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

aaccctagct	tggtccacgc	tcagagcatt	ttggccattt	gggccactca	agttatcttg	60
atggggagctg	ttgaaggcta	cagagtcgca	ggaaatgggc	cattgggaga	ggccgaggac	120
ttgctttacc	ccggtggcag	cttcgaccca	ttgggtcttg	ctaccgaccc	agaggcttcc	180
gcggagttga	agggtgaagga	gctcaagaac	ggaagattgg	ctatgttctc	tatgtttgga	240
ttcttcgttc	aagccattgt	cactggtaag	ggaccgatag	agaaccttgc	tgaccatttg	300
gccgatccag	tcaacaacaa	cgcattgggc	ttcgcaacca	actttgttcc	cggaaagtga	360
gccaaagtgtt	atcagtttgt	attttgcttt	tccttcagtc	ttttgaattc	gagtgagaga	420
catgaggaga	aagagaaggt	tgGtatgtga	tggttttgaga	ctttcagatg	taaattkgca	480
agactttgta	tgattttgca	ttaatcaaac	tcatttttct	ct		

(2) INFORMATION FOR SEQ ID NO:790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1567976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

Asn	Pro	Ser	Leu	Val	His	Ala	Gln	Ser	Ile	Leu	Ala	Ile	Trp	Ala	Thr
1			5						10					15	
Gln	Val	Ile	Leu	Met	Gly	Ala	Val	Glu	Gly	Tyr	Arg	Val	Ala	Gly	Asn
			20					25					30		
Gly	Pro	Leu	Gly	Glu	Ala	Glu	Asp	Leu	Leu	Tyr	Pro	Gly	Gly	Ser	Phe
			35				40					45			
Asp	Pro	Leu	Gly	Leu	Ala	Thr	Asp	Pro	Glu	Ala	Phe	Ala	Glu	Leu	Lys
			50			55					60				
Val	Lys	Glu	Leu	Lys	Asn	Gly	Arg	Leu	Ala	Met	Phe	Ser	Met	Phe	Gly
65					70				75					80	
Phe	Phe	Val	Gln	Ala	Ile	Val	Thr	Gly	Lys	Gly	Pro	Ile	Glu	Asn	Leu
			85						90				95		
Ala	Asp	His	Leu	Ala	Asp	Pro	Val	Asn	Asn	Asn	Ala	Trp	Ala	Phe	Ala
			100				105						110		
Thr	Asn	Phe	Val	Pro	Gly	Lys									
			115												

(2) INFORMATION FOR SEQ ID NO:791:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1567977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

Met	Gly	Ala	Val	Glu	Gly	Tyr	Arg	Val	Ala	Gly	Asn	Gly	Pro	Leu	Gly
1			5						10					15	
Glu	Ala	Glu	Asp	Leu	Leu	Tyr	Pro	Gly	Gly	Ser	Phe	Asp	Pro	Leu	Gly
			20					25					30		
Leu	Ala	Thr	Asp	Pro	Glu	Ala	Phe	Ala	Glu	Leu	Lys	Val	Lys	Glu	Leu
			35			40					45				
Lys	Asn	Gly	Arg	Leu	Ala	Met	Phe	Ser	Met	Phe	Gly	Phe	Phe	Val	Gln
			50			55				60					
Ala	Ile	Val	Thr	Gly	Lys	Gly	Pro	Ile	Glu	Asn	Leu	Ala	Asp	His	Leu
65					70				75					80	
Ala	Asp	Pro	Val	Asn	Asn	Asn	Ala	Trp	Ala	Phe	Ala	Thr	Asn	Phe	Val
			85				90						95		
Pro	Gly	Lys													

(2) INFORMATION FOR SEQ ID NO:792:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 852 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..852

(D) OTHER INFORMATION: / Ceres Seq. ID 1567993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

ctttggaggt	cagggaaaagg	aaaaatcacg	ttctacctcg	atcctgaggt	agattttaca	60
caggagaaat	ctgataactca	ggaaaattca	gggaaaagag	gagaagttat	gttcctctcca	120
caaaagccct	atatggttct	gggatctttg	cgtaGcaat	tgttttatcc	tacctggagt	180
gcaactgtgg	aggagacgac	acctggtggc	agtaatatg	acggttcacc	acctctgctg	240
attagagagg	acggaaatga	aaagccgaca	acagatgatc	tgatgcggac	tctagagaag	300

gtttgtctttg gacatatagc ggatcgcttt ggtggctctg attcgataca cgagtggctcc 360
agtgttctct cacttgggtga gcagcagcgc cttgcctttg caccggttatt gctgtctcag 420
ccaaagctgg cgtctctgga tgaatccacc agtgcgttgg atgaagctaa tgaggcgcttc 480
ctgtaccagc aaatccagtc ggctggcatt acatatataa gcattggcca ccgccggact 540
ttaacgaaat tcataacaa gatettacaa atctcaacgg cagaccggaa gagcaatgaa 600
cgtaactggc gaataagagga cgtggatgcc caagattctt tgtacggtag attgaatcaa 660
aaggagggtgc caagtggaa cgtgatcaaaa cctgattgat tacataagag acagaagcag 720
caggtaaatc tgcaaacggg tgtcatgaaa catataagaa acatgtttgg tgtccatttt 780
gtataatac taccagactt gacgttgact gaagatgcaa gtaaatagag agattaatac 840
agatacgagt gc

(2) INFORMATION FOR SEQ ID NO:793:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..227

(D) OTHER INFORMATION: / Ceres Seq. ID 1567994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

Leu Trp Arg Ser Gly Lys Gly Lys Ile Thr Phe Tyr Leu Asp Pro Glu
1 5 10 15
Val Asp Phe Thr Gln Glu Lys Ser Asp Thr Gln Glu Asn Ser Gly Lys
20 25 30
Arg Gly Asp Val Leu Phe Leu Pro Gln Arg Pro Tyr Met Val Leu Gly
35 40 45
Ser Leu Arg Gln Gln Leu Leu Tyr Pro Thr Trp Ser Ala Thr Val Glu
50 55 60
Glu Thr Thr Pro Gly Gly Ser Asn Ile Asp Gly Ser Pro Pro Leu Leu
65 70 75 80
Ile Arg Glu Asp Gly Asn Glu Lys Pro Thr Thr Asp Asp Leu Met Arg
85 90 95
Thr Leu Glu Lys Val Cys Leu Gly His Ile Ala Asp Arg Phe Gly Gly
100 105 110
Leu Asp Ser Ile His Glu Trp Ser Ser Val Leu Ser Leu Gly Glu Gln
115 120 125
Gln Arg Leu Ala Phe Ala Arg Leu Leu Leu Ser Gln Pro Lys Leu Ala
130 135 140
Leu Leu Asp Glu Ser Thr Ser Ala Leu Asp Glu Ala Asn Glu Ala Phe
145 150 155 160
Leu Tyr Gln Gln Ile Gln Ser Ala Gly Ile Thr Tyr Ile Ser Ile Gly
165 170 175
His Arg Arg Thr Leu Thr Lys Phe His Asn Lys Ile Leu Gln Ile Ser
180 185 190
Thr Ala Asp Pro Lys Ser Asn Glu Arg Asn Trp Arg Ile Glu Asp Val
195 200 205
Asp Ala Gln Asp Ser Leu Tyr Gly Arg Leu Asn Gln Lys Glu Val Pro
210 215 220
Ser Gly Ser
225

(2) INFORMATION FOR SEQ ID NO:794:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..183

(D) OTHER INFORMATION: / Ceres Seq. ID 1567995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

Met Val Leu Gly Ser Leu Arg Gln Gln Leu Leu Tyr Pro Thr Trp Ser
1 5 10 15
Ala Thr Val Glu Glu Thr Thr Pro Gly Gly Ser Asn Ile Asp Gly Ser
20 25 30
Pro Pro Leu Leu Ile Arg Glu Asp Gly Asn Glu Lys Pro Thr Thr Asp
35 40 45
Asp Leu Met Arg Thr Leu Glu Lys Val Cys Leu Gly His Ile Ala Asp
50 55 60
Arg Phe Gly Gly Leu Asp Ser Ile His Glu Trp Ser Ser Val Leu Ser
65 70 75 80
Leu Gly Glu Gln Gln Arg Leu Ala Phe Ala Arg Leu Leu Ser Gln
85 90 95
Pro Lys Leu Ala Leu Leu Asp Glu Ser Thr Ser Ala Leu Asp Glu Ala
100 105 110
Asn Glu Ala Phe Leu Tyr Gln Gln Ile Gln Ser Ala Gly Ile Thr Tyr
115 120 125
Ile Ser Ile Gly His Arg Arg Thr Leu Thr Lys Phe His Asn Lys Ile
130 135 140
Leu Gln Ile Ser Thr Ala Asp Pro Lys Ser Asn Glu Arg Asn Trp Arg
145 150 155 160
Ile Glu Asp Val Asp Ala Gln Asp Ser Leu Tyr Gly Arg Leu Asn Gln
165 170 175
Lys Glu Val Pro Ser Gly Ser
180

(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1567996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

Met Arg Thr Leu Glu Lys Val Cys Leu Gly His Ile Ala Asp Arg Phe
1 5 10 15
Gly Gly Leu Asp Ser Ile His Glu Trp Ser Ser Val Leu Ser Leu Gly
20 25 30
Glu Gln Gln Arg Leu Ala Phe Ala Arg Leu Leu Ser Gln Pro Lys
35 40 45
Leu Ala Leu Leu Asp Glu Ser Thr Ser Ala Leu Asp Glu Ala Asn Glu
50 55 60
Ala Phe Leu Tyr Gln Gln Ile Gln Ser Ala Gly Ile Thr Tyr Ile Ser
65 70 75 80
Ile Gly His Arg Arg Thr Leu Thr Lys Phe His Asn Lys Ile Leu Gln
85 90 95
Ile Ser Thr Ala Asp Pro Lys Ser Asn Glu Arg Asn Trp Arg Ile Glu
100 105 110
Asp Val Asp Ala Gln Asp Ser Leu Tyr Gly Arg Leu Asn Gln Lys Glu
115 120 125
Val Pro Ser Gly Ser
130

(2) INFORMATION FOR SEQ ID NO:796:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1336 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1336
(D) OTHER INFORMATION: / Ceres Seq. ID 1567997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

caacatattg	ccaagacc	ctttgattgc	ttggaaaatt	atattttgc	atggagcatt	60
tgaagctatt	cttcagctgc	tctgcctg	taaaagagtt	gaggggtccaa	tatctccagc	120
cggaaccga	ccagtttaca	aggccaatgg	tctggctgct	tactttgtga	cactagcaac	180
ctatcttgg	ctttgttgg	ttggaatctt	caaccctgca	attgtctatg	atcacttggg	240
tgaataattt	tccgcaactaa	tattcgggaag	cttcataattt	tgtgttttgt	tgtacataaa	300
agggcattgt	gcaccttcac	caagtgaact	tgggttcattg	ggtaacctaa	taattgactt	360
ctattggggc	atggagttgt	accctcgaa	tggtaagagc	tttgacatca	aggtgtttac	420
taattgcaga	tccggaatga	tgtcttgggc	agttcttgca	gtcacgtact	gcataaaaaca	480
gtatgaaata	aattggcaaa	tatctgattc	aatgctgggt	aacaccatcc	tgatgtgtgt	540
gtatgtcaca	aaattctctt	gggtgggaagc	tgggttatgg	aacaccatgg	acattgcaca	600
tgaccgagct	ggattctata	tatgctgggg	ttgtctagtg	tgggtgcctt	ctgtctacac	660
tcttcacagg	atgtaccttg	tgaaccaccc	cgtcgaaactc	ggaactcagt	tggcaataata	720
cattctcgtt	gcaggaaatc	tgtgcattta	cataaactat	gactgtgata	gacaaaaggca	780
agagttcagg	aggacaaaac	ggaaatgttt	ggtttgggga	agagcccccgt	caagattgtt	840
ggcgctgat	actacaacat	ctgggtgaaac	taaaactagt	cttctcttaa	cgtctgtgatg	900
tgctgggattg	gctgcctcatt	tccattatgt	tccgtgagac	tttaagtgtct	tcttctggac	960
Cgtaccggct	ctcttcgata	actctctggc	atactcttac	gtcatatttc	tcacctctct	1020
tctctttgat	cgagccaaga	gagacgatga	ccgatgccga	tcaaagtatg	ggaaaatttg	1080
gaagctgat	tgtgagaag	tcaaatcacg	gatcattccg	ggaattttat	gattgtaacg	1140
aagtctgttg	tctcattttt	ctactattta	cgtaaatgg	aacgttggaa	tcatacaaaag	1200
accgtgcaca	aacaaaaattt	caaattgatg	cgatagacat	tcttttgcgt	atttgtatgc	1260
tataggtttt	caaatctcta	gCtacgotta	tgtatttccc	tagattatca	aagttagcct	1320
gccgttttct	aatttt					

(2) INFORMATION FOR SEQ ID NO:797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..376
(D) OTHER INFORMATION: / Ceres Seq. ID 1567998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

Asn	Ile	Trp	Pro	Arg	Pro	Thr	Leu	Ile	Ala	Trp	Lys	Ile	Ile	Phe	Cys
1				5					10					15	
Tyr	Gly	Ala	Phe	Glu	Ala	Ile	Leu	Gln	Leu	Leu	Pro	Gly	Lys	Arg	
				20				25				30			
Val	Glu	Gly	Pro	Ile	Ser	Pro	Ala	Gly	Asn	Arg	Pro	Val	Trp	Lys	Ala
				35			40				45				
Asn	Gly	Leu	Ala	Ala	Tyr	Phe	Val	Thr	Leu	Ala	Thr	Trp	Leu	Gly	Leu
				50			55				60				
Trp	Trp	Phe	Gly	Ile	Phe	Asn	Pro	Ala	Ile	Val	Tyr	Asp	His	Leu	Gly
				65			70			75				80	
Glu	Ile	Phe	Ser	Ala	Leu	Ile	Phe	Gly	Ser	Phe	Ile	Phe	Cys	Val	Leu
				85				90						95	
Leu	Tyr	Ile	Lys	Gly	His	Val	Ala	Pro	Ser	Ser	Ser	Asp	Ser	Gly	Ser
				100				105						110	
Cys	Gly	Asn	Leu	Ile	Ile	Asp	Phe	Tyr	Trp	Gly	Met	Glu	Leu	Tyr	Pro
				115			120					125			
Arg	Ile	Gly	Lys	Ser	Phe	Asp	Ile	Lys	Val	Phe	Thr	Asn	Cys	Arg	Phe
				130			135					140			

Gly Met Met Ser Trp Ala Val Leu Ala Val Thr Tyr Cys Ile Lys Gln
145 150 155 160
Tyr Glu Ile Asn Gly Lys Val Ser Asp Ser Met Leu Val Asn Thr Ile
165 170 175
Leu Met Leu Val Tyr Val Thr Lys Phe Trp Trp Glu Ala Gly Tyr
180 185 190
Trp Asn Thr Met Asp Ile Ala His Asp Arg Ala Gly Phe Tyr Ile Cys
195 200 205
Trp Gly Cys Leu Val Trp Val Pro Ser Val Tyr Thr Ser Pro Gly Met
210 215 220
Tyr Leu Val Asn His Pro Val Glu Leu Gly Thr Gln Leu Ala Ile Tyr
225 230 235 240
Ile Leu Val Ala Gly Ile Leu Cys Ile Tyr Ile Asn Tyr Asp Cys Asp
245 250 255
Arg Gln Arg Gln Glu Phe Arg Arg Thr Asn Gly Lys Cys Leu Val Trp
260 265 270
Gly Arg Ala Pro Ser Lys Ile Val Ala Ser Tyr Thr Thr Thr Ser Gly
275 280 285
Glu Thr Lys Thr Ser Leu Leu Leu Thr Ser Gly Trp Trp Gly Leu Ala
290 295 300
Arg His Phe His Tyr Val Pro Glu Ile Leu Ser Ala Phe Phe Trp Thr
305 310 315 320
Val Pro Ala Leu Phe Asp Asn Phe Leu Ala Tyr Phe Tyr Val Ile Phe
325 330 335
Leu Thr Leu Leu Leu Phe Asp Arg Ala Lys Arg Asp Asp Arg Cys
340 345 350
Arg Ser Lys Tyr Gly Lys Tyr Trp Lys Leu Tyr Cys Glu Lys Val Lys
355 360 365
Tyr Arg Ile Ile Pro Gly Ile Tyr
370 375

(2) INFORMATION FOR SEQ ID NO:798:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..253
(D) OTHER INFORMATION: / Ceres Seq. ID 1567999
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:
Met Glu Leu Tyr Pro Arg Ile Gly Lys Ser Phe Asp Ile Lys Val Phe
1 5 10 15
Thr Asn Cys Arg Phe Gly Met Met Ser Trp Ala Val Leu Ala Val Thr
20 25 30
Tyr Cys Ile Lys Gln Tyr Glu Ile Asn Gly Lys Val Ser Asp Ser Met
35 40 45
Leu Val Asn Thr Ile Leu Met Leu Val Tyr Val Thr Lys Phe Phe Trp
50 55 60
Trp Glu Ala Gly Tyr Trp Asn Thr Met Asp Ile Ala His Asp Arg Ala
65 70 75 80
Gly Phe Tyr Ile Cys Trp Gly Cys Leu Val Trp Val Pro Ser Val Tyr
85 90 95
Thr Ser Pro Gly Met Tyr Leu Val Asn His Pro Val Glu Leu Gly Thr
100 105 110
Gln Leu Ala Ile Tyr Ile Leu Val Ala Gly Ile Leu Cys Ile Tyr Ile
115 120 125
Asn Tyr Asp Cys Asp Arg Gln Arg Gln Glu Phe Arg Arg Thr Asn Gly
130 135 140
Lys Cys Leu Val Trp Gly Arg Ala Pro Ser Lys Ile Val Ala Ser Tyr

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(2) INFORMATION FOR SEQ ID NO:799:
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 231 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: peptide
  (ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..231
      (D) OTHER INFORMATION: / Ceres Seq. ID 1568000
```

(2) INFORMATION FOR SEQ ID NO:800:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 564 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..564

SEQUENCE DESCRIPTION: SEQ ID NO:800:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

attcaaatctg	tagcgtctga	tgtcggccct	aggatctgtc	tgggtaaaga	tctggcgat	60
ctacaattga	aatcaattgc	atcggcggtc	ttgtccgcgc	accgggtgac	ggtgtgtagc	120
gggcatacgg	tgggaacaga	gatgtcgtta	aacttattca	tgaagatcgc	tcttttttag	180
aacgtccaag	aacgggattt	aacggcgaac	ggcggcgatc	tacagagatt	taaaatcaac	240
ctgtccaatg	acgggggttt	taacggcgct	tcgaattagg	tagggtgagc	gaatcaaatc	300
catctatcat	ttaactgtct	ttagagagtt	gcactcgctt	tttgggcgct	gtttaaatac	360
gcggtctctt	ggccaactca	caaaagtcgc	cccaagtgtc	gtcgggttgt	tgggtcgaat	420
attcaataga	tgctattttg	cgaagtcgag	ttgttctgtt	ctcttttttt	tactcaatgt	480
ccttggtaat	tcagacagta	aaatttgatt	tcattatttt	gtaagcatct	ctcaaatgtg	540
tttaagtaat	cttatcttaa	aagc				

(2) INFORMATION FOR SEO ID NO:801:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1568008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

1	Ile	Lys	Phe	Val	Ala	Phe	Asn	Ala	Gly	Pro	Arg	Ile	Cys	Leu	Gly	Lys
15				5						10					15	
Asp	Leu	Ala	Thr	Leu	Gln	Met	Lys	Ser	Ile	Ala	Ser	Ala	Val	Leu	Leu	
20				20				25						30		
Arg	His	Arg	Leu	Thr	Val	Val	Thr	Gly	His	Lys	Val	Glu	Gln	Lys	Met	
35							40						45			
Ser	Leu	Thr	Leu	Phe	Met	Lys	Tyr	Gly	Leu	Leu	Val	Asn	Val	His	Glu	
50						55					60					
Arg	Asp	Leu	Thr	Ala	Ile	Ala	Ala	Asp	Leu	Arg	Glu	Cys	Lys	Ser	Asn	
65				70						75					80	
Val	Val	Asn	Asp	Gly	Val	Gly	Asn	Gly	Val	Ser	Ser					
85									90							

(2) INFORMATION FOR SEQ ID NO:802:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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{A} NAME/KEY: peptide

(B) LOCATION: 1.70

(D) OTHER INFORMATION: / Ceres Seq. ID 1568009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

[illegible]

65

70

(2) INFORMATION FOR SEQ ID NO:803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1364

(D) OTHER INFORMATION: / Ceres Seq. ID 1568029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

ctataaatagg	aacaccatgg	aaaggaaaaag	agacacacac	aaataaagaa	aacgaaaaaca	60
ctttttact	tatatgtcag	ccatggctcc	gactttgcaa	ggccagtgga	tcaaggtggg	120
gcagaaagga	ggaacgggac	caggacctag	aagttcacac	ggcatagccg	cggtcggaga	180
caagctctac	agtttcggcg	gcgagttaac	accaaacaaa	cacatcgaca	aagacctota	240
cgtctttgac	ttcaacactc	aaacttggtc	aatcgctcaa	cccaaggagg	acgccccaac	300
tgatctctgc	taggcgtg	gcattggtgc	cggtggaaat	aagatctata	tctttggagg	360
ccgcgatgag	aaccgcaact	tcgaaaactt	tcgctcctac	gatacgggtg	catccgagtg	420
gaacatctctg	acgaagcttg	atgaggtggg	aggaccggag	gctcgtaact	tccattcgat	480
ggcttcggat	gaaaaccatg	tgatatgatt	cggtgggggt	agcaaaaggcg	gtactatgaa	540
tactcccacg	cggttcagga	caatcgaggc	gtataacatt	gctggggaaa	tgggctcagc	600
taccggatcc	aggagataac	ttcgagaaaa	gaggaggagc	gggattcgct	gtggtacaag	660
ggaagatttt	gggtgtttat	gggtttgcga	ccctcgattg	gcccggaggc	aaagatgact	720
atgagttctaa	tgtctgtcaa	ttctatgac	cggtctccaa	aaagtggacc	gaagttagaga	780
ctacaggagc	gaacaccttc	gcaaggagcg	tgtttgcaca	tcggttagtg	ggaaagtata	840
taataaattg	tgcaagtgag	gtatggcctg	atctcaatgg	gcattatggt	ccgaggacgc	900
tgctcaatga	gggatatgcc	ttggacaccg	agacactggt	gtgggaaaaa	ttgggagaaa	960
aaggtgcacc	agccatacac	cgaggtttga	ctgcctatac	tgctgccact	gtcgatggaa	1020
agaaatggcct	cctcatgcat	ggcggaagag	ttccgaccaa	cgagcggaact	gatgatctct	1080
acttctatgc	ggatcaattc	gcttaatgag	tgctcaagatt	gtgtgtgtgt	gtgtgtgtgt	1140
ttaatattta	ttactatcca	ataaggagcc	ctaattggtt	gctgtattat	tcaaaattat	1200
ctgtgtgtgg	gactcgtcga	gcttttttac	tctaattgag	cctactcatg	gtgtgtgtgag	1260
tggttctcca	agtatcattg	tccaataagg	agccaattta	tttatggctg	gctgttttat	1320
tcaaaattat	gtgtatgtgt	taataattaa	agattgaatt	atct		

(2) INFORMATION FOR SEQ ID NO:804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1568030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

Met	Ala	Pro	Thr	Leu	Gln	Gly	Gln	Trp	Ile	Lys	Val	Gly	Gln	Lys	Gly
1				5				10						15	
Gly	Thr	Gly	Pro	Gly	Pro	Arg	Ser	Ser	His	Gly	Ile	Ala	Ala	Val	Gly
				20				25						30	
Asp	Lys	Leu	Tyr	Ser	Phe	Gly	Gly	Glu	Leu	Thr	Pro	Asn	Lys	His	Ile
				35				40						45	
Asp	Lys	Asp	Leu	Tyr	Val	Phe	Asp	Phe	Asn	Thr	Gln	Thr	Trp	Ser	Ile
				50				55						60	
Ala	Gln	Pro	Lys	Gly	Asp	Ala	Pro	Thr	Val	Ser	Cys	Leu	Gly	Val	Arg
				70				75						80	
Met	Val	Ala	Val	Gly	Thr	Lys	Ile	Tyr	Ile	Phe	Gly	Gly	Arg	Asp	Glu
				85				90						95	
Asn	Arg	Asn	Phe	Glu	Asn	Phe	Arg	Ser	Tyr	Asp	Thr	Val	Thr	Ser	Glu

Met	Gly	Ile	Met	Val	Pro	Gly	Arg	Cys	Pro	Met	Arg	Asp	Met	Arg	Trp
1				5					10					15	
Thr	Pro	Arg	His	Trp	Cys	Gly	Lys	Ser	Trp	Glu	Lys	Lys	Val	His	Gln
			20					25					30		
Pro	Tyr	His	Glu	Val	Gly	Leu	Pro	Ile	Leu	Leu	Pro	Leu	Ser	Met	Glu
			35				40					45			
Arg	Met	Ala	Ser	Ser	Cys	Met	Ala	Glu	Ser	Phe	Arg	Pro	Thr	Ser	Glu
	50					55				60					
Leu	Met	Ile	Ser	Thr	Ser	Met	Arg	Ser	Ile	Gln	Leu	Asn	Ala	Cys	Gln
					70					75					80
Asp	Leu	Cys	Cys	Val	Cys	Gly	Ser	Leu	Ile	Phe	Ile	Thr	Ile	Gln	
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1127

(D) OTHER INFORMATION: / Ceres Seq. ID 1568037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

```
aatcgaaaaa acctcggtc gatctcacat ttataatctc tcaactctctc tctttctctg      60
gtaaatcatc aagtgtgaaga atgggtggctg tgaggcgaaag gagaacacaa gcgtcaaaccc      120
ctagatccga accaccgcgaa cacatgtcgg atcatgattc cgattccgat tgggatacacg      180
ctcgcgaaaga atgcagttcc ggtaaacacac cagcaaaagct gcttctttgc gacaaatgcg      240
ataaaagggtt Ctcactctttt ctgtctcaga ccgatcctcg ttccagttcc caaagggtctc      300
tggttctgcc cttctgtgtc caaacatcag atccctaaat ctttccctct tattcagact      360
aaaattatag atttcttcgc gattaagcgg ttccagattt catctcaaat ctcaagttct      420
tcagatagta ttgggaagaa acggaaaaaag actagcttgg tgatgtcaaa gaagaagaga      480
aggctttctc catacaatcc tagcaatgat cctcaaagga ggctagagca aatggcgctc      540
ctggccactg cgttgagagc ttccaacacc aagttcagca atgagcttac ttatgtatct      600
ggaaaggctc caagatctgc aaaccaagct gcttttgaga aaggaggcat gcaggttcta      660
tctaaagaag gcgtagagac cttagccttg tgcaagaaaa tgatggacct cggtgaatgc      720
ccgcacacta tggctgctct cgatccttat gaagggttca cagtagaggc ggacagggtt      780
ataaaagact ggacaattat cacagagtat gttggagatg ttgattatct gagcaataga      840
gaagatgact atgatggaga cagtatgatg actctacttc atgcctctga tctctcgaga      900
tgtctcgtaa tttgcctgca cagacgcagt aacatcgccc ggttcatcag tggcatcaac      960
aatcactcac cagaaggagc gaagaagcag aacctgaagt gtgtgaggtt caacatcaac      1020
ggagaagcta gggttcttct cgtagctaatt agagacatat cgaaagggga aagattgtag      1080
tatgattaca acggatatga acatgagtat ccaactgaac attttgt
```

(2) INFORMATION FOR SEQ ID NO:808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..324

(D) OTHER INFORMATION: / Ceres Seq. ID 1568038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

```
Met Ile Pro Ile Pro Ile Gly Ile Gln Ser Ala Lys Asn Ala Val Pro
1      5      10      15
Val Asn Asn Gln Gln Ser Cys Phe Phe Ala Thr Asn Ala Ile Lys Xaa
20      25      30
Ser His Leu Phe Cys Leu Arg Pro Ile Leu Val Ser Val Pro Lys Gly
35      40      45
Ser Trp Phe Cys Pro Ser Cys Ser Lys His Gln Ile Pro Lys Ser Phe
50      55      60
Pro Leu Ile Gln Thr Lys Ile Ile Asp Phe Phe Arg Ile Lys Arg Ser
65      70      75      80
Pro Asp Ser Ser Gln Ile Ser Ser Ser Ser Asp Ser Ile Gly Lys Lys
85      90      95
Arg Lys Lys Thr Ser Leu Val Met Ser Lys Lys Lys Arg Arg Leu Leu
100      105      110
Pro Tyr Asn Pro Ser Asn Asp Pro Gln Arg Arg Leu Glu Gln Met Ala
115      120      125
Ser Leu Ala Thr Ala Leu Arg Ala Ser Asn Thr Lys Phe Ser Asn Glu
130      135      140
```

```

Leu Thr Tyr Val Ser Gly Lys Ala Pro Arg Ser Ala Asn Gln Ala Ala
145                      150                      155                      160
Phe Glu Lys Gly Gly Met Gln Val Leu Ser Lys Glu Gly Val Glu Thr
                      165                      170                      175
Leu Ala Leu Cys Lys Lys Met Met Asp Leu Gly Glu Cys Pro Pro Leu
                      180                      185                      190
Met Val Val Phe Asp Pro Tyr Glu Gly Phe Thr Val Glu Ala Asp Arg
                      195                      200                      205
Phe Ile Lys Asp Trp Thr Ile Ile Thr Glu Tyr Val Gly Asp Val Asp
210                      215                      220
Tyr Leu Ser Asn Arg Glu Asp Asp Tyr Asp Gly Asp Ser Met Met Thr
225                      230                      235                      240
Leu Leu His Ala Ser Asp Pro Ser Arg Cys Leu Val Ile Cys Pro Asp
                      245                      250                      255
Arg Arg Ser Asn Ile Ala Arg Phe Ile Ser Gly Ile Asn Asn His Ser
260                      265                      270
Pro Glu Gly Arg Lys Lys Gln Asn Leu Lys Cys Val Arg Phe Asn Ile
275                      280                      285
Asn Gly Glu Ala Arg Val Leu Leu Val Ala Asn Arg Asp Ile Ser Lys
290                      295                      300
Gly Glu Arg Leu Tyr Tyr Asp Tyr Asn Gly Tyr Glu His Glu Tyr Pro
305                      310                      315                      320
Thr Glu His Phe

```

(2) INFORMATION FOR SEQ ID NO:809:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..221

(D) OTHER INFORMATION: / Ceres Seq. ID 1568039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

```

Met Ser Lys Lys Lys Arg Arg Leu Leu Pro Tyr Asn Pro Ser Asn Asp
1                      5                      10                      15
Pro Gln Arg Arg Leu Glu Gln Met Ala Ser Leu Ala Thr Ala Leu Arg
20                      25                      30
Ala Ser Asn Thr Lys Phe Ser Asn Glu Leu Thr Tyr Val Ser Gly Lys
35                      40                      45
Ala Pro Arg Ser Ala Asn Gln Ala Ala Phe Glu Lys Gly Gly Met Gln
50                      55                      60
Val Leu Ser Lys Glu Gly Val Glu Thr Leu Ala Leu Cys Lys Lys Met
65                      70                      75                      80
Met Asp Leu Gly Glu Cys Pro Pro Leu Met Val Val Phe Asp Pro Tyr
85                      90                      95
Glu Gly Phe Thr Val Glu Ala Asp Arg Phe Ile Lys Asp Trp Thr Ile
100                      105                      110
Ile Thr Glu Tyr Val Gly Asp Val Asp Tyr Leu Ser Asn Arg Glu Asp
115                      120                      125
Asp Tyr Asp Gly Asp Ser Met Met Thr Leu Leu His Ala Ser Asp Pro
130                      135                      140
Ser Arg Cys Leu Val Ile Cys Pro Asp Arg Arg Ser Asn Ile Ala Arg
145                      150                      155                      160
Phe Ile Ser Gly Ile Asn Asn His Ser Pro Glu Gly Arg Lys Lys Gln
165                      170                      175
Asn Leu Lys Cys Val Arg Phe Asn Ile Asn Gly Glu Ala Arg Val Leu
180                      185                      190
Leu Val Ala Asn Arg Asp Ile Ser Lys Gly Glu Arg Leu Tyr Tyr Asp

```


195 200 205
Tyr Asn Gly Tyr Glu His Glu Tyr Pro Thr Glu His Phe
210 215 220
(2) INFORMATION FOR SEQ ID NO:810:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..198
(D) OTHER INFORMATION: / Ceres Seq. ID 1568040
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:
Met Ala Ser Leu Ala Thr Ala Leu Arg Ala Ser Asn Thr Lys Phe Ser
1 5 10 15
Asn Glu Leu Thr Tyr Val Ser Gly Lys Ala Pro Arg Ser Ala Asn Gln
20 25 30
Ala Ala Phe Glu Lys Gly Gly Met Gln Val Leu Ser Lys Glu Gly Val
35 40 45
Glu Thr Leu Ala Leu Cys Lys Lys Met Met Asp Leu Gly Glu Cys Pro
50 55 60
Pro Leu Met Val Val Phe Asp Pro Tyr Glu Gly Phe Thr Val Glu Ala
65 70 75 80
Asp Arg Phe Ile Lys Asp Trp Thr Ile Ile Thr Glu Tyr Val Gly Asp
85 90 95
Val Asp Tyr Leu Ser Asn Arg Glu Asp Asp Tyr Asp Gly Asp Ser Met
100 105 110
Met Thr Leu Leu His Ala Ser Asp Pro Ser Arg Cys Leu Val Ile Cys
115 120 125
Pro Asp Arg Arg Ser Asn Ile Ala Arg Phe Ile Ser Gly Ile Asn Asn
130 135 140
His Ser Pro Glu Gly Arg Lys Lys Gln Asn Leu Lys Cys Val Arg Phe
145 150 155 160
Asn Ile Asn Gly Glu Ala Arg Val Leu Leu Val Ala Asn Arg Asp Ile
165 170 175
Ser Lys Gly Glu Arg Leu Tyr Tyr Asp Tyr Asn Gly Tyr Glu His Glu
180 185 190
Tyr Pro Thr Glu His Phe

195
(2) INFORMATION FOR SEQ ID NO:811:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1714 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1714
(D) OTHER INFORMATION: / Ceres Seq. ID 1568045
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:
acactgttta tctgattcgt cttctctgat aatcaagagt agtagtgccg ttctctggaa 60
aatattcgat ttttaaaaga cttctgatgat gacattaaac tcactatctc cagctgaatc 120
caaagctatt tctttcttgg atacctccag gtccaatcca atccctaaac tctcaggctg 180
gtttagtgtt aggaggaggga atcaaggagg aggttttggg aaaggtgtta agtgttcagt 240
gaaagtgcag cagcaacaac aacctctctc agcatggcct gggagagctg tccctgaggc 300
gcctcgtcaa tcttgggatg gaccaaaacc catctctatc gttggatcta ctggttctat 360
tggaactcag acattggata ttgtggctga gaatcctgac aaattcagag ttgtgctct 420
agctgctggt tcgaatgtta ctctacttgc tgatcaggta aggagattta agcctgcatt 480

ggtgtgctgtt	agaaacgagt	cactgattaa	tgagcttaaa	gaggctttat	ctgattttgga	540
ctataaaact	gagattattc	caggagagca	aggagtgtat	gaggttgccc	gacatcctga	600
agctgtaacc	gttgttaacc	gaatagtagg	ttgtgcggga	ctaaagccta	cggttgtgcg	660
aattgaagca	ggaaaggaca	ttgctcttgc	aaacaaagag	acattaatcg	caggtgtgtcc	720
ttctgtcgtt	ccgcttgcca	acaaacataa	tgtaaagatt	cttcgggcag	attcagaaca	780
ttctgccata	tttcagtgta	ttcaagggtt	gctctgaagg	gctctgocga	agataatctt	840
gactgcacat	gggtggagctt	ttagggtatt	gctctgcgaa	aagctaaagg	aagtttaagt	900
agcggatgcy	ttgaagcatt	caaaactggaa	catgggaaaag	aaaatcactg	tggactctgc	960
tacgcttttc	aacaagggtc	ttgaggtcat	tgaagcgcat	tattgttttg	gagctgagta	1020
tgacgatata	gattgtcatt	catccgcgaa	gtatcatata	ttccatgatt	gaacacacag	1080
attcatctgt	gcttgcctcaa	ttgggttgcc	ctgatatgcy	tttccagatt	ctctacacaa	1140
tgctatggcc	cgatagagtt	cctgtgtctg	aagtaacttg	gccaaagctt	gaccttttga	1200
aactcggttc	attgactttc	aagaaaccag	acaatgtgaa	atacccatcc	atggatctgt	1260
cttatctgtc	tggacgagct	ggaggcacaa	tgactggagt	tctcagcgcc	gccaatgaga	1320
aagctgttga	aatgttcaat	gatgaaaaga	taagctattt	ggatactctc	aaggttgttg	1380
aattaaacat	cgataaacat	cgaaaacgag	ttgttaacat	acgcctctct	gaagagatgt	1440
ttcactatga	cttctgggca	cgtgaatatg	ccgcgaatgt	cgagctttct	tctggtgcta	1500
ggccagttca	tgcataga	attggttgtt	ggaagaacat	aaggaaagctt	ctgagggaaat	1560
gttgaagaaa	gattagtgtg	gagaatgggg	tactacttaa	tagcgttttt	ggcaaggatt	1620
atggattgtg	tagctaattt	atctgtgato	cgaaacagcc	aaactgataa	tttgaaccac	1680
ttttaccaaa	taaaacgag	cttaattGtt	tcac			

(2) INFORMATION FOR SEQ ID NO:812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..328

(D) OTHER INFORMATION: / Ceres Seq. ID 1568046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

Met	Met	Thr	Leu	Asn	Ser	Leu	Ser	Pro	Ala	Glu	Ser	Lys	Ala	Ile	Ser
1				5				10						15	
Phe	Leu	Asp	Thr	Ser	Arg	Phe	Asn	Pro	Ile	Pro	Lys	Leu	Ser	Gly	Gly
			20					25						30	
Phe	Ser	Leu	Arg	Arg	Arg	Asn	Gln	Gly	Arg	Gly	Phe	Gly	Lys	Gly	Val
			35				40					45			
Lys	Cys	Ser	Val	Lys	Val	Gln	Gln	Gln	Gln	Pro	Pro	Pro	Ala	Trp	
	50					55				60					
Pro	Gly	Arg	Ala	Val	Pro	Glu	Ala	Pro	Arg	Gln	Ser	Trp	Asp	Gly	Pro
65				70				75						80	
Lys	Pro	Ile	Ser	Ile	Val	Gly	Ser	Thr	Gly	Ser	Ile	Gly	Thr	Gln	Thr
			85					90						95	
Leu	Asp	Ile	Val	Ala	Glu	Asn	Pro	Asp	Lys	Phe	Arg	Val	Val	Ala	Leu
			100					105						110	
Ala	Ala	Gly	Ser	Asn	Val	Thr	Leu	Leu	Ala	Asp	Gln	Val	Arg	Arg	Phe
			115				120					125			
Lys	Pro	Ala	Leu	Val	Ala	Val	Arg	Asn	Glu	Ser	Leu	Ile	Asn	Glu	Leu
			130				135				140				
Lys	Glu	Ala	Leu	Ala	Asp	Leu	Asp	Tyr	Lys	Leu	Glu	Ile	Ile	Pro	Gly
145				150				155						160	
Glu	Gln	Gly	Val	Ile	Glu	Val	Ala	Arg	His	Pro	Glu	Ala	Val	Thr	Val
			165					170						175	
Val	Thr	Gly	Ile	Val	Gly	Cys	Ala	Gly	Leu	Lys	Pro	Thr	Val	Ala	Ala
			180					185						190	
Ile	Glu	Ala	Gly	Lys	Asp	Ile	Ala	Leu	Ala	Asn	Lys	Glu	Thr	Leu	Ile
			195				200					205			
Ala	Gly	Gly	Pro	Phe	Val	Leu	Pro	Leu	Ala	Asn	Lys	His	Asn	Val	Lys
	210						215					220			

```

Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln
225                      230                      235                      240
Gly Leu Pro Glu Gly Ala Leu Arg Lys Ile Ile Leu Thr Ala Ser Gly
                      245                      250                      255
Gly Ala Phe Arg Asp Trp Pro Val Glu Lys Leu Lys Glu Val Lys Val
                      260                      265                      270
Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr
                      275                      280                      285
Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala
290                      295                      300
His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Asp Cys His Ser Ser
305                      310                      315                      320
Ala Lys Tyr His Thr Phe His Asp
                      325

```

(2) INFORMATION FOR SEQ ID NO:813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..327

(D) OTHER INFORMATION: / Ceres Seq. ID 1568047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

```

Met Thr Leu Asn Ser Leu Ser Pro Ala Glu Ser Lys Ala Ile Ser Phe
1                      5                      10                      15
Leu Asp Thr Ser Arg Phe Asn Pro Ile Pro Lys Leu Ser Gly Gly Phe
                      20                      25                      30
Ser Leu Arg Arg Arg Asn Gln Gly Arg Gly Phe Gly Lys Gly Val Lys
35                      40                      45
Cys Ser Val Lys Val Gln Gln Gln Gln Pro Pro Pro Ala Trp Pro
50                      55                      60
Gly Arg Ala Val Pro Glu Ala Pro Arg Gln Ser Trp Asp Gly Pro Lys
65                      70                      75                      80
Pro Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu
                      85                      90                      95
Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu Ala
100                      105                      110
Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Arg Arg Phe Lys
115                      120                      125
Pro Ala Leu Val Ala Val Arg Asn Glu Ser Leu Ile Asn Glu Leu Lys
130                      135                      140
Glu Ala Leu Ala Asp Leu Asp Tyr Lys Leu Glu Ile Ile Pro Gly Glu
145                      150                      155                      160
Gln Gly Val Ile Glu Val Ala Arg His Pro Glu Ala Val Thr Val Val
165                      170                      175
Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala Ile
180                      185                      190
Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala
195                      200                      205
Gly Gly Pro Phe Val Leu Pro Leu Ala Asn Lys His Asn Val Lys Ile
210                      215                      220
Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln Gly
225                      230                      235                      240
Leu Pro Glu Gly Ala Leu Arg Lys Ile Ile Leu Thr Ala Ser Gly Gly
245                      250                      255
Ala Phe Arg Asp Trp Pro Val Glu Lys Leu Lys Glu Val Lys Val Ala
260                      265                      270
Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr Val

```

	275		280		285	
Asp	Ser	Ala	Thr	Leu	Phe	Asn
290					295	
Tyr	Leu	Phe	Gly	Ala	Glu	Tyr
305					310	
Lys	Tyr	His	Thr	Phe	His	Asp
					325	

(2) INFORMATION FOR SEQ ID NO:814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1428
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

ccccaccct	caaagatctc	tcaaaagaatg	gcttcgcg	ctgttcgcatc	gatggttctt	60
gaccctaaag	catcacgcgc	cttgatggat	ctatccaccg	cagacgaaga	agatctctat	120
ggccgcctca	aatcgcttga	acgacaacta	gagttaccg	atatccaaga	agaatattgt	180
aaagacgagc	aaaagaattc	caaacgagag	ctgttacgag	cacaagaaga	ggtcaaacga	240
attcaatccg	tgccctttgt	gataggtcag	ttcatggaga	tgatagatca	gaacaacggc	300
atcgctggat	ctactactgg	ctccaattac	taagtccaga	ttctcagcac	aatcaataga	360
gaactcttaa	agcctttctg	ttccgtcgct	cttcaccgtc	actccaacgc	ctttgttgat	420
gttttgcctc	cgaggagctga	ttctagcatc	tcctttctca	gccaatctga	gaagcctgac	480
gtctcctaca	atgatattgg	aggatgcgat	attcagaaaac	aggaaattcg	tgaggctgtt	540
gaattgcctc	ttaccacaca	cgagctttac	aaacagattg	gtattgaccc	acctcgtgga	600
gtcttgctct	atggacctcc	tggtacttga	aagactatgt	tggtcaaggc	tgttgccaat	660
cacacaaact	ctgccttcat	tagggttgtt	ggatccgagt	tttgcaaaaa	gtatctcggc	720
gagggacctc	gtatggttgc	tgatgtcttc	cgctttgcca	aggaaaaatg	tccagctatc	780
atcttcattg	atgaggtaga	tgccatcgct	actgttaggt	ttgatgtcca	aacaggagcc	840
gatagggaag	ttcagcgat	tctcatggag	cttottaatc	agatggatgg	atttgaccag	900
accgtgaatg	tcaaggctcat	aatggcaaca	aacaggggac	acactctaga	tcctgctctc	960
ttacgtctcg	gaagacttga	tcgtaagatt	gagttccccc	ttcctgatag	acgtcaaaaa	1020
aggcttggtt	tccagggtat	caactccaaa	atgaacctta	gcgatgaggt	tgacttggaa	1080
gactatgttt	cacggcctga	taaaattagc	gctgctgaga	tagcagcaat	ttgccaggaa	1140
gctgtgatgc	atgcggtgcg	aaagaacaga	tatgtgatac	taacctaaag	tttcgagaag	1200
ggctaccgcg	caaatgttaa	gaagccagac	acggactttg	agttttacaa	gtgaagagaa	1260
agcagaagtg	gaaccagatt	atggctgttg	ttaaaattcc	agtggtgttt	gagaattatt	1320
aaggacatgg	aatcaaat	gcagtttaaa	taagaactaa	gttgcatNct	cctaatttct	1380
gtaactcgag	ttcacatttg	tttttagtct	atcacgtttt	tacagttc		

(2) INFORMATION FOR SEQ ID NO:815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..205
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

Met	Leu	Ala	Lys	Ala	Val	Ala	Asn	His	Thr	Thr	Ala	Ala	Phe	Ile	Arg
1			5				10						15		
Val	Val	Gly	Ser	Glu	Phe	Val	Gln	Lys	Tyr	Leu	Gly	Glu	Gly	Pro	Arg
			20				25						30		
Met	Val	Arg	Asp	Val	Phe	Arg	Leu	Ala	Lys	Glu	Asn	Ala	Pro	Ala	Ile
			35				40						45		

```

Ile Phe Ile Asp Glu Val Asp Ala Ile Ala Thr Ala Arg Phe Asp Ala
 50                               55                               60
Gln Thr Gly Ala Asp Arg Glu Val Gln Arg Ile Leu Met Glu Leu Leu
 65                               70                               75                               80
Asn Gln Met Asp Gly Phe Asp Gln Thr Val Asn Val Lys Val Ile Met
                               85                               90                               95
Ala Thr Asn Arg Ala Asp Thr Leu Asp Pro Ala Leu Leu Arg Pro Gly
                               100                              105                              110
Arg Leu Asp Arg Lys Ile Glu Phe Pro Leu Pro Asp Arg Arg Gln Lys
                               115                              120                              125
Arg Leu Val Phe Gln Val Cys Thr Ser Lys Met Asn Leu Ser Asp Glu
                               130                              135                              140
Val Asp Leu Glu Asp Tyr Val Ser Arg Pro Asp Lys Ile Ser Ala Ala
 145                               150                               155                               160
Glu Ile Ala Ala Ile Cys Gln Glu Ala Gly Met His Ala Val Arg Lys
                               165                              170                              175
Asn Arg Tyr Val Ile Leu Pro Lys Asp Phe Glu Lys Gly Tyr Arg Ala
                               180                              185                              190
Asn Val Lys Lys Pro Asp Thr Asp Phe Glu Phe Tyr Lys
                               195                              200                              205

```

(2) INFORMATION FOR SEQ ID NO:816:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1568060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

```

Met Val Arg Asp Val Phe Arg Leu Ala Lys Glu Asn Ala Pro Ala Ile
 1                               5                               10                               15
Ile Phe Ile Asp Glu Val Asp Ala Ile Ala Thr Ala Arg Phe Asp Ala
 20                               25                               30
Gln Thr Gly Ala Asp Arg Glu Val Gln Arg Ile Leu Met Glu Leu Leu
 35                               40                               45
Asn Gln Met Asp Gly Phe Asp Gln Thr Val Asn Val Lys Val Ile Met
 50                               55                               60
Ala Thr Asn Arg Ala Asp Thr Leu Asp Pro Ala Leu Leu Arg Pro Gly
 65                               70                               75                               80
Arg Leu Asp Arg Lys Ile Glu Phe Pro Leu Pro Asp Arg Arg Gln Lys
 85                               90                               95
Arg Leu Val Phe Gln Val Cys Thr Ser Lys Met Asn Leu Ser Asp Glu
 100                              105                              110
Val Asp Leu Glu Asp Tyr Val Ser Arg Pro Asp Lys Ile Ser Ala Ala
 115                              120                              125
Glu Ile Ala Ala Ile Cys Gln Glu Ala Gly Met His Ala Val Arg Lys
 130                              135                              140
Asn Arg Tyr Val Ile Leu Pro Lys Asp Phe Glu Lys Gly Tyr Arg Ala
 145                              150                              155                              160
Asn Val Lys Lys Pro Asp Thr Asp Phe Glu Phe Tyr Lys
 165                              170

```

(2) INFORMATION FOR SEQ ID NO:817:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568061

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

```
Met Glu Leu Leu Asn Gln Met Asp Gly Phe Asp Gln Thr Val Asn Val
1      5      10      15
Lys Val Ile Met Ala Thr Asn Arg Ala Asp Thr Leu Asp Pro Ala Leu
20      25      30
Leu Arg Pro Gly Arg Leu Asp Arg Lys Ile Glu Phe Pro Leu Pro Asp
35      40      45
Arg Arg Gln Lys Arg Leu Val Phe Gln Val Cys Thr Ser Lys Met Asn
50      55      60
Leu Ser Asp Glu Val Asp Leu Glu Asp Tyr Val Ser Arg Pro Asp Lys
65      70      75      80
Ile Ser Ala Ala Glu Ile Ala Ala Ile Cys Gln Glu Ala Gly Met His
85      90      95
Ala Val Arg Lys Asn Arg Tyr Val Ile Leu Pro Lys Asp Phe Glu Lys
100      105      110
Gly Tyr Arg Ala Asn Val Lys Lys Pro Asp Thr Asp Phe Glu Phe Tyr
115      120      125
Lys
```

(2) INFORMATION FOR SEQ ID NO:818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..883
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

```
aaaacaaaag aggaacttga gaattttatg cttgagacaa aatggcagaa gatacgtacg      60
aggaagagtg cgactacttg tttaaaggcg tgttgatcgg agactcagcc gtcggaaaaat      120
caaacctcct gtctagattt tctaaagacg agttccgggt tgactctaaa ccaaccatcg      180
gagtagagtt tgcttacccg aatgttcacg tcggagataa aatcatcaag gctcagattt      240
gggacacccg cggccaagaa agatttcgag caatcacaag ttcgactact cgtggagcat      300
taggggcatt actgattttc gacatcacta gacgaacaac ttctgacaac atcaagaaaat      360
gctcttttga gcttagagac ttgcaccaat ccgaaaacgt cgttgtcttc gtcggaaaaca      420
aatctgactc ccgacaatct agagaagttg aagaagacga gggttaagact ctagcagaat      480
cagaaggtct ctactctctc gagacttcgg ctttagagaa tgttaacgtc gaagaagcgt      540
ttctagtgtg gatcggaagg atacatgagg ttgttactca gaggatagct tcggaaaaaca      600
aatccaacgg tgcctgcgac cctcacatta acggtaatgg gaacggtacg gtccctcccg      660
ttggtaaaga aattgtgaat atacacgaag tcaactgctac tcaacccotta ttaagctcat      720
cttccaactg ttggttttaa taaataatta atgtattttt ttogttttatt gttttggaat      780
actttgatga tgtttttatt tgccctgtgKA tctcgtgaaaa ttttgccctg gttgagtaca      840
tgaattttaa tcatacaat atattccaaat aaatatgaaa atc
```

(2) INFORMATION FOR SEQ ID NO:819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568088

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1246

(D) OTHER INFORMATION: / Ceres Seq. ID 1568089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

aaagagattta	acgtatGttgt	ggtgagagag	tatgatccaa	agagagacatt	aacgagtgtgt	60
gaagagcgtt	aggaagaatcg	tgaagtcgga	tctttattag	tggatctact	gggtgacctc	120
cttgcgccga	tcgcacaatc	tctctcttct	ccatgctgtg	tggcagaagt	cggtaaatga	180
atagtcggga	tgatcagag	gaagatacaa	atggtgacac	tgtgtgttaa	tgcatttact	240
caacgcgcga	acgttttcgc	aaacataaac	tctgcctgtc	ctccgcgctt		300
agagttctct	ttctttcacg	gaggtatgga	atttgactga	aactgtgtga	agaacttgaa	360
gagtggtgtc	tacgaaacga	cgcctgtttac	tctacgtctc	aaactgaaaa	cgacaacata	420
gttctgccta	aaactcttca	cgaagaaagt	ggttactcca	aactcgtcat	accaactttc	480
tttgttcaca	cgtgtcttca	ccacgcagtc	actgtctctc	gagtcgtcaa	aatacatcaa	540
ctctctctct	ccgcagctga	gtcactctac	cgcaaacgat	tctcaaccac	cggagttttc	600
cccttcggca	tcaactcaat	ctctcacoa	aaactctccc	tgcgcataa	ctcggctgtg	660
ccacgtggag	gagacaaagt	ttccgggtgc	ttaccgcacc	agacccgggt	atgggcccgt	720
ataagtaatt	ggaacagtaa	agatgtttac	agactccaag	tcaaaaggag	gtcgcgtctt	780
aaacgcattg	tagctaagtc	aacccgcgtc	tccgacggag	cgttctcggt	tctgaaatac	840
ccgtgtctgt	ccaactcttt	caagtctcgt	gcgatgcatt	ttatgaagc	tatcgtgtgc	900
gagggcgca	gagcggcgga	gcgcttctgt	ctaacgcaca	tacactgaag		960
agaaaagacg	gttgtgcgct	cgtgcctcgt	cgctgtgagc	gctcagagtt		1020
cgattctcac	tttgaagagt	actctccgc	gaggaattgt	ggtgtgtgaa	acgtctccga	1080

tatgacgatg acgcgctaga ctggaccaag tcaccacctg gattgtctat tttcgttgac 1140
cctagagaaa tataataatt tgtatagaat atattaagag gactctaaca attgcaacca 1200
aacacacaaa caaaaattac agaattaaat accaaatctc agtctc

(2) INFORMATION FOR SEQ ID NO:821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..384
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

Lys	Gly	Phe	Asn	Val	Val	Val	Val	Arg	Glu	Tyr	Asp	Pro	Lys	Arg	Asp
1			5						10					15	
Leu	Thr	Ser	Val	Glu	Glu	Leu	Glu	Ser	Cys	Glu	Val	Gly	Ser	Leu	
			20					25					30		
Leu	Val	Asp	Leu	Met	Gly	Asp	Pro	Leu	Ala	Arg	Ile	Arg	Gln	Ser	Pro
			35				40					45			
Ser	Phe	His	Met	Leu	Val	Ala	Glu	Ile	Gly	Asn	Glu	Ile	Val	Gly	Met
			50				55				60				
Ile	Arg	Gly	Thr	Ile	Lys	Met	Val	Thr	Arg	Gly	Val	Asn	Ala	Leu	Arg
			65				70				75			80	
Gln	Ala	Asp	Asp	Val	Ser	Pro	Glu	Ile	Asn	Thr	Thr	Lys	Leu	Ala	Phe
							85			90				95	
Val	Ser	Gly	Leu	Arg	Val	Ser	Pro	Phe	Tyr	Arg	Arg	Met	Gly	Ile	Gly
			100					105					110		
Leu	Lys	Leu	Val	Gln	Arg	Leu	Glu	Glu	Trp	Phe	Leu	Arg	Asn	Asp	Ala
			115				120					125			
Val	Tyr	Ser	Tyr	Val	Gln	Thr	Glu	Asn	Asp	Asn	Ile	Ala	Ser	Val	Lys
			130				135				140				
Leu	Phe	Thr	Glu	Lys	Ser	Gly	Tyr	Ser	Lys	Phe	Arg	Thr	Pro	Thr	Phe
			145				150				155			160	
Leu	Val	Asn	Pro	Val	Phe	Asn	His	Arg	Val	Thr	Val	Ser	Arg	Arg	Val
							165			170				175	
Lys	Ile	Ile	Lys	Leu	Ala	Pro	Ser	Asp	Ala	Glu	Ser	Leu	Tyr	Arg	Asn
			180					185					190		
Arg	Phe	Ser	Thr	Thr	Glu	Phe	Phe	Pro	Ser	Asp	Ile	Asn	Ser	Ile	Leu
			195				200					205			
Thr	Asn	Lys	Leu	Ser	Leu	Gly	Thr	Tyr	Leu	Ala	Val	Pro	Arg	Gly	Gly
			210				215				220				
Asp	Asn	Val	Ser	Gly	Ser	Leu	Pro	Asp	Gln	Thr	Gly	Ser	Trp	Ala	Val
							230				235			240	
Ile	Ser	Ile	Trp	Asn	Ser	Lys	Asp	Val	Tyr	Arg	Leu	Gln	Val	Lys	Gly
							245			250				255	
Ala	Ser	Arg	Leu	Lys	Arg	Met	Leu	Ala	Lys	Ser	Thr	Arg	Val	Phe	Asp
			260					265				270			
Gly	Ala	Phe	Pro	Phe	Leu	Lys	Ile	Pro	Ser	Phe	Pro	Asn	Leu	Phe	Lys
			275				280					285			
Ser	Phe	Ala	Met	His	Phe	Met	Tyr	Gly	Ile	Gly	Gly	Glu	Gly	Pro	Arg
			290				295				300				
Ala	Ala	Glu	Met	Val	Glu	Ala	Leu	Cys	Ser	His	Ala	His	Asn	Leu	Ala
							310				315			320	
Arg	Lys	Ser	Gly	Cys	Ala	Val	Val	Ala	Ala	Glu	Val	Ala	Ser	Cys	Glu
			325					330						335	
Pro	Leu	Arg	Val	Gly	Ile	Pro	His	Trp	Lys	Val	Leu	Ser	Pro	Glu	Asp
			340					345					350		
Leu	Trp	Cys	Leu	Lys	Arg	Leu	Arg	Tyr	Asp	Asp	Asp	Gly	Val	Asp	Trp
			355				360						365		

Thr Lys Ser Pro Pro Gly Leu Ser Ile Phe Val Asp Pro Arg Glu Ile
370 375 380

(2) INFORMATION FOR SEQ ID NO:822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1568091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

Met	Gly	Asp	Pro	Leu	Ala	Arg	Ile	Arg	Gln	Ser	Pro	Ser	Phe	His	Met
1				5					10					15	
Leu	Val	Ala	Glu	Ile	Gly	Asn	Glu	Ile	Val	Gly	Met	Ile	Arg	Gly	Thr
			20					25					30		
Ile	Lys	Met	Val	Thr	Arg	Gly	Val	Asn	Ala	Leu	Arg	Gln	Ala	Asp	Asp
			35				40					45			
Val	Ser	Pro	Glu	Ile	Asn	Thr	Thr	Lys	Leu	Ala	Phe	Val	Ser	Gly	Leu
			50			55					60				
Arg	Val	Ser	Pro	Phe	Tyr	Arg	Arg	Met	Gly	Ile	Gly	Leu	Lys	Leu	Val
			65		70				75					80	
Gln	Arg	Leu	Glu	Glu	Trp	Phe	Leu	Arg	Asn	Asp	Ala	Val	Tyr	Ser	Tyr
				85					90					95	
Val	Gln	Thr	Glu	Asn	Asp	Asn	Ile	Ala	Ser	Val	Lys	Leu	Phe	Thr	Glu
			100					105					110		
Lys	Ser	Gly	Tyr	Ser	Lys	Phe	Arg	Thr	Pro	Thr	Phe	Leu	Val	Asn	Pro
			115				120					125			
Val	Phe	Asn	His	Arg	Val	Thr	Val	Ser	Arg	Arg	Val	Lys	Ile	Ile	Lys
			130				135					140			
Leu	Ala	Pro	Ser	Asp	Ala	Glu	Ser	Leu	Tyr	Arg	Asn	Arg	Phe	Ser	Thr
			145			150				155					160
Thr	Glu	Phe	Phe	Pro	Ser	Asp	Ile	Asn	Ser	Ile	Leu	Thr	Asn	Lys	Leu
			165					170					175		
Ser	Leu	Gly	Thr	Tyr	Leu	Ala	Val	Pro	Arg	Gly	Gly	Asp	Asn	Val	Ser
			180				185					190			
Gly	Ser	Leu	Pro	Asp	Gln	Thr	Gly	Ser	Trp	Ala	Val	Ile	Ser	Ile	Trp
			195				200					205			
Asn	Ser	Lys	Asp	Val	Tyr	Arg	Leu	Gln	Val	Lys	Gly	Ala	Ser	Arg	Leu
			210			215					220				
Lys	Arg	Met	Leu	Ala	Lys	Ser	Thr	Arg	Val	Phe	Asp	Gly	Ala	Phe	Pro
			225			230				235				240	
Phe	Leu	Lys	Ile	Pro	Ser	Phe	Pro	Asn	Leu	Phe	Lys	Ser	Phe	Ala	Met
			245					250					255		
His	Phe	Met	Tyr	Gly	Ile	Gly	Gly	Glu	Gly	Pro	Arg	Ala	Ala	Glu	Met
			260				265						270		
Val	Glu	Ala	Leu	Cys	Ser	His	Ala	His	Asn	Leu	Ala	Arg	Lys	Ser	Gly
			275				280					285			
Cys	Ala	Val	Val	Ala	Ala	Glu	Val	Ala	Ser	Cys	Glu	Pro	Leu	Arg	Val
			290			295					300				
Gly	Ile	Pro	His	Trp	Lys	Val	Leu	Ser	Pro	Glu	Asp	Leu	Trp	Cys	Leu
			305			310				315					320
Lys	Arg	Leu	Arg	Tyr	Asp	Asp	Asp	Gly	Val	Asp	Trp	Thr	Lys	Ser	Pro
			325						330				335		
Pro	Gly	Leu	Ser	Ile	Phe	Val	Asp	Pro	Arg	Glu	Ile				
			340				345								

(2) INFORMATION FOR SEQ ID NO:823:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..333
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568092
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

Met	Leu	Val	Ala	Glu	Ile	Gly	Asn	Glu	Ile	Val	Gly	Met	Ile	Arg	Gly	
1				5				10						15		
Thr	Ile	Lys	Met	Val	Thr	Arg	Gly	Val	Asn	Ala	Leu	Arg	Gln	Ala	Asp	
			20					25					30			
Asp	Val	Ser	Pro	Glu	Ile	Asn	Thr	Thr	Lys	Leu	Ala	Phe	Val	Ser	Gly	
			35				40					45				
Leu	Arg	Val	Ser	Pro	Phe	Tyr	Arg	Arg	Met	Gly	Ile	Gly	Leu	Lys	Leu	
	50					55				60						
Val	Gln	Arg	Leu	Glu	Glu	Trp	Phe	Leu	Arg	Asn	Asp	Ala	Val	Tyr	Ser	
65					70				75					80		
Tyr	Val	Gln	Thr	Glu	Asn	Asp	Asn	Ile	Ala	Ser	Val	Lys	Leu	Phe	Thr	
				85				90					95			
Glu	Lys	Ser	Gly	Tyr	Ser	Lys	Phe	Arg	Thr	Pro	Thr	Phe	Leu	Val	Asn	
			100					105					110			
Pro	Val	Phe	Asn	His	Arg	Val	Thr	Val	Ser	Arg	Arg	Val	Lys	Ile	Ile	
			115				120					125				
Lys	Leu	Ala	Pro	Ser	Asp	Ala	Glu	Ser	Leu	Tyr	Arg	Asn	Arg	Phe	Ser	
	130					135					140					
Thr	Thr	Glu	Phe	Phe	Pro	Ser	Asp	Ile	Asn	Ser	Ile	Leu	Thr	Asn	Lys	
145					150				155					160		
Leu	Ser	Leu	Gly	Thr	Tyr	Leu	Ala	Val	Pro	Arg	Gly	Gly	Asp	Asn	Val	
			165					170					175			
Ser	Gly	Ser	Leu	Pro	Asp	Gln	Thr	Gly	Ser	Trp	Ala	Val	Ile	Ser	Ile	
			180				185					190				
Trp	Asn	Ser	Lys	Asp	Val	Tyr	Arg	Leu	Gln	Val	Lys	Gly	Ala	Ser	Arg	
			195				200					205				
Leu	Lys	Arg	Met	Leu	Ala	Lys	Ser	Thr	Arg	Val	Phe	Asp	Gly	Ala	Phe	
	210					215					220					
Pro	Phe	Leu	Lys	Ile	Pro	Ser	Phe	Pro	Asn	Leu	Phe	Lys	Ser	Phe	Ala	
225					230				235					240		
Met	His	Phe	Met	Tyr	Gly	Ile	Gly	Gly	Glu	Gly	Pro	Arg	Ala	Ala	Glu	
			245						250				255			
Met	Val	Glu	Ala	Leu	Cys	Ser	His	Ala	His	Asn	Leu	Ala	Arg	Lys	Ser	
			260					265					270			
Gly	Cys	Ala	Val	Val	Ala	Ala	Glu	Val	Ala	Ser	Cys	Glu	Pro	Leu	Arg	
			275				280					285				
Val	Gly	Ile	Pro	His	Trp	Lys	Val	Leu	Ser	Pro	Glu	Asp	Leu	Trp	Cys	
	290					295					300					
Leu	Lys	Arg	Leu	Arg	Tyr	Asp	Asp	Gly	Val	Asp	Trp	Thr	Lys	Ser		
			310					315					320			
Pro	Pro	Gly	Leu	Ser	Ile	Phe	Val	Asp	Pro	Arg	Glu	Ile				
			325					330								

(2) INFORMATION FOR SEQ ID NO:824:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1183 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1183

(D) OTHER INFORMATION: / Ceres Seq. ID 1568093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

acatcatctt	cattaatctg	atcaataaat	agggttaatc	aaaagtcacg	aaaccaaacac	60
agttcaattt	tacgaaaact	ctcagaaatg	gagaagtagc	agaagctaga	gaaggtcggg	120
ctgaagaaaa	ctcgtctcga	gatggacgaa	gaaggtatct	gaactcgtga	gcttcttgct	180
atctcgtctc	tccagatggt	atcaaacctg	atctatgttg	tccgattact	ctcggtcgaa	240
catgttctac	aaccatcaac	caaatctcaa	tctaccaaat	ccaatctcta	tctcgttttc	300
gagtatctcg	atactgatct	taagaaatct	atcgattcgt	ataggaaaag	acctaatcct	360
aagcctcttg	agcctttttt	gattcagaag	ttgatgtttc	agcctttgta	aggtgttcgc	420
catgttcaat	gtcactggtg	gcttcacagt	gatcttaaac	cgcagaatct	tctctcgttg	480
aaaagataag	agcttcttta	gattgctgat	ttgggtcttg	gtcgtgcttt	tactgttctc	540
cttaagctct	atacgcatag	gattgttact	ctttggtata	gagctcctga	agttctctct	600
ggatctactc	attattcaac	tggtgttgac	atgtggtctg	ttggttgat	ctttgctgag	660
atggttcgga	ggcaagctct	tttccctggt	gattctgagt	ttcagcaatt	gcttcacatc	720
tgcaggttgc	taggaacacc	aactgagcag	caatggcctg	gtgtttccac	Attcgctgac	780
ttgcagtgtt	accctaagtg	ggagcgcgaa	gacttaactc	ttgctgttcc	tctcttttca	840
cctcaaggag	ttgatcttct	cacgaaaatg	ctcaagtaca	atccagccga	aagaatttca	900
gcacaaaacg	cacttgatca	cccatatttt	gcacagcctg	acaagctctc	gttctgaagt	960
ctattgtctg	atctgtgtgc	atcgtcttgg	tgaattttaa	catttgatct	atctttgttt	1020
cgcagacatt	agtgctcttat	gtttggttta	gagatttgta	gtctttcaga	agaaactggt	1080
aaaagcttga	ttctcaagtg	aatgtaaaaa	acaatggtgt	ggt		1140

(2) INFORMATION FOR SEQ ID NO:825:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..309

(D) OTHER INFORMATION: / Ceres Seq. ID 1568094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

Met	Glu	Lys	Tyr	Glu	Lys	Leu	Glu	Lys	Val	Gly	Glu	Gly	Thr	Tyr	Gly
1				5					10					15	
Lys	Val	Tyr	Lys	Ala	Met	Glu	Lys	Gly	Thr	Gly	Lys	Leu	Val	Ala	Leu
			20					25					30		
Lys	Lys	Thr	Arg	Leu	Glu	Met	Asp	Glu	Gly	Ile	Pro	Pro	Thr	Ala	
			35				40			45					
Leu	Arg	Glu	Ile	Ser	Leu	Leu	Gln	Met	Leu	Ser	Thr	Ser	Ile	Tyr	Val
			50				55			60					
Val	Arg	Leu	Leu	Cys	Val	Glu	His	Val	His	Gln	Pro	Ser	Thr	Lys	Ser
			65				70			75				80	
Gln	Ser	Thr	Lys	Ser	Asn	Leu	Tyr	Leu	Val	Phe	Glu	Tyr	Leu	Asp	Thr
			85					90						95	
Asp	Leu	Lys	Lys	Phe	Ile	Asp	Ser	Tyr	Arg	Lys	Gly	Pro	Asn	Pro	Lys
			100					105					110		
Pro	Leu	Glu	Pro	Phe	Leu	Ile	Gln	Lys	Leu	Met	Phe	Gln	Leu	Cys	Lys
			115				120					125			
Gly	Val	Ala	His	Cys	His	Ser	His	Gly	Val	Leu	His	Arg	Asp	Leu	Lys
			130				135					140			
Pro	Gln	Asn	Leu	Leu	Leu	Val	Lys	Asp	Lys	Glu	Leu	Leu	Lys	Ile	Ala
			145				150			155				160	
Asp	Leu	Gly	Leu	Gly	Arg	Ala	Phe	Thr	Val	Pro	Leu	Lys	Ser	Tyr	Thr
			165					170						175	
His	Glu	Ile	Val	Thr	Leu	Trp	Tyr	Arg	Ala	Pro	Glu	Val	Leu	Leu	Gly
			180					185					190		
Ser	Thr	His	Tyr	Ser	Thr	Gly	Val	Asp	Met	Trp	Ser	Val	Gly	Cys	Ile

(2) INFORMATION FOR SEQ ID NO:826:

(A) LENGTH: 288 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

(1X) FEATURE.
(A) NAME

(B) LOCATION: 1-288

(D) OTHER INFORMATION

(D) OTHER INFORMATION: / Ceres Seq. ID 13688093
SEQUENCE DESCRIPTION: SEQ ID NO:826:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:826:
Gln Lys Gly Thr Gly Lys Leu Val Ala Leu I

Met	Glu	Lys	Gly	5	nr	Gly	Lys	Leu	Val	Ala	Leu	Lys	Lys	nr	Arg	Leu
1										10					15	
Glu	Met	Asp	Glu	20	Gly	Ile	Pro	Pro	Thr	Ala	Leu	Arg	Glu	Ile	Ser	
								25					30			
Leu	Leu	Gln	Met	Leu	Ser	Thr	Ser	Ile	Tyr	Val	Val	Arg	Leu	Leu	Cys	
		35						40				45				
Val	Glu	His	Val	His	Gln	Pro	Ser	Thr	Lys	Ser	Gln	Ser	Thr	Lys	Ser	
	50					55					60					
Asn	Leu	Tyr	Leu	Val	Phe	Glu	Tyr	Leu	Asp	Thr	Asp	Leu	Lys	Lys	Phe	
					70					75					80	
Ile	Asp	Ser	Tyr	Arg	Lys	Gly	Pro	Asn	Pro	Lys	Pro	Leu	Glu	Pro	Phe	
				85					90					95		
Leu	Ile	Gln	Lys	Leu	Met	Phe	Gln	Leu	Cys	Lys	Gly	Val	Ala	His	Cys	
			100					105					110			
His	Ser	His	Gly	Val	Leu	His	Arg	Asp	Leu	Lys	Pro	Gln	Asn	Leu	Leu	
		115						120				125				
Leu	Val	Lys	Asp	Lys	Glu	Leu	Leu	Lys	Ile	Ala	Asp	Leu	Gln	Leu	Gly	
	130					135					140					
Arg	Ala	Phe	Thr	Val	Pro	Leu	Lys	Ser	Tyr	Thr	His	Glu	Ile	Val	Thr	
145					150					155					160	
Leu	Trp	Tyr	Arg	Ala	Pro	Glu	Val	Leu	Leu	Gly	Ser	Thr	His	Tyr	Ser	
			165						170					175		
Thr	Gly	Val	Asp	Met	Trp	Ser	Val	Gly	Cys	Ile	Phe	Ala	Glu	Met	Val	
			180					185					190			
Arg	Arg	Gln	Ala	Leu	Phe	Pro	Gly	Asp	Ser	Glu	Phe	Gln	Gln	Leu	Leu	
		195					200					205				
His	Ile	Phe	Arg	Leu	Leu	Gly	Thr	Pro	Thr	Glu	Gln	Gln	Trp	Pro	Gly	
	210					215					220					
Val	Ser	Thr	Leu	Arg	Asp	Trp	His	Val	Tyr	Pro	Lys	Trp	Glu	Pro	Gln	
225					230					235				240		
Asp	Leu	Thr	Leu	Ala	Val	Pro	Ser	Leu	Ser	Pro	Gln	Gly	Val	Asp	Leu	
			245						250					255		
Leu	Thr	Lys	Met	Leu	Lys	Tyr	Asn	Pro	Ala	Glu	Arg	Ile	Ser	Ala	Lys	
			260					265					270			

Thr Ala Leu Asp His Pro Tyr Phe Asp Ser Leu Asp Lys Ser Gln Phe
275 280 285

(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..271
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

```
Met Asp Glu Glu Gly Ile Pro Pro Thr Ala Leu Arg Glu Ile Ser Leu
1      5      10      15
Leu Gln Met Leu Ser Thr Ser Ile Tyr Val Val Arg Leu Leu Cys Val
20      25      30
Glu His Val His Gln Pro Ser Thr Lys Ser Gln Ser Thr Lys Ser Asn
35      40      45
Leu Tyr Leu Val Phe Glu Tyr Leu Asp Thr Asp Leu Lys Lys Phe Ile
50      55      60
Asp Ser Tyr Arg Lys Gly Pro Asn Pro Lys Pro Leu Glu Pro Phe Leu
65      70      75      80
Ile Gln Lys Leu Met Phe Gln Leu Cys Lys Gly Val Ala His Cys His
85      90      95
Ser His Gly Val Leu His Arg Asp Leu Lys Pro Gln Asn Leu Leu Leu
100      105      110
Val Lys Asp Lys Glu Leu Leu Lys Ile Ala Asp Leu Gly Leu Gly Arg
115      120      125
Ala Phe Thr Val Pro Leu Lys Ser Tyr Thr His Glu Ile Val Thr Leu
130      135      140
Trp Tyr Arg Ala Pro Glu Val Leu Leu Gly Ser Thr His Tyr Ser Thr
145      150      155      160
Gly Val Asp Met Trp Ser Val Gly Cys Ile Phe Ala Glu Met Val Arg
165      170      175
Arg Gln Ala Leu His Pro Gly Asp Ser Glu Phe Gln Gln Leu Leu His
180      185      190
Ile Phe Arg Leu Leu Gly Thr Pro Thr Glu Gln Gln Trp Pro Gly Val
195      200      205      210
Ser Thr Leu Arg Asp Trp His Val Tyr Pro Lys Trp Glu Pro Gln Asp
215      220      225
Leu Thr Leu Ala Val Pro Ser Leu Ser Pro Gln Gly Val Asp Leu Leu
230      235      240
Thr Lys Met Leu Lys Tyr Asn Pro Ala Glu Arg Ile Ser Ala Lys Thr
245      250      255
Ala Leu Asp His Pro Tyr Phe Asp Ser Leu Asp Lys Ser Gln Phe
260      265      270
```

(2) INFORMATION FOR SEQ ID NO:828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1212
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

ctgtctctct	tcagtgacac	aaacccaaa	aaaagtagtg	agaaacaaaa	tcgaggtaac	60
tactagatga	agacagtaga	gcaattaaat	attgcggttg	trgttgtagt	gacggtctct	120
attggaatgt	tgagatcatc	ggaggctcaa	cttcaaatga	atttctacgc	gaagagctgt	180
ccaaacgcag	agaaaatcat	ttcagatcat	attcaaaaatc	atatccacaa	tggtcctctt	240
cttcagctc	ctctcatccg	aatgcacttc	catgattgct	tcggtagggg	atgtgacgga	300
tcggtgttga	taaatccaac	atctggtaac	gcagagagag	atgcaccacc	gaattctaac	360
cttagaggat	tcggtttctg	ggaaaaggatt	aaggctcttc	ttgaaaaagt	gtgtccttaag	420
actgtttctt	gcgcagatat	cattgctttg	actgctagag	acacagttgt	cgccaccgga	480
ggtccttcat	ggagtgttcc	aacgggaaga	agagacggtg	ggatctcaaa	tttgaaggag	540
gctacgaata	acttccacc	tccaacgagt	aatttccaga	ctttacgacg	acttttcaaa	600
aaccaagccc	ttaatctcaa	ggaccttgtt	ctgctctctg	gggctcacac	gactgtgtgc	660
tcacattggt	cttccatgaa	tactcgtctc	tacaactctc	cgaactacagt	caaacaagat	720
ccatctctcg	atagccagta	cgcagcta	ctaaaggcta	acaaatgtaa	gagcctaacc	780
gcaaatagca	ccatcctgga	gatggatccc	ggtagtagca	gaagcttcga	tctcagttat	840
tataggctgt	tcttgaagag	gagagccttg	ttccaatctg	attctgcctt	gacacagaac	900
tcagcgagct	tgaagggtgat	caacgacttg	gtcaaacggtt	ctgaaaaagaa	gtttttcaaa	960
gcttttgtta	agtcgaatrg	agaagatggg	gagagttaaw	gtgaCaGact	ggctcagctg	1020
gtgtgatcag	gacacgggtg	tctgtcgtcg	gaagttagta	agcttggtcg	gaatgtgggt	1080
tgttatggtc	attgtgtgtt	tgtgtgactt	tcggaaaaaa	caaatgttgt	taatttaatt	1140
ttgttgttgt	tgtatttgtg	tttatgcacc	caagaatgat	gtgttatggt	tcaattaata	1200
tgtgaatcat	tt					

(2) INFORMATION FOR SEQ ID NO:829:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 310 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..310

(D) OTHER INFORMATION: / Ceres Seq. ID 1568101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

Met	Lys	Thr	Met	Thr	Gln	Leu	Asn	Ile	Ala	Val	Xaa	Val	Val	Val	Thr
1					5				10					15	
Val	Leu	Ile	Gly	Met	Leu	Arg	Ser	Ser	Glu	Ala	Gln	Leu	Gln	Met	Asn
			20					25					30		
Phe	Tyr	Ala	Lys	Ser	Cys	Pro	Asn	Ala	Glu	Lys	Ile	Ile	Ser	Asp	His
		35					40					45			
Ile	Gln	Asn	His	Ile	His	Asn	Gly	Pro	Ser	Leu	Ala	Ala	Pro	Leu	Ile
		50				55					60				
Arg	Met	His	Phe	His	Asp	Cys	Phe	Val	Arg	Gly	Cys	Asp	Gly	Ser	Val
		65				70				75				80	
Leu	Ile	Asn	Ser	Thr	Ser	Gly	Asn	Ala	Glu	Arg	Asp	Ala	Pro	Pro	Asn
			85						90					95	
Leu	Thr	Leu	Arg	Gly	Phe	Gly	Phe	Val	Glu	Arg	Ile	Lys	Ala	Leu	Leu
			100					105					110		
Glu	Lys	Val	Cys	Pro	Lys	Thr	Val	Ser	Cys	Ala	Asp	Ile	Ile	Ala	Leu
		115					120					125			
Thr	Ala	Arg	Asp	Thr	Val	Val	Ala	Thr	Gly	Gly	Pro	Ser	Trp	Ser	Val
		130					135					140			
Pro	Thr	Gly	Arg	Arg	Asp	Gly	Arg	Ile	Ser	Asn	Leu	Lys	Glu	Ala	Thr
		145				150				155					160
Asn	Asn	Ile	Pro	Pro	Pro	Thr	Ser	Asn	Phe	Thr	Thr	Leu	Arg	Arg	Leu
			165					170					175		
Phe	Lys	Asn	Gln	Gly	Leu	Asn	Leu	Lys	Asp	Leu	Val	Leu	Leu	Ser	Gly
		180						185					190		
Ala	His	Thr	Ile	Gly	Val	Ser	His	Cys	Ser	Ser	Met	Asn	Thr	Arg	Leu
		195					200					205			
Tyr	Asn	Phe	Ser	Thr	Thr	Val	Lys	Gln	Asp	Pro	Ser	Leu	Asp	Ser	Gln

210	215	220
Tyr Ala Ala Asn Leu Lys	Ala Asn Lys Cys	Lys Ser Leu Asn Asp Asn
225	230	235
Ser Thr Ile Leu Glu Met	Asp Pro Gly Ser	Ser Arg Ser Phe Asp Leu
245	250	255
Ser Tyr Tyr Arg Leu Val	Leu Lys Arg Arg	Gly Leu Phe Gln Ser Asp
260	265	270
Ser Ala Leu Thr Thr Asn	Ser Ala Thr Leu Lys Val	Ile Asn Asp Leu
275	280	285
Val Asn Gly Ser Glu Lys	Lys Phe Phe Lys Ala	Phe Ala Lys Ser Met
290	295	300
Xaa Glu Asp Gly Glu Ser		
305	310	

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..307

- (D) OTHER INFORMATION: / Ceres Seq. ID 1568102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

Met Thr Gln Leu Asn Ile Ala Val Xaa Val Val Val Thr Val Leu Ile	
1	5 10 15
Gly Met Leu Arg Ser Ser Glu Ala Gln Leu Gln Met Asn Phe Tyr Ala	
	20 25 30
Lys Ser Cys Pro Asn Ala Glu Lys Ile Ile Ser Asp His Ile Gln Asn	
	35 40 45
His Ile His Asn Gly Pro Ser Leu Ala Ala Pro Leu Ile Arg Met His	
	50 55 60
Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Ile Asn	
	65 70 75 80
Ser Thr Ser Gly Asn Ala Glu Arg Asp Ala Pro Pro Asn Leu Thr Leu	
	85 90 95
Arg Gly Phe Gly Phe Val Glu Arg Ile Lys Ala Leu Leu Glu Lys Val	
	100 105 110
Cys Pro Lys Thr Val Ser Cys Ala Asp Ile Ile Ala Leu Thr Ala Arg	
	115 120 125
Asp Thr Val Val Ala Thr Gly Gly Pro Ser Trp Ser Val Pro Thr Gly	
	130 135 140
Arg Arg Asp Gly Arg Ile Ser Asn Leu Lys Glu Ala Thr Asn Asn Ile	
	145 150 155 160
Pro Pro Pro Thr Ser Asn Phe Thr Thr Leu Arg Arg Leu Phe Lys Asn	
	165 170 175
Gln Gly Leu Asn Leu Lys Asp Leu Val Leu Leu Ser Gly Ala His Thr	
	180 185 190
Ile Gly Val Ser His Cys Ser Ser Met Asn Thr Arg Leu Tyr Asn Phe	
	195 200 205
Ser Thr Thr Val Lys Gln Asp Pro Ser Leu Asp Ser Gln Tyr Ala Ala	
	210 215 220
Asn Leu Lys Ala Asn Lys Cys Lys Ser Leu Asn Asp Asn Ser Thr Ile	
	225 230 235
Leu Glu Met Asp Pro Gly Ser Ser Arg Ser Phe Asp Leu Ser Tyr Tyr	
	240 245 250 255
Arg Leu Val Leu Lys Arg Arg Gly Leu Phe Gln Ser Asp Ser Ala Leu	
	260 265 270
Thr Thr Asn Ser Ala Thr Leu Lys Val Ile Asn Asp Leu Val Asn Gly	
	275 280 285

Ser Glu Lys Lys Phe Phe Lys Ala Phe Ala Lys Ser Met Xaa Glu Asp
290 295 300
Gly Glu Ser
305

(2) INFORMATION FOR SEQ ID NO:831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..290

(D) OTHER INFORMATION: / Ceres Seq. ID 1568103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

Met Leu Arg Ser Ser Glu Ala Gln Leu Gln Met Asn Phe Tyr Ala Lys
1 5 10 15
Ser Cys Pro Asn Ala Glu Lys Ile Ile Ser Asp His Ile Gln Asn His
20 25 30
Ile His Asn Gly Pro Ser Leu Ala Ala Pro Leu Ile Arg Met His Phe
35 40 45
His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Ile Asn Ser
50 55 60
Thr Ser Gly Asn Ala Glu Arg Asp Ala Pro Pro Asn Leu Thr Leu Arg
65 70 75 80
Gly Phe Gly Phe Val Glu Arg Ile Lys Ala Leu Leu Glu Lys Val Cys
85 90 95
Pro Lys Thr Val Ser Cys Ala Asp Ile Ile Ala Leu Thr Ala Arg Asp
100 105 110
Thr Val Val Ala Thr Gly Gly Pro Ser Trp Ser Val Pro Thr Gly Arg
115 120 125
Arg Asp Gly Arg Ile Ser Asn Leu Lys Glu Ala Thr Asn Asn Ile Pro
130 135 140
Pro Pro Thr Ser Asn Phe Thr Thr Leu Arg Arg Leu Phe Lys Asn Gln
145 150 155 160
Gly Leu Asn Leu Lys Asp Leu Val Leu Leu Ser Gly Ala His Thr Ile
165 170 175
Gly Val Ser His Cys Ser Ser Met Asn Thr Arg Leu Tyr Asn Phe Ser
180 185 190
Thr Thr Val Lys Gln Asp Pro Ser Leu Asp Ser Gln Tyr Ala Ala Asn
195 200 205
Leu Lys Ala Asn Lys Cys Lys Ser Leu Asn Asp Asn Ser Thr Ile Leu
210 215 220
Glu Met Asp Pro Gly Ser Ser Arg Ser Phe Asp Leu Ser Tyr Tyr Arg
225 230 235 240
Leu Val Leu Lys Arg Arg Gly Leu Phe Gln Ser Asp Ser Ala Leu Thr
245 250 255
Thr Asn Ser Ala Thr Leu Lys Val Ile Asn Asp Leu Val Asn Gly Ser
260 265 270
Glu Lys Lys Phe Phe Lys Ala Phe Ala Lys Ser Met Xaa Glu Asp Gly
275 280 285
Glu Ser
290

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1734 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1734

(D) OTHER INFORMATION: / Ceres Seq. ID 1568104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

```
atcaatggct ctgatgcatt tcttcttcatt cgtctctctta tcttctctgt ttcogtcacc 60
atcccgctga gaatccacta ctacagtttgc tagtgacagg agagagaagt gtgtgggacc 120
ttgtgggttt tcatcgacga ggattttgat taaaggaggt actggtgtca atgcacacca 180
tcaagaacttt gctgatgttt atgtggaaaaa tgggtattatt gtcgctgtgc agccaatact 240
taagggttggg gatgaagtca ctgtcctcga tgcctactgga aagtttgtca tgcaggagg 300
aattgacccc cacacgcacc tgcctatgga atttatgggt accgagacta ttgatgttt 360
cttcagtggg caggcagcgg cattagctgg tggaaacaact atgcataag actttgttat 420
acctgtcaat ggggaatctg tggctggttt tgaagcctat gaaaacaaat ctagagaatc 480
ttgtatggat tacggttttc atatggcaat cacaaagtgg gatgaaggtg ttccacaggga 540
catggagatg ttggtcaagg aaaagggtat caactcttcc aagtttttcc tagcgtataa 600
aggatctctt atggttaact atgacctact cctagaagga cttaaaaagt gcaaatccct 660
cgggtcctgt gccatggttc atgctgaaaa tggagatgca gtattcgaag gacagaaaaa 720
aatgattgar ctgggcatct Acagggtccag agggctcatg tctttTcaAG gccctcgtgt 780
ctcgaggagc agggccactgc tagagcaatt cgtttggctc gttttattaa cacgcctctc 840
tatgttgttc atgtgatgag tgttgatgca atggacgaga ttgctaaggc tcgaaaaatca 900
ggacagaagg ttattggaga ctcgtgttgt tctggattaa tccttgatga tcattggctt 960
tgggatcctg acctccaact tgcgtccaag tatgtcatga tcccaacctat cacagcagta 1020
ggacatggga aagccctaca agatgcctct tccacaggaa tctctcagct tctaggaaat 1080
gatcactgca ctttccaattc tacacaaaaa gctctaggac ttgatgattt ccgcaaaaata 1140
cctaattggt ttaattggcct tagggaacgg atgcacttga tatgggacac gatgtggagg 1200
tctggccaac tctcagctac tgattatgtt cgaataacca gcactgagtg tctagaatt 1260
tccaacatat atccacggaa agggagctatc ctgtgctgctc cggatgcaga tatattcata 1320
ttgaattcaa actcaagcta cgagattagc tcaaaagtctc atcattcaag atcagacata 1380
aacgtctacg agggcagaag aggaaaaggga aaggttgaag tgaacaatgc agggagacga 1440
attgtgtggg aaaaacgaga acctaaagtt gttccaagaa gtggcaagta tatagagatg 1500
ctctcttttc gattaccttt cgatgggtatt gagaatacag atgctaatta tctatctctc 1560
cttcagctca cgtttaacgc tgtcagaact gaagctacgt aaagtgcagg tatctatctt 1620
tcgtgatctt gtaagaacaa ttgtacataa tttgtattaa aagtattgaa agagcgatta 1680
tgaataatgt gcatgtagtc tggttttgag aaaaaataaa agattgtaaa attt
```

(2) INFORMATION FOR SEQ ID NO:833:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..284

(D) OTHER INFORMATION: / Ceres Seq. ID 1568105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

```
Ser Met Ala Leu Asp Ala Phe Phe Phe Ile Val Ser Leu Phe Leu Leu
1      5      10      15
Phe Pro Ser Pro Ser Ala Ser Glu Ser Thr Thr Gln Phe Cys Ser Ala
20     25     30
Gly Arg Glu Asn Gly Val Gly Ser Cys Gly Val Ser Ser Thr Arg Ile
35     40     45
Leu Ile Lys Gly Gly Thr Val Val Asn Ala His His Gln Glu Leu Ala
50     55     60
Asp Val Tyr Val Glu Asn Gly Ile Ile Val Ala Val Gln Pro Asn Ile
65     70     75
Lys Val Gly Asp Glu Val Thr Val Leu Asp Ala Thr Gly Lys Phe Val
85     90     95
Met Pro Gly Gly Ile Asp Pro His Thr His Leu Ala Met Glu Phe Met
100    105    110
Gly Thr Glu Thr Ile Asp Asp Phe Phe Ser Gly Gln Ala Ala Leu
```

115	120	125
Ala Gly Gly Thr Thr Met His Ile Asp Phe Val Ile Pro Val Asn Gly		
130	135	140
Asn Leu Val Ala Gly Phe Glu Ala Tyr Glu Asn Lys Ser Arg Glu Ser		
145	150	155
Cys Met Asp Tyr Gly Phe His Met Ala Ile Thr Lys Trp Asp Glu Gly		
165	170	175
Val Ser Arg Asp Met Glu Met Leu Val Lys Glu Lys Gly Ile Asn Ser		
180	185	190
Phe Lys Phe Phe Leu Ala Tyr Lys Gly Ser Leu Met Val Thr Asp Asp		
195	200	205
Leu Leu Leu Glu Gly Leu Lys Arg Cys Lys Ser Leu Gly Ala Leu Ala		
210	215	220
Met Val His Ala Glu Asn Gly Asp Ala Val Phe Glu Gly Gln Lys Arg		
225	230	235
Met Ile Xaa Leu Gly Ile Tyr Arg Ser Arg Gly Ser Cys Ser Phe Gln		
245	250	255
Gly Leu Leu Cys Ser Arg Glu Arg Pro Leu Leu Glu Gln Phe Val Trp		
260	265	270
Leu Val Leu Leu Thr Arg Leu Ser Met Leu Phe Met		
275	280	

(2) INFORMATION FOR SEQ ID NO:834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..283
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

Met Ala Leu Asp Ala Phe Phe Phe Ile Val Ser Leu Phe Leu Phe	1	5	10	15
Pro Ser Pro Ser Ala Ser Glu Ser Thr Thr Gln Phe Cys Ser Ala Gly	20	25	30	
Arg Glu Asn Gly Val Gly Ser Cys Gly Val Ser Ser Thr Arg Ile Leu	35	40	45	
Ile Lys Gly Gly Thr Val Val Asn Ala His His Gln Glu Leu Ala Asp	50	55	60	
Val Tyr Val Glu Asn Gly Ile Ile Val Ala Val Gln Pro Asn Ile Lys	65	70	75	80
Val Gly Asp Glu Val Thr Val Leu Asp Ala Thr Gly Lys Phe Val Met	85	90	95	
Pro Gly Gly Ile Asp Pro His Thr His Leu Ala Met Glu Phe Met Gly	100	105	110	
Thr Glu Thr Ile Asp Asp Phe Phe Ser Gly Gln Ala Ala Ala Leu Ala	115	120	125	
Gly Gly Thr Thr Met His Ile Asp Phe Val Ile Pro Val Asn Gly Asn	130	135	140	
Leu Val Ala Gly Phe Glu Ala Tyr Glu Asn Lys Ser Arg Glu Ser Cys	145	150	155	160
Met Asp Tyr Gly Phe His Met Ala Ile Thr Lys Trp Asp Glu Gly Val	165	170	175	
Ser Arg Asp Met Glu Met Leu Val Lys Glu Lys Gly Ile Asn Ser Phe	180	185	190	
Lys Phe Phe Leu Ala Tyr Lys Gly Ser Leu Met Val Thr Asp Asp Leu	195	200	205	
Leu Leu Glu Gly Leu Lys Arg Cys Lys Ser Leu Gly Ala Leu Ala Met	210	215	220	

Val His Ala Glu Asn Gly Asp Ala Val Phe Glu Gly Gln Lys Arg Met
225 230 235 240
Ile Xaa Leu Gly Ile Tyr Arg Ser Arg Gly Ser Cys Ser Phe Gln Gly
245 250 255
Leu Leu Cys Ser Arg Glu Arg Pro Leu Leu Glu Gln Phe Val Trp Leu
260 265 270
Val Leu Leu Thr Arg Leu Ser Met Leu Phe Met
275 280

(2) INFORMATION FOR SEQ ID NO:835:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 281 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..281

(D) OTHER INFORMATION: / Ceres Seq. ID 1568107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

Met Leu Phe Ser Arg Pro Pro Val Leu Glu Gly Glu Ala Thr Ala Arg
1 5 10 15
Ala Ile Arg Leu Ala Arg Phe Ile Asn Thr Pro Leu Tyr Val Val His
20 25 30
Val Met Ser Val Asp Ala Met Asp Glu Ile Ala Lys Ala Arg Lys Ser
35 40 45
Gly Gln Lys Val Ile Gly Glu Pro Val Val Ser Gly Leu Ile Leu Asp
50 55 60
Asp His Trp Leu Trp Asp Pro Asp Phe Thr Ile Ala Ser Lys Tyr Val
65 70 75 80
Met Ser Pro Pro Ile Arg Pro Val Gly His Gly Lys Ala Leu Gln Asp
85 90 95
Ala Leu Ser Thr Gly Ile Leu Gln Leu Val Gly Thr Asp His Cys Thr
100 105 110
Phe Asn Ser Thr Gln Lys Ala Leu Gly Leu Asp Asp Phe Arg Lys Ile
115 120 125
Pro Asn Gly Val Asn Gly Leu Glu Glu Arg Met His Leu Ile Trp Asp
130 135 140
Thr Met Val Glu Ser Gly Gln Leu Ser Ala Thr Asp Tyr Val Arg Ile
145 150 155 160
Thr Ser Thr Glu Cys Ala Arg Ile Phe Asn Ile Tyr Pro Arg Lys Gly
165 170 175
Ala Ile Leu Ala Gly Ser Asp Ala Asp Ile Ile Ile Leu Asn Pro Asn
180 185 190
Ser Ser Tyr Glu Ile Ser Ser Lys Ser His His Ser Arg Ser Asp Thr
195 200 205
Asn Val Tyr Glu Gly Arg Arg Gly Lys Gly Lys Val Glu Val Thr Ile
210 215 220
Ala Gly Gly Arg Ile Val Trp Glu Asn Glu Glu Leu Lys Val Val Pro
225 230 235 240
Arg Ser Gly Lys Tyr Ile Glu Met Pro Pro Phe Ser Tyr Leu Phe Asp
245 250 255
Gly Ile Glu Lys Ser Asp Ala Asn Tyr Leu Ser Ser Leu Arg Ala Pro
260 265 270
Val Lys Arg Val Arg Thr Glu Ala Thr
275 280

(2) INFORMATION FOR SEQ ID NO:836:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 659 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..659

(D) OTHER INFORMATION: / Ceres Seq. ID 1568124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

ctctttttct	tcattcttca	tctctctcc	cacaaaagag	gacaaaaaac	caaataacga	60
gaagtcocat	ttctctttgt	tgtcttaggt	gttaccttca	tcaaccaaac	gcaatggcga	120
acgcggcgtc	ggggatggcg	gtggaggacg	agtgttaagct	gaagtttttg	gagctaaaag	180
cgaaagaaaa	ctatagggtc	ataatattca	ggatagatgg	acaacaagtg	gtggtagaaa	240
agctgggaag	cccccaagag	aactacgacg	atttacccaa	ttacctaccg	ccaaaatgaat	300
gcgcgtacgc	cgtttatgac	ttcgacttca	ccactgctga	gaatatccag	aagagcaaga	360
tctttctcat	agcatggtca	ccggattcat	ctagagtaag	gatgaagatg	gtgtatgcga	420
gtctaaagga	caggttccaag	agggaaattgg	atgggtattca	gggtggagtta	caagccactg	480
acccgagcga	gatgagttct	gacatcatca	aaagtgcgaac	ttcttagatc	tccttgcctt	540
tcataattata	tatccataat	cattgtcatt	caaacatttt	cctcatctta	tgttaactttc	600
gatcttggtt	tcatttcatt	ttgttcttga	ctgttttttt	ctatGtttat	ttacatttt	

(2) INFORMATION FOR SEQ ID NO:837:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..174

(D) OTHER INFORMATION: / Ceres Seq. ID 1568125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

Leu	Phe	Leu	His	Ser	Ser	Ser	Leu	Leu	Pro	Gln	Lys	Arg	Thr	Lys	Asn
1			5						10					15	
Gln	Ile	Thr	Arg	Ser	Pro	Ile	Ser	Leu	Cys	Cys	Leu	Arg	Cys	Tyr	Leu
			20					25						30	
His	Gln	Pro	Asn	Ala	Met	Ala	Asn	Ala	Ala	Ser	Gly	Met	Ala	Val	Glu
			35				40					45			
Asp	Glu	Cys	Lys	Leu	Lys	Phe	Leu	Glu	Leu	Lys	Ala	Lys	Arg	Asn	Tyr
			50			55					60				
Arg	Phe	Ile	Ile	Phe	Arg	Ile	Asp	Gly	Gln	Gln	Val	Val	Val	Glu	Lys
			65		70			75						80	
Leu	Gly	Ser	Pro	Gln	Glu	Asn	Tyr	Asp	Asp	Phe	Thr	Asn	Tyr	Leu	Pro
			85					90					95		
Pro	Asn	Glu	Cys	Arg	Tyr	Ala	Val	Tyr	Asp	Phe	Asp	Phe	Thr	Thr	Ala
			100					105					110		
Glu	Asn	Ile	Gln	Lys	Ser	Lys	Ile	Phe	Phe	Ile	Ala	Trp	Ser	Pro	Asp
			115				120					125			
Ser	Ser	Arg	Val	Arg	Met	Lys	Met	Val	Tyr	Ala	Ser	Ser	Lys	Asp	Arg
			130			135					140				
Phe	Lys	Arg	Glu	Leu	Asp	Gly	Ile	Gln	Val	Glu	Leu	Gln	Ala	Thr	Asp
			145		150					155				160	
Pro	Ser	Glu	Met	Ser	Leu	Asp	Ile	Ile	Lys	Ser	Arg	Thr	Leu		
			165					170							

(2) INFORMATION FOR SEQ ID NO:838:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1568126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

```
Met Ala Asn Ala Ala Ser Gly Met Ala Val Glu Asp Glu Cys Lys Leu
1      5      10
Lys Phe Leu Glu Leu Lys Ala Lys Arg Asn Tyr Arg Phe Ile Ile Phe
20     25     30
Arg Ile Asp Gly Gln Gln Val Val Val Glu Lys Leu Gly Ser Pro Gln
35     40     45
Glu Asn Tyr Asp Asp Phe Thr Asn Tyr Leu Pro Pro Asn Glu Cys Arg
50     55     60
Tyr Ala Val Tyr Asp Phe Asp Phe Thr Thr Ala Glu Asn Ile Gln Lys
65     70     75     80
Ser Lys Ile Phe Phe Ile Ala Trp Ser Pro Asp Ser Ser Arg Val Arg
85     90     95
Met Lys Met Val Tyr Ala Ser Ser Lys Asp Arg Phe Lys Arg Glu Leu
100    105    110
Asp Gly Ile Gln Val Glu Leu Gln Ala Thr Asp Pro Ser Glu Met Ser
115    120    125
Leu Asp Ile Ile Lys Ser Arg Thr Leu
130    135
```

(2) INFORMATION FOR SEQ ID NO:839:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1568127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

```
Met Ala Val Glu Asp Glu Cys Lys Leu Lys Phe Leu Glu Leu Lys Ala
1      5      10
Lys Arg Asn Tyr Arg Phe Ile Ile Phe Arg Ile Asp Gly Gln Gln Val
20     25     30
Val Val Glu Lys Leu Gly Ser Pro Gln Glu Asn Tyr Asp Asp Phe Thr
35     40     45
Asn Tyr Leu Pro Pro Asn Glu Cys Arg Tyr Ala Val Tyr Asp Phe Asp
50     55     60
Phe Thr Thr Ala Glu Asn Ile Gln Lys Ser Lys Ile Phe Phe Ile Ala
65     70     75     80
Trp Ser Pro Asp Ser Ser Arg Val Arg Met Lys Met Val Tyr Ala Ser
85     90     95
Ser Lys Asp Arg Phe Lys Arg Glu Leu Asp Gly Ile Gln Val Glu Leu
100    105    110
Gln Ala Thr Asp Pro Ser Glu Met Ser Leu Asp Ile Ile Lys Ser Arg
115    120    125
Thr Leu
130
```

(2) INFORMATION FOR SEQ ID NO:840:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1320 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1320

(D) OTHER INFORMATION: / Ceres Seq. ID 1568128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

ataagcggatt	tcattattatt	cttcttcatc	gattcttgat	tttgcaagaa	gacaattc	caa	60
gaaagcggatt	tagaagacgg	aggagttctt	accggagatc	ttatacttat	ggatggaatg		120
tacaatttcc	attcgggccc	tgattattca	gataagtcgg	ttctgatgat	gtcacccggg		180
agtctcaatgt	ttccttccga	tlaccaagct	ttgctatggt	ctcccgccgg	tgaaaatcgt		240
gtctctgatg	ttttcggatc	cgacgagcta	ctctcagtag	cctgtctcgc	tttgtcgtcg		300
gaggcggtt	cgatcgctcc	ggagatccga	agaaatgatg	ataacgtttc	tctaactgtc		360
atcacaagcta	aaatcgcttg	tcattccttcg	tatcctcgct	tacttcaagc	ttacatcgat		420
tgccaaaaga	aacaggtcgg	agcaccaccg	gagatagcgt	gtttactaga	ggagattcaa		480
cgggagagtg	atgtttataa	gcaagaggtt	gttccttctt	cttgctttgg	agctgatcct		540
gagcttgatg	aattttatga	aacgtactgc	gatatattag	tgaatacaaa	atcgatcata		600
gcaagaccgt	ttgacgaggg	aacgtgtttc	ttgaacaaga	ttgagatgca	gtacaggaa		660
ctatgtactc	gtgtcggagt	tgccaggggg	gtttctgagg	atggtgtaat	atcatctgac		720
gaggaaactga	gtggaggtga	tcattgaggtg	gcagagggatg	ggagacaaag	atgtggaagac		780
cgggacacctca	aaagataggtt	Gctacgc	tttggagacc	gtattagtag	tttaaaagctt		840
gagttctcaa	agaagaagaa	gaaaggaaag	ttacctagag	aagcaagaca	agctcttctc		900
gatttgtgta	atctccatta	taagtggcct	taccctactg	aaggagataa	gatagcatta		960
gctgatgc	cggtgttaga	ccagaaacaa	atcaacaatt	ggtttataaa	ccaaaggaaa		1020
cgctattgga	agccatcaga	gaatatgcct	tttgctatga	tgtagtattc	tagtggatca		1080
ttctttaccg	aggaatgaat	ttatttaccg	tatttattta	acgttactta	aaaagatgga		1140
tgatataattc	tgcttgcctt	tgccgacaat	caaaagaaaa	aagaaagaaa	agagtgaaag		1200
atgggacgca	caatgaatta	tgaattattc	actcactcac	atgtagtaga	aggaacaagg		1260
gaacaagtca	aaatgctttg	taactattat	tatcggtgaa	taaaaataac	ttcttttgtc		1320

(2) INFORMATION FOR SEQ ID NO:841:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..329

(D) OTHER INFORMATION: / Ceres Seq. ID 1568129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

Met	Asp	Gly	Met	Tyr	Asn	Phe	His	Ser	Ala	Gly	Asp	Tyr	Ser	Asp	Lys
1			5					10					15		
Ser	Val	Leu	Met	Met	Ser	Pro	Glu	Ser	Leu	Met	Phe	Pro	Ser	Asp	Tyr
			20					25					30		
Gln	Ala	Leu	Leu	Cys	Ser	Ser	Ala	Gly	Glu	Asn	Arg	Val	Ser	Asp	Val
			35					40					45		
Phe	Gly	Ser	Asp	Glu	Leu	Leu	Ser	Val	Ala	Val	Ser	Ala	Leu	Ser	Ser
			50					55					60		
Glu	Ala	Ala	Ser	Ile	Ala	Pro	Glu	Ile	Arg	Arg	Asn	Asp	Asp	Asn	Val
			65					70					75		
Ser	Leu	Thr	Val	Ile	Lys	Ala	Lys	Ile	Ala	Cys	His	Pro	Ser	Tyr	Pro
			85					90					95		
Arg	Leu	Leu	Gln	Ala	Tyr	Ile	Asp	Cys	Gln	Lys	Lys	Gln	Val	Gly	Ala
			100					105					110		
Pro	Pro	Glu	Ile	Ala	Cys	Leu	Leu	Glu	Glu	Ile	Gln	Arg	Glu	Ser	Asp
			115					120					125		
Val	Tyr	Lys	Gln	Glu	Val	Val	Pro	Ser	Ser	Cys	Phe	Gly	Ala	Asp	Pro
			130					135					140		
Glu	Leu	Asp	Glu	Phe	Met	Glu	Thr	Tyr	Cys	Asp	Ile	Leu	Val	Lys	Tyr
			145					150					155		
Lys	Ser	Asp	Leu	Ala	Arg	Pro	Phe	Asp	Glu	Ala	Thr	Cys	Phe	Leu	Asn
			165					170					175		
Lys	Ile	Glu	Met	Gln	Leu	Arg	Asn	Leu	Cys	Thr	Gly	Val	Glu	Ser	Ala
			180					185					190		

[illegible]

(2) INFORMATION FOR SEQ ID NO:842:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 326 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

{ix} FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..326

(D) OTHER INFORMATION: / Ceres Seq. ID 1568130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

Met	Tyr	Asn	Phe	His	Ser	Ala	Gly	Asp	Tyr	Ser	Asp	Lys	Ser	Val	Leu
1				5				10						15	
Met	Met	Ser	Pro	Glu	Ser	Leu	Met	Phe	Pro	Ser	Asp	Tyr	Gln	Ala	Leu
			20					25					30		
Leu	Cys	Ser	Ser	Ala	Gly	Glu	Asn	Arg	Val	Ser	Asp	Val	Phe	Gly	Ser
		35					40					45			
Asp	Glu	Leu	Leu	Ser	Val	Ala	Val	Ser	Ala	Leu	Ser	Ser	Glu	Ala	Ala
	50					55					60				
Ser	Ile	Ala	Pro	Glu	Ile	Arg	Arg	Asn	Asp	Asp	Asn	Val	Ser	Leu	Thr
65					70					75					80
Val	Ile	Lys	Ala	Lys	Ile	Ala	Cys	His	Pro	Ser	Tyr	Pro	Arg	Leu	Leu
				85					90					95	
Gln	Ala	Tyr	Ile	Asp	Cys	Gln	Lys	Lys	Gln	Val	Gly	Ala	Pro	Pro	Glu
			100					105					110		
Ile	Ala	Cys	Leu	Leu	Glu	Glu	Ile	Gln	Arg	Glu	Ser	Asp	Val	Tyr	Lys
		115					120					125			
Gln	Glu	Val	Val	Pro	Ser	Ser	Cys	Phe	Gly	Ala	Asp	Pro	Glu	Leu	Asp
		130				135					140				
Glu	Phe	Met	Glu	Thr	Tyr	Cys	Asp	Ile	Leu	Val	Lys	Tyr	Lys	Ser	Asp
145					150					155					160
Leu	Ala	Arg	Pro	Phe	Asp	Glu	Ala	Thr	Cys	Phe	Leu	Asn	Lys	Ile	Glu
				165					170					175	
Met	Gln	Leu	Arg	Asn	Leu	Cys	Thr	Gly	Val	Glu	Ser	Ala	Arg	Gly	Val
			180					185					190		
Ser	Glu	Asp	Gly	Val	Ile	Ser	Ser	Asp	Glu	Glu	Leu	Ser	Gly	Gly	Asp
		195					200					205			
His	Glu	Val	Ala	Glu	Asp	Gly	Arg	Gln	Arg	Cys	Glu	Asp	Arg	Asp	Leu
		210				215					220				
Lys	Asp	Arg	Leu	Leu	Arg	Lys	Phe	Gly	Ser	Arg	Ile	Ser	Thr	Leu	Lys
225					230					235					240
Leu	Glu	Phe	Ser	Lys	Lys	Lys	Lys	Gly	Lys	Lys	Leu	Pro	Arg	Glu	Ala

1	Met	Met	Ser	Pro	5	Glu	Ser	Leu	Met	Phe	Pro	Ser	Asp	Tyr	Gln	Ala	Leu
1	Leu	Cys	Ser	Ser	20	Ala	Gly	Glu	Asn	Arg	Val	Ser	Asp	Val	Phe	Gly	Ser
Asp	Glu	Leu	Leu	Ser	Val	Ala	Val	Ser	Ala	Ser	Ala	Leu	Ser	Ser	Glu	Ala	Ala
Ser	Ile	Ala	Pro	Glu	Ile	Arg	Arg	Asn	Asp	Asp	Asn	Val	Ser	Leu	Thr		
Val	Ile	Lys	Ala	Lys	Ile	Ala	Cys	His	Pro	Ser	Tyr	Pro	Arg	Leu	Leu		
65	Gln	Ala	Tyr	Ile	Asp	Cys	Gln	Lys	Lys	Gln	Val	Gly	Ala	Pro	Pro	Glu	
Ile	Ala	Cys	Leu	Leu	Glu	Glu	Ile	Gln	Arg	Glu	Ser	Asp	Val	Tyr	Lys		
Gln	Glu	Val	Val	Pro	Ser	Ser	Cys	Phe	Gly	Ala	Asp	Pro	Glu	Leu	Asp		
Glu	Phe	Met	Glu	Thr	Tyr	Cys	Asp	Ile	Leu	Val	Lys	Tyr	Lys	Ser	Asp		
Leu	Ala	Arg	Pro	Phe	Asp	Glu	Ala	Thr	Cys	Phe	Leu	Asn	Lys	Ile	Glu		
145	Met	Gln	Leu	Arg	Asn	Leu	Cys	Thr	Gly	Val	Glu	Ser	Ala	Arg	Gly	Val	
Ser	Glu	Asp	Gly	Val	Ile	Ser	Ser	Asp	Glu	Glu	Leu	Ser	Gly	Gly	Asp		
His	Glu	Val	Ala	Glu	Asp	Gly	Arg	Gln	Arg	Cys	Glu	Asp	Arg	Asp	Leu		
Lys	Asp	Arg	Leu	Leu	Arg	Lys	Phe	Gly	Ser	Arg	Ile	Ser	Thr	Leu	Lys		
Leu	Glu	Phe	Ser	Lys	Lys	Lys	Lys	Lys	Gly	Lys	Leu	Pro	Arg	Glu	Ala		
225	Arg	Gln	Ala	Leu	Leu	Asp	Trp	Trp	Asn	Leu	Ala	Asp	Ala	Thr	Gly	Leu	Asp
Arg	Gln	Ala	Leu	Leu	Asp	Trp	Trp	Asn	Leu	Ala	Asp	Ala	Thr	Gly	Leu	Asp	
Pro	Thr	Glu	Gly	Asp	Lys	Ile	Ala	Leu	Ala	Asp	Ala	Thr	Gly	Leu	Asp		
Gln	Lys	Gln	Ile	Asn	Asn	Trp	Phe	Ile	Asn	Gln	Arg	Lys	Arg	His	Trp		
Lys	Pro	Ser	Glu	Asn	Met	Pro	Phe	Ala	Met	Met	Asp	Asp	Ser	Ser	Gly		

Ser Phe Phe Thr Glu Glu
305 310

(2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

tctctatggt	gtagttcttg	tacagttggc	tctcttttca	agaatcgctcg	cggttgaccc	60
ccgtgcctct	ccgatcaact	tccattctct	ttaaagtacg	agagattcat	caaggaacag	120
ctcattaaag	ccatggcctc	gaaagaggtt	tctttttcct	tctgttgtga	ttgtcattgt	180
tggtggaatc	gtggcggttt	cttatcagtc	caagttgaaa	ccacctccgc	cgaagctatg	240
tggtctctcc	ggtggtccac	cgatcacagc	gccgcggata	aagcttcaag	atggggaggta	300
tttggcttcc	aaagagcatg	gaattccaag	agagaaagct	aaccgcaaaa	tcgtcttcat	360
ccatggatcc	gattgttgtg	gacacgatgc	cgttttcgcc	actctgcttt	ctccggattt	420
agtagaggaa	ctaggtgtat	atatggttcc	attcgacaga	ccgggctatt	gtgagagtga	480
tcgcgaccca	agtctgtacc	cgcgaaagct	ggtttcggat	attgaagagc	tagctgatca	540
gttgagtcta	ggatcgaaat	tttatgtgct	cggtgtactc	atggggaggac	aagcagcatg	600
gggatgtctt	aaatacattc	ctcataggtt	agccggagta	acactagtgt	ctccagtggg	660
taactattat	tgggaagata	tacctttgaa	cgttttccact	gaaggtttta	actttcaaca	720
aaagagagat	caattggcag	ttcgtgttgc	tcactatact	ctctgggtta	ttctatttgtg	780
gaacacacaa	aaatGgttcc	ctggttcgag	tattgcaaac	cgagatcaca	gtctcttgcc	840
acagccggat	aaagatatca	tttcgaagct	tggtttcttc	aggaaaccac	attgggcaga	900
ggtaaggcag	caaggaatac	atgagagtat	taaccgtgac	atgatcggtt	gttttgggaa	960
ctgggaattt	gatcctttag	acctcgagaa	tccgtttttg	aataaggaag	gtctctgtgc	1020
tttgggcaca	ggagatgagg	acatgttagt	acctgcgaag	ctgcagcggtt	acctttgtca	1080
tcagcttcca	tgggttcact	atcatgaggt	tccgagaagt	ggccactctt	tcacatcac	1140
taaaggtgta	gttgatgaca	ttgtaaaagt	gctcttaacc	tccggtgtaa	gagcatctag	1200
agttgttatt	tgatcattgt	tagcttccaa	aaactctgaa	aaaaatcccc	aaaaaataca	1260
cggtacacaa	agagttatgt	actagtata	tttgacagca	tcgtagttaa	tt	

(2) INFORMATION FOR SEQ ID NO:845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..372
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

Met	Thr	Arg	Asp	Ser	Ser	Arg	Asn	Ser	Ser	Leu	Lys	Pro	Trp	Pro	Arg
1			5				10				15				
Lys	Ser	Phe	Leu	Phe	Pro	Ser	Val	Val	Ile	Val	Ile	Val	Gly	Ile	Ile
			20				25					30			
Val	Ala	Phe	Thr	Tyr	Gln	Ser	Lys	Leu	Lys	Pro	Pro	Pro	Pro	Lys	Leu
			35				40				45				
Cys	Gly	Ser	Ser	Gly	Gly	Pro	Pro	Ile	Thr	Ala	Pro	Arg	Ile	Lys	Leu
			50				55				60				
Gln	Asp	Gly	Arg	Tyr	Leu	Ala	Tyr	Lys	Glu	His	Gly	Leu	Pro	Arg	Glu
			65				70				75				80
Lys	Ala	Asn	Arg	Lys	Ile	Val	Phe	Ile	His	Gly	Ser	Asp	Cys	Cys	Arg
			85				90				95				
His	Asp	Ala	Val	Phe	Ala	Thr	Leu	Leu	Ser	Pro	Asp	Leu	Val	Glu	Glu

Met	Val	Ser	Phe	Asp	Arg	Pro	Gly	Tyr	Cys	Glu	Ser	Asp	Pro	His	Pro
1				5					10					15	
Ser	Arg	Thr	Pro	Arg	Ser	Leu	Val	Ser	Asp	Ile	Glu	Glu	Leu	Ala	Asp
			20					25					30		
Gln	Leu	Ser	Leu	Gly	Ser	Lys	Phe	Tyr	Val	Leu	Gly	Tyr	Ser	Met	Gly
		35					40					45			
Gly	Gln	Ala	Ala	Trp	Gly	Cys	Leu	Lys	Tyr	Ile	Pro	His	Arg	Leu	Ala
	50					55					60				
Gly	Val	Thr	Leu	Val	Ala	Pro	Val	Val	Asn	Tyr	Tyr	Trp	Lys	Asn	Leu
65					70				75					80	
Pro	Leu	Asn	Val	Ser	Thr	Glu	Gly	Phe	Asn	Phe	Gln	Gln	Lys	Arg	Asp
			85						90					95	
Gln	Leu	Ala	Val	Arg	Val	Ala	His	Tyr	Thr	Pro	Trp	Leu	Ile	Tyr	Trp
			100					105					110		

Trp	Asn	Thr	Gln	Lys	Trp	Phe	Pro	Gly	Ser	Ser	Ile	Ala	Asn	Arg	Asp
	115						120					125			
His	Ser	Leu	Leu	Ala	Gln	Pro	Asp	Lys	Asp	Ile	Ile	Ser	Lys	Leu	Gly
	130					135					140				
Ser	Ser	Arg	Lys	Pro	His	Trp	Ala	Glu	Val	Arg	Gln	Gln	Gly	Ile	His
	145				150					155					160
Glu	Ser	Ile	Asn	Arg	Asp	Met	Ile	Val	Gly	Phe	Gly	Asn	Trp	Glu	Phe
			165						170					175	
Asp	Pro	Leu	Asp	Leu	Glu	Asn	Pro	Phe	Leu	Asn	Lys	Glu	Gly	Ser	Val
			180					185					190		
His	Leu	Trp	Gln	Gly	Asp	Glu	Asp	Met	Leu	Val	Pro	Ala	Lys	Leu	Gln
		195					200					205			
Arg	Tyr	Leu	Ala	His	Gln	Leu	Pro	Trp	Val	His	Tyr	His	Glu	Val	Pro
	210					215					220				
Arg	Ser	Gly	His	Phe	Phe	His	Tyr	Thr	Lys	Gly	Val	Val	Asp	Asp	Ile
	225				230					235					240
Val	Lys	Ser	Leu	Leu	Thr	Ser	Gly	Val	Arg	Ala	Ser	Arg	Val	Cys	Ile
			245					250						255	

(2) INFORMATION FOR SEQ ID NO:847:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..210

(D) OTHER INFORMATION: / Ceres Seq. ID 1568155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

Met	Gly	Gly	Gln	Ala	Ala	Trp	Gly	Cys	Leu	Lys	Tyr	Ile	Pro	His	Arg
1			5					10					15		
Leu	Ala	Gly	Val	Thr	Leu	Val	Ala	Pro	Val	Val	Asn	Tyr	Tyr	Trp	Lys
			20				25					30			
Asn	Leu	Pro	Leu	Asn	Val	Ser	Thr	Glu	Gly	Phe	Asn	Phe	Gln	Gln	Lys
		35				40					45				
Arg	Asp	Gln	Leu	Ala	Val	Arg	Val	Ala	His	Tyr	Thr	Pro	Trp	Leu	Ile
	50				55					60					
Tyr	Trp	Trp	Asn	Thr	Gln	Lys	Trp	Phe	Pro	Gly	Ser	Ser	Ile	Ala	Asn
	65			70				75					80		
Arg	Asp	His	Ser	Leu	Ala	Gln	Pro	Asp	Lys	Asp	Ile	Ile	Ser	Lys	
		85					90					95			
Leu	Gly	Ser	Ser	Arg	Lys	Pro	His	Trp	Ala	Glu	Val	Arg	Gln	Gln	Gly
		100					105					110			
Ile	His	Glu	Ser	Ile	Asn	Arg	Asp	Met	Ile	Val	Gly	Phe	Gly	Asn	Trp
	115					120					125				
Glu	Phe	Asp	Pro	Leu	Asp	Leu	Glu	Asn	Pro	Phe	Leu	Asn	Lys	Glu	Gly
	130					135					140				
Ser	Val	His	Leu	Trp	Gln	Gly	Asp	Glu	Asp	Met	Leu	Val	Pro	Ala	Lys
	145				150					155					160
Leu	Gln	Arg	Tyr	Leu	Ala	His	Gln	Leu	Pro	Trp	Val	His	Tyr	His	Glu
			165						170				175		
Val	Pro	Arg	Ser	Gly	His	Phe	Phe	His	Tyr	Thr	Lys	Gly	Val	Val	Asp
		180					185					190			
Asp	Ile	Val	Lys	Ser	Leu	Leu	Thr	Ser	Gly	Val	Arg	Ala	Ser	Arg	Val
		195					200					205			
Cys	Ile														
	210														

(2) INFORMATION FOR SEQ ID NO:848:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1261
(D) OTHER INFORMATION: / Ceres Seq. ID 1568160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

gaaaacccaaa	ttaggggtttt	taatttcocag	attgttttgt	ttatttgaat	aaatctccgc	60
aagtttcaat	taggttgcaa	aaatcgaga	aMattttctt	cgattccaaa	aaatgggaa	120
aaattttgtt	cttcacttcc	gcttctgagg	ttgtgggagg	acaatcatca	tcacgatcac	180
gtaaaagaa	aagtgatgaa	gggatgatca	agtatggttt	tagtctagt	aaaggaaaa	240
ctaaccatcc	aatggaagat	tatcatgttg	ctaactttat	caacatccaa	gaccatgaat	300
tgggtctttt	tgtctattat	gatggtcata	tgggtgatag	tgtccctgct	tacttcaga	360
aacgtctctt	ctccaatctc	cttaaggagg	gagagtgttg	ggttgatcct	cgaaggtcta	420
ttgcaaaagc	ttatgagaag	acggaagcga	ttctatcgaa	tagttctgac	ttgggtcgtg	480
gtggtttctac	tgctgtgact	gctatattga	ttaatgggag	aaagtgttgg	atagctaatg	540
ttggtgattc	acgaagctgtt	ctttctaatg	gtggcgctat	aacgcagatg	agtcacagtc	600
atgagcctcg	tactgaaaag	tcgagtattg	aagatagagg	tggattttga	tcacatctac	660
caggtgatgt	tctctgggtg	aatggtccat	tagctgtgtc	tcgtgctttt	ggagataaag	720
gacttaagac	acacttgagt	tcagagcctg	acataaaaag	agctactgta	gatagccaga	780
cagatgttct	ctctctggct	agtgatggca	tcctggaagg	gatgacaaat	gaagagccaa	840
tggagatagc	gagaagagtg	agaagatccac	agaaagcggc	aaaggaatta	acagctgaag	900
cattgagaag	agagagataa	gacgacatat	cttgtgtcgt	ggctcgattc	agatgacaaa	960
ctctctgaaa	ggatacttca	ggggagatgg	gttctctata	taataatttc	aatcaaaagt	1020
tcacatgagc	aaaaaagctg	gttttcaact	gatttcgact	tgatgatctt	gggtcggttt	1080
aggacctgtc	taagtttcaa	tttgtgatta	gctgcttctt	gctatagctt	atgtgcgttc	1140
gttgtgtaaa	ttgtgtgttt	taaagacgat	aagaaaaatga	acaaaaaagg	agtggggaat	1200
ggagttttgt	gggtgggtgat	gggggggttt	gttattataa	ttggttgatt	tgttatatYt	1260

(2) INFORMATION FOR SEQ ID NO:849:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..280
(D) OTHER INFORMATION: / Ceres Seq. ID 1568161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

Met	Gly	Lys	Phe	Cys	Cys	Phe	Thr	Ser	Ala	Ser	Glu	Val	Val	Gly	Gly
1				5						10				15	
Gln	Ser	Ser	Ser	Arg	Ser	Gly	Lys	Gly	Arg	Ser	Asp	Glu	Gly	Met	Ile
			20					25					30		
Lys	Tyr	Gly	Phe	Ser	Leu	Val	Lys	Gly	Lys	Ala	Asn	His	Pro	Met	Glu
			35				40					45			
Asp	Tyr	His	Val	Ala	Asn	Phe	Ile	Asn	Ile	Gln	Asp	His	Glu	Leu	Gly
			50				55				60				
Leu	Phe	Ala	Ile	Tyr	Asp	Gly	His	Met	Gly	Asp	Ser	Val	Pro	Ala	Tyr
			65				70				75			80	
Leu	Gln	Lys	Arg	Leu	Phe	Ser	Asn	Ile	Leu	Lys	Glu	Gly	Glu	Phe	Trp
			85					90					95		
Val	Asp	Pro	Arg	Arg	Ser	Ile	Ala	Lys	Ala	Tyr	Glu	Lys	Thr	Glu	Ala
			100					105					110		
Ile	Leu	Ser	Asn	Ser	Ser	Asp	Leu	Gly	Arg	Gly	Gly	Ser	Thr	Ala	Val
			115				120						125		

Thr Ala Ile Leu Ile Asn Gly Arg Lys Leu Trp Ile Ala Asn Val Gly
130 135 140
Asp Ser Arg Ala Val Leu Ser His Gly Gly Ala Ile Thr Gln Met Ser
145 150 155 160
Thr Asp His Glu Pro Arg Thr Glu Arg Ser Ser Ile Glu Asp Arg Gly
165 170 175
Gly Phe Val Ser Asn Leu Pro Gly Asp Val Pro Arg Val Asn Gly Gln
180 185 190
Leu Ala Val Ser Arg Ala Phe Gly Asp Lys Gly Leu Lys Thr His Leu
195 200 205
Ser Ser Glu Pro Asp Ile Lys Glu Ala Thr Val Asp Ser Gln Thr Asp
210 215 220
Val Leu Leu Leu Ala Ser Asp Gly Ile Trp Lys Val Met Thr Asn Glu
225 230 235
Glu Ala Met Glu Ile Ala Arg Arg Val Lys Asp Pro Gln Lys Ala Ala
245 250 255
Lys Glu Leu Thr Ala Glu Ala Leu Arg Arg Glu Ser Lys Asp Ile
260 265 270
Ser Cys Val Val Val Arg Phe Arg
275 280

(2) INFORMATION FOR SEQ ID NO:850:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..250

(D) OTHER INFORMATION: / Ceres Seq. ID 1568162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

Met Ile Lys Tyr Gly Phe Ser Leu Val Lys Gly Lys Ala Asn His Pro
1 5 10 15
Met Glu Asp Tyr His Val Ala Asn Phe Ile Asn Ile Gln Asp His Glu
20 25 30
Leu Gly Leu Phe Ala Ile Tyr Asp Gly His Met Gly Asp Ser Val Pro
35 40 45
Ala Tyr Leu Gln Lys Arg Leu Phe Ser Asn Ile Leu Lys Glu Gly Glu
50 55 60
Phe Trp Val Asp Pro Arg Arg Ser Ile Ala Lys Ala Tyr Glu Lys Thr
65 70 75 80
Glu Ala Ile Leu Ser Asn Ser Ser Asp Leu Gly Arg Gly Ser Thr
85 90 95
Ala Val Thr Ala Ile Leu Ile Asn Gly Arg Lys Leu Trp Ile Ala Asn
100 105 110
Val Gly Asp Ser Arg Ala Val Leu Ser His Gly Gly Ala Ile Thr Gln
115 120 125
Met Ser Thr Asp His Glu Pro Arg Thr Glu Arg Ser Ser Ile Glu Asp
130 135 140
Arg Gly Gly Phe Val Ser Asn Leu Pro Gly Asp Val Pro Arg Val Asn
145 150 155 160
Gly Gln Leu Ala Val Ser Arg Ala Phe Gly Asp Lys Gly Leu Lys Thr
165 170 175
His Leu Ser Ser Glu Pro Asp Ile Lys Glu Ala Thr Val Asp Ser Gln
180 185 190
Thr Asp Val Leu Leu Leu Ala Ser Asp Gly Ile Trp Lys Val Met Thr
195 200 205
Asn Glu Glu Ala Met Glu Ile Ala Arg Arg Val Lys Asp Pro Gln Lys
210 215 220
Ala Ala Lys Glu Leu Thr Ala Glu Ala Leu Arg Arg Glu Ser Lys Asp

(2) INFORMATION FOR SEO ID NO:851:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino ac

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: \lim

MOLECULE TYPE: peptide

(1x) FEATURE:

(1A) NAME:

(A) NAME/KEY: peptide
(B) LOCATION: 1 234

(D) OTHER INFORMATION

(D) OTHER INFORMATION: / Cefes Seq. ID 1568163
SEQUENCE DESCRIPTION: SEQ ID NO:851:

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:851:
Gaa Aca Taa Tta Gaa Gaa Gaa Gaa Gaa Gaa Gaa Gaa

[illegible]

(2) INFORMATION FOR SEO ID NO:852:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1128 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1 1128

(D) OTHER INFORMATION: / Ceres Seq. ID 1568176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

acacatacaa	gactctctct	acagaacgat	ttagatttaa	tccggaaaaa	gttcagtcag	60
tgacacataa	gttgaactcg	aacatgtgtc	ttcaaacact	atctctctct	tctctccaa	120
ttcacccgtt	ctatcttcac	cattcttcga	ttctcccttc	ttctgggtga	cccgaacaga	180
tttctcttca	ctatatacga	aggactcttc	cttcacgact	tctcttcgat	tatagtcttg	240

cagaaatttc	tgctagaggt	ttaccggcgt	tgaacaaagc	ttccttgaag	aagctaccaa	300
tcaaaggatc	tacottttctg	ctggggcgaga	gcttgttgat	ggttttctgct	caccacagct	360
tggcagcagc	agcagaaatc	ataaagcctt	aaccgattta	cgAagttgga	gagttatttg	420
aacttagtat	tcagctttct	tacttgctgt	tactactggg	gttgcttgga	gttggtactt	480
tctatgtgat	cogtcaagta	ctgttacgca	gagaactaga	cctctccgct	aaagaattgc	540
aggagcaagt	aaggagcgga	gatgcaaagt	caacagagct	ctttgagctt	ggcgagctga	600
tgttgaggaa	gtttttatcct	gcagccaaca	agtttttgca	acaagctatc	cagaaatggg	660
acgggtgatga	tcaagatcct	gctcaggtct	ataacgctct	tggaagtctg	tatgtacgag	720
aggataaact	tgacaaagga	attgctcagt	ttgaaatggc	ggtagaagctg	caaccgggtt	780
atgtaacagc	ttggaacaac	cttggggatg	cttatgagaa	gaagaaggag	ttgcctttgg	840
cattgaatgc	gtttgaagaa	gttttgttgt	ttgatccaaa	caataagggtg	gctcgccoty	900
ggcgagatgc	gttgaaggat	cgcgtgaagc	tttataaagg	gtttgtggct	gttaagctca	960
agaaacgggtg	acggctcaaa	caagatgcaa	actctgaacc	aagaacgggt	ggtctctctc	1020
ccctctgtgt	atttttttgg	tttggttaata	tgtatggaga	ttttgtgtta	atatgaaaat	1080
gaaaactttgt	tgttttttgt	aaccaataaa	atcagatggt	taaaactt		

(2) INFORMATION FOR SEQ ID NO:853:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 322 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..322

(D) OTHER INFORMATION: / Ceres Seq. ID 1568177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

Thr	Tyr	Lys	Thr	Leu	Leu	Thr	Glu	Arg	Phe	Arg	Phe	Asn	Arg	Glu	Lys
1			5					10						15	
Val	Gln	Ser	Val	Thr	Leu	Met	Phe	Glu	Ser	Asn	Met	Val	Leu	Gln	Thr
			20					25					30		
Leu	Ser	Ser	Ser	Pro	Pro	Ile	His	Arg	Leu	Tyr	Leu	His	His	Ser	
			35				40					45			
Gln	Ile	Leu	Pro	Ser	Ser	Gly	Ser	Pro	Ser	Lys	Ile	Ser	Leu	Gln	Ile
			50			55					60				
His	Gly	Arg	Thr	Leu	Ala	Ile	Arg	Ser	Phe	His	Asp	Tyr	Val	Phe	Ala
			65			70				75				80	
Glu	Ile	Ser	Ala	Arg	Gly	Leu	Pro	Ala	Leu	Asn	Lys	Ala	Ser	Leu	Lys
			85						90				95		
Lys	Leu	Pro	Ile	Lys	Gly	Ser	Thr	Phe	Leu	Leu	Gly	Gln	Ser	Leu	Leu
			100				105					110			
Met	Val	Ser	Ala	His	Pro	Gln	Leu	Ala	Ala	Ala	Ala	Glu	Ile	Ile	Lys
			115			120						125			
Pro	Glu	Pro	Ile	Tyr	Glu	Val	Gly	Glu	Leu	Phe	Glu	Leu	Ser	Ile	Gln
			130			135					140				
Leu	Ser	Tyr	Leu	Leu	Leu	Leu	Gly	Leu	Leu	Gly	Val	Gly	Thr	Phe	
			145			150				155				160	
Tyr	Val	Ile	Arg	Gln	Val	Leu	Val	Arg	Arg	Glu	Leu	Asp	Leu	Ser	Ala
			165						170					175	
Lys	Glu	Leu	Gln	Glu	Gln	Val	Arg	Ser	Gly	Asp	Ala	Ser	Ala	Thr	Glu
			180				185						190		
Leu	Phe	Glu	Gly	Ala	Val	Met	Leu	Arg	Lys	Phe	Tyr	Pro	Ala	Ala	
			195			200					205				
Asn	Lys	Phe	Leu	Gln	Gln	Ala	Ile	Gln	Lys	Trp	Asp	Gly	Asp	Asp	Gln
			210			215					220				
Asp	Leu	Ala	Gln	Val	Tyr	Asn	Ala	Leu	Gly	Val	Ser	Tyr	Val	Arg	Glu
			225			230				235				240	
Asp	Lys	Leu	Asp	Lys	Gly	Ile	Ala	Gln	Phe	Glu	Met	Ala	Val	Lys	Leu
			245						250					255	
Gln	Pro	Gly	Tyr	Val	Thr	Ala	Trp	Asn	Asn	Leu	Gly	Asp	Ala	Tyr	Glu
			260					265					270		

Lys	Lys	Lys	Glu	Leu	Pro	Leu	Ala	Leu	Asn	Ala	Phe	Glu	Glu	Val	Leu
	275						280					285			
Leu	Phe	Asp	Pro	Asn	Asn	Lys	Val	Ala	Arg	Pro	Xaa	Arg	Asp	Ala	Leu
	290					295					300				
Lys	Asp	Arg	Val	Lys	Leu	Tyr	Lys	Gly	Val	Val	Ala	Val	Lys	Ser	Lys
	305				310					315					320
Lys	Arg														

(2) INFORMATION FOR SEQ ID NO:854:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..300

(D) OTHER INFORMATION: / Ceres Seq. ID 1568178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

Met	Phe	Glu	Ser	Asn	Met	Val	Leu	Gln	Thr	Leu	Ser	Ser	Ser	Pro	
1				5					10					15	
Pro	Ile	His	Arg	Leu	Tyr	Leu	His	His	Ser	Gln	Ile	Leu	Pro	Ser	Ser
			20				25						30		
Gly	Ser	Pro	Ser	Lys	Ile	Ser	Leu	Gln	Ile	His	Gly	Arg	Thr	Leu	Ala
			35				40					45			
Ile	Arg	Ser	Phe	His	Asp	Tyr	Val	Phe	Ala	Glu	Ile	Ser	Ala	Arg	Gly
	50				55						60				
Leu	Pro	Ala	Leu	Asn	Lys	Ala	Ser	Leu	Lys	Lys	Leu	Pro	Ile	Lys	Gly
65				70					75					80	
Ser	Thr	Phe	Leu	Leu	Gly	Gln	Ser	Leu	Leu	Met	Val	Ser	Ala	His	Pro
			85						90					95	
Gln	Leu	Ala	Ala	Ala	Ala	Glu	Ile	Ile	Lys	Pro	Glu	Pro	Ile	Tyr	Glu
			100						105					110	
Val	Gly	Glu	Leu	Phe	Glu	Leu	Ser	Ile	Gln	Leu	Ser	Tyr	Leu	Leu	
	115						120					125			
Leu	Leu	Gly	Leu	Leu	Gly	Val	Gly	Thr	Phe	Tyr	Val	Ile	Arg	Gln	Val
	130				135						140				
Leu	Val	Arg	Arg	Glu	Leu	Asp	Leu	Ser	Ala	Lys	Glu	Leu	Gln	Glu	Gln
	145			150					155					160	
Val	Arg	Ser	Gly	Asp	Ala	Ser	Ala	Thr	Glu	Leu	Phe	Glu	Leu	Gly	Ala
			165					170						175	
Val	Met	Leu	Arg	Lys	Phe	Tyr	Pro	Ala	Ala	Asn	Lys	Phe	Leu	Gln	Gln
	180						185						190		
Ala	Ile	Gln	Lys	Trp	Asp	Gly	Asp	Asp	Gln	Asp	Leu	Ala	Gln	Val	Tyr
	195						200					205			
Asn	Ala	Leu	Gly	Val	Ser	Tyr	Val	Arg	Glu	Asp	Lys	Leu	Asp	Lys	Gly
	210				215						220				
Ile	Ala	Gln	Phe	Glu	Met	Ala	Val	Lys	Leu	Gln	Pro	Gly	Tyr	Val	Thr
225				230						235				240	
Ala	Trp	Asn	Asn	Leu	Gly	Asp	Ala	Tyr	Glu	Lys	Lys	Lys	Glu	Leu	Pro
			245						250					255	
Leu	Ala	Leu	Asn	Ala	Phe	Glu	Glu	Val	Leu	Leu	Phe	Asp	Pro	Asn	Asn
			260					265					270		
Lys	Val	Ala	Arg	Pro	Xaa	Arg	Asp	Ala	Leu	Lys	Asp	Arg	Val	Lys	Leu
	275						280					285			
Tyr	Lys	Gly	Val	Val	Ala	Val	Lys	Ser	Lys	Lys	Arg				
	290					295					300				

(2) INFORMATION FOR SEQ ID NO:855:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 295 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..295
(D) OTHER INFORMATION: / Ceres Seq. ID 1568179
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

Met	Val	Leu	Gln	Thr	Leu	Ser	Ser	Ser	Ser	Pro	Pro	Ile	His	Arg	Leu
1			5						10					15	
Tyr	Leu	His	His	Ser	Gln	Ile	Leu	Pro	Ser	Ser	Gly	Ser	Pro	Ser	Lys
			20				25						30		
Ile	Ser	Leu	Gln	Ile	His	Gly	Arg	Thr	Leu	Ala	Ile	Arg	Ser	Phe	His
			35				40					45			
Asp	Tyr	Val	Phe	Ala	Glu	Ile	Ser	Ala	Arg	Gly	Leu	Pro	Ala	Leu	Asn
	50					55				60					
Lys	Ala	Ser	Leu	Lys	Lys	Leu	Pro	Ile	Lys	Gly	Ser	Thr	Phe	Leu	Leu
65					70				75					80	
Gly	Gln	Ser	Leu	Leu	Met	Val	Ser	Ala	His	Pro	Gln	Leu	Ala	Ala	Ala
				85					90					95	
Ala	Glu	Ile	Ile	Lys	Pro	Glu	Pro	Ile	Tyr	Glu	Val	Gly	Glu	Leu	Phe
			100					105					110		
Glu	Leu	Ser	Ile	Gln	Leu	Ser	Tyr	Leu	Leu	Leu	Leu	Gly	Leu	Leu	
			115				120					125			
Gly	Val	Gly	Thr	Phe	Tyr	Val	Ile	Arg	Gln	Val	Leu	Val	Arg	Arg	Glu
	130					135					140				
Leu	Asp	Leu	Ser	Ala	Lys	Glu	Leu	Gln	Glu	Gln	Val	Arg	Ser	Gly	Asp
	145				150				155					160	
Ala	Ser	Ala	Thr	Glu	Leu	Phe	Glu	Leu	Gly	Ala	Val	Met	Leu	Arg	Lys
			165					170					175		
Phe	Tyr	Pro	Ala	Ala	Asn	Lys	Phe	Leu	Gln	Gln	Ala	Ile	Gln	Lys	Trp
			180				185						190		
Asp	Gly	Asp	Asp	Gln	Asp	Leu	Ala	Gln	Val	Tyr	Asn	Ala	Leu	Gly	Val
	195					200					205				
Ser	Tyr	Val	Arg	Glu	Asp	Lys	Leu	Asp	Lys	Gly	Ile	Ala	Gln	Phe	Glu
	210					215					220				
Met	Ala	Val	Lys	Leu	Gln	Pro	Gly	Tyr	Val	Thr	Ala	Trp	Asn	Asn	Leu
225					230					235				240	
Gly	Asp	Ala	Tyr	Glu	Lys	Lys	Lys	Glu	Leu	Pro	Leu	Ala	Leu	Asn	Ala
			245					250					255		
Phe	Glu	Glu	Val	Leu	Leu	Phe	Asp	Pro	Asn	Asn	Lys	Val	Ala	Arg	Pro
	260						265						270		
Xaa	Arg	Asp	Ala	Leu	Lys	Asp	Arg	Val	Lys	Leu	Tyr	Lys	Gly	Val	Val
	275					280						285			
Ala	Val	Lys	Ser	Lys	Lys	Arg									
	290				295										

(2) INFORMATION FOR SEQ ID NO:856:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1525 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1525
(D) OTHER INFORMATION: / Ceres Seq. ID 1568180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

gaatgctgct	tacctcatgt	gatgctcgta	tcattcccag	ggcaaggctca	cataagccct	60
ctctcttcgtc	toggaaagat	catgctctct	aaaggcttaa	togtcacctt	tgtatccaca	120

(2) INFORMATION FOR SEQ ID NO:857:

(A) LENGTH: 296 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..296

(D) OTHER INFORMATION: / Ceres Seq. ID 1568181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

1	Thr	Xaa	Ile	Pro	Ser	Phe	Leu	His	Pro	Ser	Ser	Pro	Leu	Ser	Ser
1	Ile	Gly	Gly	Thr	5	Leu	Gln	Ile	10	Lys	Arg	Leu	His	15	Pro
				20				25					30		
Ser	Val	Leu	Ile	Glu	Thr	Phe	Gln	Glu	Leu	Glu	Lys	Asp	Thr	Ile	Asp
		35				40						45			
His	Met	Ser	Gln	Leu	Cys	Pro	Gln	Val	Asn	Phe	Asn	Pro	Ile	Gly	Pro
	50					55				60					
Leu	Phe	Thr	Met	Ala	Lys	Thr	Ile	Arg	Ser	Asp	Ile	Lys	Gly	Asp	Ile
65					70					75				80	
Ser	Lys	Pro	Asp	Ser	Asp	Cys	Ile	Glu	Trp	Leu	His	Ser	Arg	Glu	Pro
				85					90					95	
Ser	Ser	Val	Val	Tyr	Ile	Ser	Phe	Gly	Thr	Leu	Ala	Phe	Leu	Lys	Gln
			100					105					110		
Asn	Gln	Ile	Asp	Glu	Ile	Ala	His	Gly	Ile	Leu	Asn	Ser	Gly	Leu	Ser
		115				120						125			
Cys	Leu	Trp	Val	Leu	Arg	Pro	Pro	Leu	Glu	Gly	Leu	Ala	Ile	Glu	Pro
	130					135				140					
His	Val	Leu	Pro	Leu	Glu	Leu	Glu	Glu	Lys	Gly	Lys	Ile	Val	Glu	Trp
145					150					155				160	
Cys	Gln	Gln	Glu	Lys	Xaa	Leu	Ala	His	Pro	Ala	Val	Ala	Cys	Phe	Leu
				165					170					175	
Ser	His	Cys	Gly	Trp	Asn	Ser	Thr	Met	Glu	Ala	Leu	Thr	Ser	Gly	Val
			180					185					190		
Pro	Val	Ile	Cys	Phe	Pro	Gln	Trp	Gly	Asp	Gln	Val	Thr	Asn	Ala	Val

	195		200		205
Tyr	Leu	Ile	Gly	Val	Phe
210					Lys
Ser	Asp	Glu	Arg	Ile	Val
225					Pro
Glu	Ala	Thr	Val	Gly	Glu
					230
Arg	Trp	Lys	Glu	Ala	Glu
					245
Glu	Arg	Asn	Phe	Gln	Glu
					260
Met	Thr	Asn	Ile	Asn	Asn
					275
					290
					295

(2) INFORMATION FOR SEQ ID NO:858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..247
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

Met	Ser	Gln	Leu	Cys	Pro	Gln	Val	Asn	Phe	Asn	Pro	Ile	Gly	Pro	Leu
1				5							10			15	
Phe	Thr	Met	Ala	Lys	Thr	Ile	Arg	Ser	Asp	Ile	Lys	Gly	Asp	Ile	Ser
				20						25			30		
Lys	Pro	Asp	Ser	Asp	Cys	Ile	Glu	Trp	Leu	His	Ser	Arg	Glu	Pro	Ser
				35				40				45			
Ser	Val	Val	Tyr	Ile	Ser	Phe	Gly	Thr	Leu	Ala	Phe	Leu	Lys	Gln	Asn
				50			55				60				
Gln	Ile	Asp	Glu	Ile	Ala	His	Gly	Ile	Leu	Asn	Ser	Gly	Leu	Ser	Cys
				65			70				75			80	
Leu	Trp	Val	Leu	Arg	Pro	Pro	Leu	Glu	Gly	Leu	Ala	Ile	Glu	Pro	His
				85					90				95		
Val	Leu	Pro	Leu	Glu	Leu	Glu	Glu	Lys	Gly	Lys	Ile	Val	Glu	Trp	Cys
				100				105					110		
Gln	Gln	Glu	Lys	Xaa	Leu	Ala	His	Pro	Ala	Val	Ala	Cys	Phe	Leu	Ser
				115			120					125			
His	Cys	Gly	Trp	Asn	Ser	Thr	Met	Glu	Ala	Leu	Thr	Ser	Gly	Val	Pro
				130			135				140				
Val	Ile	Cys	Phe	Pro	Gln	Trp	Gly	Asp	Gln	Val	Thr	Asn	Ala	Val	Tyr
				145			150			155				160	
Leu	Ile	Gly	Val	Phe	Lys	Thr	Gly	Leu	Arg	Leu	Ser	Arg	Gly	Ala	Ser
				165			170				175				
Asp	Glu	Arg	Ile	Val	Pro	Arg	Glu	Glu	Val	Ala	Glu	Arg	Leu	Leu	Glu
				180			185				190				
Ala	Thr	Val	Gly	Glu	Lys	Ala	Val	Glu	Leu	Arg	Glu	Asn	Ala	Arg	Arg
				195			200				205				
Trp	Lys	Glu	Glu	Ala	Glu	Ser	Ala	Val	Ala	Tyr	Gly	Gly	Thr	Ser	Glu
				210			215			220					
Arg	Asn	Phe	Gln	Glu	Phe	Val	Asp	Lys	Leu	Val	Asp	Val	Lys	Thr	Met
				225			230			235				240	
Thr	Asn	Ile	Asn	Asn	Val	Val									
				245											

(2) INFORMATION FOR SEQ ID NO:859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..229
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568183
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:
Met Ala Lys Thr Ile Arg Ser Asp Ile Lys Gly Asp Ile Ser Lys Pro
1 5 10 15
Asp Ser Asp Cys Ile Glu Trp Leu His Ser Arg Glu Pro Ser Ser Val
 20 25 30
Val Tyr Ile Ser Phe Gly Thr Leu Ala Phe Leu Lys Gln Asn Gln Ile
 35 40 45
Asp Glu Ile Ala His Gly Ile Leu Asn Ser Gly Leu Ser Cys Leu Trp
 50 55 60
Val Leu Arg Pro Pro Leu Glu Gly Leu Ala Ile Glu Pro His Val Leu
 65 70 75 80
Pro Leu Glu Leu Glu Glu Lys Gly Lys Ile Val Glu Trp Cys Gln Gln
 85 90 95
Glu Lys Xaa Leu Ala His Pro Ala Val Ala Cys Phe Leu Ser His Cys
 100 105 110
Gly Trp Asn Ser Thr Met Glu Ala Leu Thr Ser Gly Val Pro Val Ile
 115 120 125
Cys Phe Pro Gln Trp Gly Asp Gln Val Thr Asn Ala Val Tyr Leu Ile
 130 135 140
Gly Val Phe Lys Thr Gly Leu Arg Leu Ser Arg Gly Ala Ser Asp Glu
 145 150 155 160
Arg Ile Val Pro Arg Glu Glu Val Ala Glu Arg Leu Leu Glu Ala Thr
 165 170 175
Val Gly Glu Lys Ala Val Glu Leu Arg Glu Asn Ala Arg Arg Trp Lys
 180 185 190
Glu Glu Ala Glu Ser Ala Val Ala Tyr Gly Gly Thr Ser Glu Arg Asn
 195 200 205
Phe Gln Glu Phe Val Asp Lys Leu Val Asp Val Lys Thr Met Thr Asn
 210 215 220
Ile Asn Asn Val Val
225

(2) INFORMATION FOR SEQ ID NO:860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1295 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1295
(D) OTHER INFORMATION: / Ceres Seq. ID 1568184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

aaaacaaaaa	aacacagcct	ttgtttcgtt	ttcttcgcgt	ttcttcgcgt	ttcttccttc	60
tcgttttgat	tttcagattt	ttttaactcg	gtcgttgccg	tgacttcaaa	tttcttaaaa	120
gagagagaga	gagagagagg	agatagttca	gaaaatctgt	cagacttggg	atctttctcg	180
gcaatgcgac	gctttgtcgc	cgcgaaatcc	ctctcccgag	aggatacaac	ctttttgtca	240
ttctcttctt	cttcgcgtgac	gcggtttctc	aaggctcttc	ctctccggtc	agatccaaga	300
gatgtccgct	aattctcatc	ctcctaattc	caaaaacgct	ctctgtaalg	cagcgcgcgg	360
tgccgcgcgc	ggggtttgtt	cggtacggtt	tgtgtgtctc	cttgatgtta	taaaaacgag	420
gttttcaggt	catgggcgtc	ctaagctcgg	tgatgcaaac	atcaaaagta	gtctaatgtt	480
tggtcagctt	gagcagatct	tcaagagaga	agggatgcgt	ggcttatacc	gcggtctctc	540
ccctactgtc	atggctcttc	tctccaattg	ggccattttt	tttacaatgt	atgaccagct	600
caagagcttt	ctttgttcaa	atgatcacaa	actcagcggt	ggagctaacg	tattgctctg	660

ttcgggagct	ggagctgc	ctaccattgc	cacaaatcct	ctttgggtgc	tcaagactag	720
acttcagaca	caagggaatga	gagtggtgat	agtgccatag	aaaagcacat	tttctgcttt	780
aaggagaata	gcttatgagg	aggggaattcg	cggtattgtac	agtggtcttg	tcctcgactg	840
agctggtatc	agtcgatgtg	ccattcagtt	tcacacatat	gagatgatca	aagtgtactt	900
ggccaagaaa	ggtgataaat	cagtcgataa	cctcaatgct	cggtgatgtg	cagttgcctc	960
ttcgattgca	aagatatattg	catccacatt	aacttaccgc	cacgaggtag	tacgagctag	1020
gcttcaagag	caaggggacac	acagtgagaa	acgttactca	ggagtaagag	attgcaccaa	1080
gaaagtgttt	gagaaagatg	ggttcctctg	tttttacaga	ggCtgcgcga	cgaacttact	1140
gagacaaact	cctgcagcag	ttataacttt	cactagcttc	gaaatgggtg	atcgtttctt	1200
cgctactcat	atacctctctg	agcaaaagctc	tatactttaa	atccggtttt	ttttttttga	1260
tgatgatgac	gattaaaaagt	tatttttaca	caggt			

- (2) INFORMATION FOR SEQ ID NO:861:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
- (A) NAME/KEY: peptide
- (B) LOCATION: 1..312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

Met	Ser	Ala	Asn	Ser	His	Pro	Pro	Asn	Ser	Lys	Asn	Val	Leu	Cys	Asn
1			5					10					15		
Ala	Ala	Ala	Gly	Ala	Ala	Ala	Gly	Val	Ala	Ala	Thr	Phe	Val	Cys	
			20					25				30			
Pro	Leu	Asp	Val	Ile	Lys	Thr	Arg	Phe	Gln	Val	His	Gly	Leu	Pro	Lys
			35				40				45				
Leu	Gly	Asp	Ala	Asn	Ile	Lys	Gly	Ser	Leu	Ile	Val	Gly	Ser	Leu	Glu
			50			55					60				
Gln	Ile	Phe	Lys	Arg	Glu	Gly	Met	Arg	Gly	Leu	Tyr	Arg	Gly	Leu	Ser
			65		70				75					80	
Pro	Thr	Val	Met	Ala	Leu	Leu	Ser	Asn	Trp	Ala	Ile	Tyr	Phe	Thr	Met
			85					90						95	
Tyr	Asp	Gln	Leu	Lys	Ser	Phe	Leu	Cys	Ser	Asn	Asp	His	Lys	Leu	Ser
			100					105					110		
Val	Gly	Ala	Asn	Val	Leu	Ala	Ala	Ser	Gly	Ala	Gly	Ala	Ala	Thr	Thr
			115				120						125		
Ile	Ala	Thr	Asn	Pro	Leu	Trp	Val	Val	Lys	Thr	Arg	Leu	Gln	Thr	Gln
			130			135					140				
Gly	Met	Arg	Val	Gly	Ile	Val	Pro	Tyr	Lys	Ser	Thr	Phe	Ser	Ala	Leu
			145		150					155				160	
Arg	Arg	Ile	Ala	Tyr	Glu	Glu	Gly	Ile	Arg	Gly	Leu	Tyr	Ser	Gly	Leu
			165					170						175	
Val	Pro	Ala	Leu	Ala	Gly	Ile	Ser	His	Val	Ala	Ile	Gln	Phe	Pro	Thr
			180				185							190	
Tyr	Glu	Met	Ile	Lys	Val	Tyr	Leu	Ala	Lys	Lys	Gly	Asp	Lys	Ser	Val
			195				200					205			
Asp	Asn	Leu	Asn	Ala	Arg	Asp	Val	Ala	Val	Ala	Ser	Ser	Ile	Ala	Lys
			210			215					220				
Ile	Phe	Ala	Ser	Thr	Leu	Thr	Tyr	Pro	His	Glu	Val	Val	Arg	Ala	Arg
			225		230				235					240	
Leu	Gln	Glu	Gln	Gly	His	His	Ser	Glu	Lys	Arg	Tyr	Ser	Gly	Val	Arg
			245					250						255	
Asp	Cys	Ile	Lys	Lys	Val	Phe	Glu	Lys	Asp	Gly	Phe	Pro	Gly	Phe	Tyr
			260				265						270		
Arg	Gly	Cys	Ala	Thr	Asn	Leu	Leu	Arg	Thr	Thr	Pro	Ala	Ala	Val	Ile
			275				280					285			
Thr	Phe	Thr	Ser	Phe	Glu	Met	Val	His	Arg	Phe	Leu	Val	Thr	His	Ile
			290			295					300				

Pro Ser Glu Gln Ser Ser Ile Leu
305 310

(2) INFORMATION FOR SEQ ID NO:862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..241
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

Met	Arg	Gly	Leu	Tyr	Arg	Gly	Leu	Ser	Pro	Thr	Val	Met	Ala	Leu	Leu
1			5						10					15	
Ser	Asn	Trp	Ala	Ile	Tyr	Phe	Thr	Met	Tyr	Asp	Gln	Leu	Lys	Ser	Phe
		20						25					30		
Leu	Cys	Ser	Asn	Asp	His	Lys	Leu	Ser	Val	Gly	Ala	Asn	Val	Leu	Ala
		35					40					45			
Ala	Ser	Gly	Ala	Gly	Ala	Ala	Thr	Thr	Ile	Ala	Thr	Asn	Pro	Leu	Trp
	50					55					60				
Val	Val	Lys	Thr	Arg	Leu	Gln	Thr	Gln	Gly	Met	Arg	Val	Gly	Ile	Val
	65				70				75					80	
Pro	Tyr	Lys	Ser	Thr	Phe	Ser	Ala	Leu	Arg	Arg	Ile	Ala	Tyr	Glu	Glu
			85						90					95	
Gly	Ile	Arg	Gly	Leu	Tyr	Ser	Gly	Leu	Val	Pro	Ala	Leu	Ala	Gly	Ile
			100					105					110		
Ser	His	Val	Ala	Ile	Gln	Phe	Pro	Thr	Tyr	Glu	Met	Ile	Lys	Val	Tyr
		115					120					125			
Leu	Ala	Lys	Lys	Gly	Asp	Lys	Ser	Val	Asp	Asn	Leu	Asn	Ala	Arg	Asp
	130					135					140				
Val	Ala	Val	Ala	Ser	Ser	Ile	Ala	Lys	Ile	Phe	Ala	Ser	Thr	Leu	Thr
	145				150					155				160	
Tyr	Pro	His	Glu	Val	Val	Arg	Ala	Arg	Leu	Gln	Glu	Gln	Gly	His	His
			165						170					175	
Ser	Glu	Lys	Arg	Tyr	Ser	Gly	Val	Arg	Asp	Cys	Ile	Lys	Lys	Val	Phe
			180				185						190		
Glu	Lys	Asp	Gly	Phe	Pro	Gly	Phe	Tyr	Arg	Gly	Cys	Ala	Thr	Asn	Leu
		195					200					205			
Leu	Arg	Thr	Thr	Pro	Ala	Ala	Val	Ile	Thr	Phe	Thr	Ser	Phe	Glu	Met
	210					215					220				
Val	His	Arg	Phe	Leu	Val	Thr	His	Ile	Pro	Ser	Glu	Gln	Ser	Ser	Ile
	225				230					235					240
Leu															

(2) INFORMATION FOR SEQ ID NO:863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..229
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

Met	Ala	Leu	Leu	Ser	Asn	Trp	Ala	Ile	Tyr	Phe	Thr	Met	Tyr	Asp	Gln
1			5						10					15	
Leu	Lys	Ser	Phe	Leu	Cys	Ser	Asn	Asp	His	Lys	Leu	Ser	Val	Gly	Ala

20	25	30
Asn Val Leu Ala Ala Ser Gly Ala Gly Ala Ala Thr Thr Ile Ala Thr		
35	40	45
Asn Pro Leu Trp Val Val Lys Thr Arg Leu Gln Thr Gln Gly Met Arg		
50	55	60
Val Gly Ile Val Pro Tyr Lys Ser Thr Phe Ser Ala Leu Arg Arg Ile		
65	70	75
Ala Tyr Glu Glu Gly Ile Arg Gly Leu Tyr Ser Gly Leu Val Pro Ala		
85	90	95
Leu Ala Gly Ile Ser His Val Ala Ile Gln Phe Pro Thr Tyr Glu Met		
100	105	110
Ile Lys Val Tyr Leu Ala Lys Lys Gly Asp Lys Ser Val Asp Asn Leu		
115	120	125
Asn Ala Arg Asp Val Ala Val Ala Ser Ser Ile Ala Lys Ile Phe Ala		
130	135	140
Ser Thr Leu Thr Tyr Pro His Glu Val Val Arg Ala Arg Leu Gln Glu		
145	150	155
Gln Gly His His Ser Glu Lys Arg Tyr Ser Gly Val Arg Asp Cys Ile		
165	170	175
Lys Lys Val Phe Glu Lys Asp Gly Phe Pro Gly Phe Tyr Arg Gly Cys		
180	185	190
Ala Thr Asn Leu Leu Arg Thr Thr Pro Ala Ala Val Ile Thr Phe Thr		
195	200	205
Ser Phe Glu Met Val His Arg Phe Leu Val Thr His Ile Pro Ser Glu		
210	215	220
Gln Ser Ser Ile Leu		
225		

(2) INFORMATION FOR SEQ ID NO:864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1302
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

aaagtttggg	tatttattga	accgagtggt	ttctttcgtt	gactcgccca	ccatggaagc	60
tgaagtagcc	caagatatca	tcactgcgtg	agcttgaatc	tcgcgccttg	caactgcaact	120
tgggtctcac	aggcttggga	tcagaagcat	agtgctggaa	tcttctgagc	agctgagagc	180
aacagagatt	gcactttcat	tatatattaa	tgcttggaa	gccatggaag	ctctcggtat	240
ttctcagcat	attcgcagtc	tcggtgatcg	cttccaagga	tgggtgtcca	gaccatttc	300
tgccaggagt	cctcctaagg	aaatgttatt	tccagaatct	gaagaatatg	aggttcgatg	360
catacagagg	aagctcttgt	tagacgctct	agcgggcgaa	ttgcctcaag	ggaccatacg	420
gttctcatct	aagcttggtc	acatcgaaat	gtcgcgacac	tacaagatgg	ttcatctctc	480
cgacgggact	atacttaaaa	ccaagggttt	ggtaggggtg	gatggagtag	agtcagtgtg	540
tggttaagtgc	ctaggtctca	agaatccgtg	taaaacttcc	cgtgtagcaa	tcgcggggat	600
cgctcatttc	cagacagggc	acgaattagg	gagaagggtc	tttcagtttt	attggcaacgg	660
gtttcgtttc	ggtttcatct	catgtgacca	aaacactgtc	tactggttcc	taacccacac	720
ctctactgat	ttagataaga	aaaatcatca	gaagatcaaa	cagtttgtgc	tgaccaagat	780
caaaagacttt	cctgacaaca	tcaagagtat	cctggagacc	actgatcttg	atagtttggg	840
gatgaatcca	ctcatgtatc	gacctccctg	ggaaacttct	tgggcaaaac	attgcaaaaga	900
caacgtatgt	gttcgacggg	atgcacttca	cccaatgact	cctgatattg	gacaagggtg	960
ttgctcggcg	atggagagcg	gagttatctc	cgctcgttgt	ctcgggtgaag	caatgaaagc	1020
taagaatatg	aaagggtgaa	cagaagatga	gaacgagagt	tataggcgga	ttgagagatg	1080
tttgaagaag	tatgcaggat	cgagggaagt	gagaagcatt	gactcttata	ctacatcata	1140
tacagtaggt	ttcatacagc	agagcagagg	caagtggagt	acctttttat	gagacacagt	1200
catgtcctct	ttcctttctt	ggttgcKgtA	gYtgaaaaag	tctcatttca	actgtggaag	1260
acttagccat	gaatgattct	caatgagcaa	gcacaatgtt	ag		

(2) INFORMATION FOR SEQ ID NO:865:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 409 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..409

(D) OTHER INFORMATION: / Ceres Seq. ID 1568189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

Lys	Phe	Gly	Tyr	Leu	Leu	Asn	Arg	Val	Val	Ser	Phe	Val	Asp	Ser	Pro
1				5					10				15		
Thr	Met	Glu	Ala	Glu	Ser	Thr	Gln	Asp	Ile	Ile	Val	Gly	Ala	Gly	
		20					25					30			
Ile	Ser	Gly	Leu	Ala	Thr	Ala	Leu	Gly	Leu	His	Arg	Leu	Gly	Ile	Arg
		35					40					45			
Ser	Ile	Val	Leu	Glu	Ser	Ser	Glu	Gln	Leu	Arg	Ala	Thr	Gly	Phe	Ala
		50				55					60				
Leu	Ser	Leu	Tyr	Phe	Asn	Ala	Trp	Lys	Ala	Met	Glu	Ala	Leu	Gly	Ile
65				70					75					80	
Ser	Gln	His	Ile	Arg	Ser	Leu	Gly	Asp	Arg	Phe	Gln	Gly	Trp	Val	Val
		85						90						95	
Arg	Pro	Ile	Ser	Ala	Gly	Asp	Pro	Pro	Lys	Glu	Met	Leu	Phe	Pro	Glu
		100					105						110		
Ser	Glu	Gly	Tyr	Glu	Val	Arg	Cys	Ile	Gln	Arg	Lys	Leu	Leu	Leu	Asp
		115					120					125			
Ala	Leu	Ala	Gly	Glu	Leu	Pro	Gln	Gly	Thr	Ile	Arg	Phe	Ser	Ser	Lys
		130				135					140				
Leu	Val	His	Ile	Glu	Leu	Ser	Gly	His	Tyr	Lys	Met	Val	His	Leu	Ser
145					150				155					160	
Asp	Gly	Thr	Ile	Leu	Lys	Thr	Lys	Val	Leu	Val	Gly	Cys	Asp	Gly	Val
		165						170						175	
Lys	Ser	Val	Val	Gly	Lys	Trp	Leu	Gly	Phe	Lys	Asn	Pro	Val	Lys	Thr
		180					185						190		
Ser	Arg	Val	Ala	Ile	Arg	Gly	Ile	Ala	His	Phe	Gln	Thr	Gly	His	Glu
		195					200					205			
Leu	Gly	Arg	Arg	Phe	Phe	Gln	Phe	Tyr	Gly	Asn	Gly	Val	Arg	Ser	Gly
		210				215					220				
Phe	Ile	Ser	Cys	Asp	Gln	Asn	Thr	Val	Tyr	Trp	Phe	Leu	Thr	His	Thr
225					230				235					240	
Ser	Thr	Asp	Leu	Asp	Lys	Lys	Asn	His	Gln	Lys	Ile	Lys	Gln	Phe	Val
		245						250						255	
Leu	Thr	Lys	Ile	Lys	Asp	Leu	Pro	Asp	Asn	Ile	Lys	Ser	Ile	Leu	Glu
		260					265						270		
Thr	Thr	Asp	Leu	Asp	Ser	Leu	Val	Met	Asn	Pro	Leu	Met	Tyr	Arg	Pro
		275					280					285			
Pro	Trp	Glu	Leu	Leu	Trp	Ala	Asn	Ile	Ala	Lys	Asp	Asn	Val	Cys	Val
		290				295					300				
Ala	Gly	Asp	Ala	Leu	His	Pro	Met	Thr	Pro	Asp	Ile	Gly	Gln	Gly	Gly
305					310				315					320	
Cys	Ser	Ala	Met	Glu	Asp	Gly	Val	Ile	Leu	Ala	Arg	Cys	Leu	Gly	Glu
		325							330				335		
Ala	Met	Lys	Ala	Lys	Asn	Met	Lys	Gly	Glu	Thr	Glu	Asp	Glu	Asn	Glu
		340						345					350		
Ser	Tyr	Arg	Arg	Ile	Glu	Asp	Gly	Leu	Lys	Lys	Tyr	Ala	Gly	Ser	Arg
		355					360					365			
Lys	Trp	Arg	Ser	Ile	Asp	Leu	Ile	Thr	Thr	Ser	Tyr	Thr	Val	Gly	Phe
		370				375					380				
Ile	Gln	Gln	Ser	Arg	Gly	Lys	Trp	Met	Thr	Leu	Phe	Arg	Asp	Lys	Phe

385 390 395 400
Met Ser Ser Phe Leu Ser Trp Leu Xaa
405
(2) INFORMATION FOR SEQ ID NO:866:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 392 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..392
(D) OTHER INFORMATION: / Ceres Seq. ID 1568190
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:
Met Glu Ala Glu Ser Thr Gln Asp Ile Ile Ile Val Gly Ala Gly Ile
1 5 10 15
Ser Gly Leu Ala Thr Ala Leu Gly Leu His Arg Leu Gly Ile Arg Ser
20 25 30
Ile Val Leu Glu Ser Ser Glu Gln Leu Arg Ala Thr Gly Phe Ala Leu
35 40 45
Ser Leu Tyr Phe Asn Ala Trp Lys Ala Met Glu Ala Leu Gly Ile Ser
50 55 60
Gln His Ile Arg Ser Leu Gly Asp Arg Phe Gln Gly Trp Val Val Arg
65 70 75 80
Pro Ile Ser Ala Gly Asp Pro Pro Lys Glu Met Leu Phe Pro Glu Ser
85 90 95
Glu Glu Tyr Glu Val Arg Cys Ile Gln Arg Lys Leu Leu Leu Asp Ala
100 105 110
Leu Ala Gly Glu Leu Pro Gln Gly Thr Ile Arg Phe Ser Ser Lys Leu
115 120 125
Val His Ile Glu Leu Ser Gly His Tyr Lys Met Val His Leu Ser Asp
130 135 140
Gly Thr Ile Leu Lys Thr Lys Val Leu Val Gly Cys Asp Gly Val Lys
145 150 155 160
Ser Val Val Gly Lys Trp Leu Gly Phe Lys Asn Pro Val Lys Thr Ser
165 170 175
Arg Val Ala Ile Arg Gly Ile Ala His Phe Gln Thr Gly His Glu Leu
180 185 190
Gly Arg Arg Phe Phe Gln Phe Tyr Gly Asn Gly Val Arg Ser Gly Phe
195 200 205
Ile Ser Cys Asp Gln Asn Thr Val Tyr Trp Phe Leu Thr His Thr Ser
210 215 220
Thr Asp Leu Asp Lys Lys Asn His Gln Lys Ile Lys Gln Phe Val Leu
225 230 235
Thr Lys Ile Lys Asp Leu Pro Asp Asn Ile Lys Ser Ile Leu Glu Thr
245 250 255
Thr Asp Leu Asp Ser Leu Val Met Asn Pro Leu Met Tyr Arg Pro Pro
260 265 270
Trp Glu Leu Leu Trp Ala Asn Ile Ala Lys Asp Asn Val Cys Val Ala
275 280 285
Gly Asp Ala Leu His Pro Met Thr Pro Asp Ile Gly Gln Gly Gly Cys
290 295 300
Ser Ala Met Glu Asp Gly Val Ile Leu Ala Arg Cys Leu Gly Glu Ala
305 310 315 320
Met Lys Ala Lys Asn Met Lys Gly Glu Thr Glu Asp Glu Asn Glu Ser
325 330 335
Tyr Arg Arg Ile Glu Asp Gly Leu Lys Lys Tyr Ala Gly Ser Arg Lys
340 345 350
Trp Arg Ser Ile Asp Leu Ile Thr Thr Ser Tyr Thr Val Gly Phe Ile
355 360 365

Gln Gln Ser Arg Gly Lys Trp Met Thr Leu Phe Arg Asp Lys Phe Met
370 375 380
Ser Ser Phe Leu Ser Trp Leu Xaa
385 390

(2) INFORMATION FOR SEQ ID NO:867:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..335

(D) OTHER INFORMATION: / Ceres Seq. ID 1568191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

Met	Glu	Ala	Leu	Gly	Ile	Ser	Gln	His	Ile	Arg	Ser	Leu	Gly	Asp	Arg
1				5					10					15	
Phe	Gln	Gly	Trp	Val	Val	Arg	Pro	Ile	Ser	Ala	Gly	Asp	Pro	Pro	Lys
			20					25				30			
Glu	Met	Leu	Phe	Pro	Glu	Ser	Glu	Glu	Tyr	Glu	Val	Arg	Cys	Ile	Gln
		35					40					45			
Arg	Lys	Leu	Leu	Leu	Asp	Ala	Leu	Ala	Gly	Glu	Leu	Pro	Gln	Gly	Thr
		50				55					60				
Ile	Arg	Phe	Ser	Ser	Lys	Leu	Val	His	Ile	Glu	Leu	Ser	Gly	His	Tyr
65					70				75					80	
Lys	Met	Val	His	Leu	Ser	Asp	Gly	Thr	Ile	Leu	Lys	Thr	Lys	Val	Leu
			85						90					95	
Val	Gly	Cys	Asp	Gly	Val	Lys	Ser	Val	Val	Gly	Lys	Trp	Leu	Gly	Phe
			100					105					110		
Lys	Asn	Pro	Val	Lys	Thr	Ser	Arg	Val	Ala	Ile	Arg	Gly	Ile	Ala	His
			115				120					125			
Phe	Gln	Thr	Gly	His	Glu	Leu	Gly	Arg	Arg	Phe	Phe	Gln	Phe	Tyr	Gly
		130				135						140			
Asn	Gly	Val	Arg	Ser	Gly	Phe	Ile	Ser	Cys	Asp	Gln	Asn	Thr	Val	Tyr
145					150				155					160	
Trp	Phe	Leu	Thr	His	Thr	Ser	Thr	Asp	Leu	Asp	Lys	Lys	Asn	His	Gln
			165					170						175	
Lys	Ile	Lys	Gln	Phe	Val	Leu	Thr	Lys	Ile	Lys	Asp	Leu	Pro	Asp	Asn
			180					185					190		
Ile	Lys	Ser	Ile	Leu	Glu	Thr	Thr	Asp	Leu	Asp	Ser	Leu	Val	Met	Asn
			195				200					205			
Pro	Leu	Met	Tyr	Arg	Pro	Pro	Trp	Glu	Leu	Leu	Trp	Ala	Asn	Ile	Ala
			210			215					220				
Lys	Asp	Asn	Val	Cys	Val	Ala	Gly	Asp	Ala	Leu	His	Pro	Met	Thr	Pro
225					230				235					240	
Asp	Ile	Gly	Gln	Gly	Gly	Cys	Ser	Ala	Met	Glu	Asp	Gly	Val	Ile	Leu
			245						250					255	
Ala	Arg	Cys	Leu	Gly	Glu	Ala	Met	Lys	Ala	Lys	Asn	Met	Lys	Gly	Glu
			260				265						270		
Thr	Glu	Asp	Glu	Asn	Glu	Ser	Tyr	Arg	Arg	Ile	Glu	Asp	Gly	Leu	Lys
		275					280					285			
Lys	Tyr	Ala	Gly	Ser	Arg	Lys	Trp	Arg	Ser	Ile	Asp	Leu	Ile	Thr	Thr
		290				295					300				
Ser	Tyr	Thr	Val	Gly	Phe	Ile	Gln	Gln	Ser	Arg	Gly	Lys	Trp	Met	Thr
305					310					315				320	
Leu	Phe	Arg	Asp	Lys	Phe	Met	Ser	Ser	Phe	Leu	Ser	Trp	Leu	Xaa	
			325						330					335	

(2) INFORMATION FOR SEQ ID NO:868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1364 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1364
(D) OTHER INFORMATION: / Ceres Seq. ID 1568192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

cwywactct	ctctttctcc	ttagcttctc	cttcaaggtt	tttttgaaaa	gctgcaaat	60
tccatagcca	tggacactgc	taaatggcct	caggagtttg	ttgtgaagcc	aatgaacgag	120
atcgtgacaa	acacatgcct	aaaacaacag	tcgaatccct	cttctcctgc	tactctgtg	180
gaaaggaagg	caagaccgga	gaaagaccag	gctttgaact	gtccaagatg	caactcotta	240
aacaccaagt	tctgttacta	caacaactac	agcctgacgc	agcccaggta	ctttgtataa	300
gactgcagga	ggatattggc	cgcaGgtggt	tccttcagga	acatcccctg	cgggtggcgc	360
gtccgcaaga	acaaagagat	ttcttccaat	tcctcttctc	cttcaccctc	ttcgtctctt	420
ctttcaaga	aaactctttt	tgccaacaac	aacacgccta	cgctctctct	tcctcatctt	480
aaacctaa	tttgtgaagc	agccgctact	aaagtccaag	acttgacgtt	ttctcaaggg	540
tttggaacg	ccacagaggt	taaagatctc	aaactggcgt	tttctcaagg	gtttgggac	600
ggtcaccatc	atcacagatg	tatcccagag	tttctgcaag	tagtaccacg	cagcagtagt	660
aagaacaacc	cactgttctc	aaacttctcg	gctttggagc	ttttagggat	ctctagttcc	720
tctgcttctc	ctaactcaag	ccctgtcttc	atgtcttctc	caaatgtcca	tgattcatcg	780
gtatcacag	catcggggtt	tggtctgagt	taccacagt	ttcaagagtt	catgagacca	840
gctttgggat	tctctcttga	tggtggggat	cctctacgtc	aagaagaggg	gtccagtggt	900
actaataagt	gaagggcggt	gctgccattt	gagagcctcc	tcaaacctcc	agtttcatca	960
tcaagaccac	atagtgtggg	gaatgggcaat	ctgaagagag	ttaatgatga	gcgtagtgat	1020
catgaacatc	agaaagaaga	aggagaagct	gaccaatctg	ttgggttttg	gagtggtgat	1080
ttaagtgcgt	gtgcttctgc	tgctgcatct	ggtggtgggt	catggcaata	attatagatca	1140
tggaaccatc	ccatgagagt	ttttagaaca	aatgattaca	tttttcatcc	atgttttaaa	1200
aagatgagag	gggttaactat	ataatctggg	tacttactat	ttttagtctc	ttccttgggt	1260
ttccttctcc	ttttctaaaa	attattatta	actttgttgg	gttgggggat	gatactgtat	1320
gtatttagac	tctcttttaa	atcaatctca	gttgtagtt	acct		

(2) INFORMATION FOR SEQ ID NO:869:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 353 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..353
(D) OTHER INFORMATION: / Ceres Seq. ID 1568193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

Met	Asp	Thr	Ala	Lys	Trp	Pro	Gln	Glu	Phe	Val	Val	Lys	Pro	Met	Asn
1				5				10						15	
Glu	Ile	Val	Thr	Asn	Thr	Cys	Leu	Lys	Gln	Gln	Ser	Asn	Pro	Pro	Ser
			20					25					30		
Pro	Ala	Thr	Pro	Val	Glu	Arg	Lys	Ala	Arg	Pro	Glu	Lys	Asp	Gln	Ala
			35				40					45			
Leu	Asn	Cys	Pro	Arg	Cys	Asn	Ser	Leu	Asn	Thr	Lys	Phe	Cys	Tyr	Tyr
			50				55				60				
Asn	Asn	Tyr	Ser	Leu	Thr	Gln	Pro	Arg	Tyr	Phe	Cys	Lys	Asp	Cys	Arg
65				70				75						80	
Arg	Tyr	Trp	Thr	Ala	Gly	Gly	Ser	Leu	Arg	Asn	Ile	Pro	Val	Gly	Gly
			85				90							95	
Gly	Val	Arg	Lys	Asn	Lys	Arg	Ser	Ser	Ser	Asn	Ser	Ser	Ser	Ser	Ser
			100				105						110		
Pro	Ser	Ser	Ser	Ser	Ser	Lys	Lys	Pro	Leu	Phe	Ala	Asn	Asn	Asn	
			115				120					125			
Thr	Pro	Thr	Pro	Pro	Leu	Pro	His	Leu	Asn	Pro	Lys	Ile	Gly	Glu	Ala

130	135	140
Ala Ala Thr Lys Val Gln Asp Leu Thr Phe Ser Gln Gly Phe Gly Asn		
145	150	155
Ala His Glu Val Lys Asp Leu Asn Leu Ala Phe Ser Gln Gly Phe Gly		
	165	170
Ile Gly His His His His Ser Ser Ile Pro Glu Phe Leu Gln Val Val		
	180	185
Pro Ser Ser Ser Met Lys Asn Asn Pro Leu Val Ser Thr Ser Ser Ala		
	195	200
Leu Glu Leu Leu Gly Ile Ser Ser Ser Ser Ala Ser Asn Ser Arg		
	210	215
Pro Ala Phe Met Ser Tyr Pro Asn Val His Asp Ser Ser Val Tyr Thr		
225	230	235
Ala Ser Gly Phe Gly Leu Ser Tyr Pro Gln Phe Gln Glu Phe Met Arg		
	245	250
Pro Ala Leu Gly Phe Ser Leu Asp Gly Gly Asp Pro Leu Arg Gln Glu		
	260	265
Glu Gly Ser Ser Gly Thr Asn Asn Gly Arg Pro Leu Leu Pro Phe Glu		
	275	280
Ser Leu Leu Lys Leu Pro Val Ser Ser Ser Ser Thr Asn Ser Gly Gly		
	290	295
Asn Gly Asn Leu Lys Glu Ile Asn Asp Glu Arg Ser Asp His Glu His		
305	310	315
Glu Lys Glu Glu Gly Glu Ala Asp Gln Ser Val Gly Phe Trp Ser Gly		
	325	330
Met Leu Ser Ala Gly Ala Ser Ala Ala Ala Ser Gly Gly Gly Ser Trp		
	340	345
		350
Gln		

(2) INFORMATION FOR SEQ ID NO:870:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..339

(D) OTHER INFORMATION: / Ceres Seq. ID 1568194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

Met	Asn	Glu	Ile	Val	Thr	Asn	Thr	Cys	Leu	Lys	Gln	Gln	Ser	Asn	Pro
1		5						10						15	
Pro	Ser	Pro	Ala	Thr	Pro	Val	Glu	Arg	Lys	Ala	Arg	Pro	Glu	Lys	Asp
		20						25						30	
Gln	Ala	Leu	Asn	Cys	Pro	Arg	Cys	Asn	Ser	Leu	Asn	Thr	Lys	Phe	Cys
		35					40						45		
Tyr	Tyr	Asn	Asn	Tyr	Ser	Leu	Thr	Gln	Pro	Arg	Tyr	Phe	Cys	Lys	Asp
	50				55					60					
Cys	Arg	Arg	Tyr	Trp	Thr	Ala	Gly	Gly	Ser	Leu	Arg	Asn	Ile	Pro	Val
	65				70				75					80	
Gly	Gly	Gly	Val	Arg	Lys	Asn	Lys	Arg	Ser	Ser	Ser	Asn	Ser	Ser	Ser
		85							90				95		
Ser	Ser	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Lys	Lys	Pro	Leu	Phe	Ala	Asn
	100						105						110		
Asn	Asn	Thr	Pro	Thr	Pro	Pro	Leu	Pro	His	Leu	Asn	Pro	Lys	Ile	Gly
	115						120					125			
Glu	Ala	Ala	Ala	Thr	Lys	Val	Gln	Asp	Leu	Thr	Phe	Ser	Gln	Gly	Phe
	130					135					140				
Gly	Asn	Ala	His	Glu	Val	Lys	Asp	Leu	Asn	Leu	Ala	Phe	Ser	Gln	Gly
145				150					155						160

Phe Gly Ile Gly His His His His Ser Ser Ile Pro Glu Phe Leu Gln
165 170 175
Val Val Pro Ser Ser Ser Met Lys Asn Asn Pro Leu Val Ser Thr Ser
180 185 190
Ser Ala Leu Glu Leu Leu Gly Ile Ser Ser Ser Ser Ala Ser Ser Asn
195 200 205
Ser Arg Pro Ala Phe Met Ser Tyr Pro Asn Val His Asp Ser Ser Val
210 215 220
Tyr Thr Ala Ser Gly Phe Gly Leu Ser Tyr Pro Gln Phe Gln Glu Phe
225 230 235 240
Met Arg Pro Ala Leu Gly Phe Ser Leu Asp Gly Gly Asp Pro Leu Arg
245 250 255
Gln Glu Glu Gly Ser Ser Gly Thr Asn Asn Gly Arg Pro Leu Leu Pro
260 265 270
Phe Glu Ser Leu Leu Lys Leu Pro Val Ser Ser Ser Ser Thr Asn Ser
275 280 285
Gly Gly Asn Gly Asn Leu Lys Glu Ile Asn Asp Glu Arg Ser Asp His
290 295 300
Glu His Glu Lys Glu Glu Gly Glu Ala Asp Gln Ser Val Gly Phe Trp
305 310 315 320
Ser Gly Met Leu Ser Ala Gly Ala Ser Ala Ala Ser Gly Gly Gly
325 330 335
Ser Trp Gln

(2) INFORMATION FOR SEQ ID NO:871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1398
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

atctaacttt	tccagataat	atattcaaaa	ttttacagag	aggaagaaga	agttcccgc	60
acttgtgaga	gactataaaa	ctatcagatc	tctctctctc	gctctcttca	gatcacaaa	120
ttttcgtttt	taggtgtctc	tcctcgatct	cggtttgtga	tcttcttttt	catcaatggc	180
gtctagtgtat	aaacaaacaa	gcccaaagcc	tccaccttca	ccgtctctct	tccgttaattc	240
caagttttgt	cagtcacaata	tgagaatttt	gatctcagga	ggagctggat	tcatgtggctc	300
tcacctgtgt	gataagctga	tgaaaaacga	aaagaatgag	gtgattgttg	ctgataaacta	360
tttcacgggt	tcaaaggaga	atctcaagaa	gtggattgtg	catccgagat	ttgaGgctta	420
tcctgcatga	tgctcacagag	Ccacttctga	tcgaggttga	tcagatttca	catcttgcat	480
gtctcgtctc	tccatgtctc	tacaagtaca	accctgtgaa	gacaatcaag	accaatgtca	540
ttggcacact	gaacatgcta	ggtcttgcca	agcgtgtttg	agcaaggatt	ttgttaact	600
caacctcaga	ggatatatga	gatctcttta	tccatcccca	gcccgagagc	tattggggag	660
atgtcaaccc	aattgggtgt	aggagctggt	atgatgaag	caagcgtgtt	gctgagacct	720
tgatgtttga	ctaccacagg	cagcatggaa	ttgaaatccg	cattgcccga	attcttaacaa	780
cttatgtgtc	acgcatgaac	attgatgatg	gacgtgtttg	aagcaacttc	attgctcaag	840
cactcogtgg	tgaggcattg	actgttcaga	aaccagggac	acagactcgc	agttctgtgt	900
atgtatctga	catgtttgat	ggacttatgc	gcctaatgga	aggagatgac	actgggtccca	960
tcaacatcgg	taacccagggt	gagttttaca	tggtggagtt	ggctgagaca	gtgaaagagc	1020
tgattaaccc	gagcatagag	ataaagatgg	ttgagaacac	accggatgat	ccaagacaga	1080
ggaagccatg	acatcacaaa	ggctaTaaga	agttttggga	tgggaaccac	aggtgaagct	1140
tcgtgaagcg	ctgcccctta	tggaagaaga	cttcaggcta	aggtcctggag	tccaagaaga	1200
ctaaaactcc	atcacccgat	atcacacgca	aacgtgaatg	ctacacataa	cccagttcta	1260
caactttcat	attctcttgt	gcaagtgtgt	tgtttccata	aatatgtttc	tactttccac	1320
agtcagaaat	tattctgata	gaaaaataaa	gattatgaac	gaatgctttt	tatatttaag	1380
gaagataaaa	attacttt					

(2) INFORMATION FOR SEQ ID NO:872:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 178 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..178
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568200
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:
Met Leu Gly Leu Ala Lys Arg Val Gly Ala Arg Ile Leu Leu Thr Ser
1 5 10 15
Thr Ser Glu Val Tyr Gly Asp Pro Leu Ile His Pro Gln Pro Glu Ser
 20 25 30
Tyr Trp Gly Asn Val Asn Pro Ile Gly Val Arg Ser Cys Tyr Asp Glu
 35 40 45
Gly Lys Arg Val Ala Glu Thr Leu Met Phe Asp Tyr His Arg Gln His
50 55 60
Gly Ile Glu Ile Arg Ile Ala Arg Ile Phe Asn Thr Tyr Gly Pro Arg
65 70 75 80
Met Asn Ile Asp Asp Gly Arg Val Val Ser Asn Phe Ile Ala Gln Ala
 85 90 95
Leu Arg Gly Glu Ala Leu Thr Val Gln Lys Pro Gly Thr Gln Thr Arg
 100 105 110
Ser Phe Cys Tyr Val Ser Asp Met Val Asp Gly Leu Met Arg Leu Met
 115 120 125
Glu Gly Asp Asp Thr Gly Pro Ile Asn Ile Gly Asn Pro Gly Glu Phe
130 135 140
Thr Met Val Glu Leu Ala Glu Thr Val Lys Glu Leu Ile Asn Pro Ser
145 150 155 160
Ile Glu Ile Lys Met Val Glu Asn Thr Pro Asp Asp Pro Arg Gln Arg
 165 170 175
Lys Pro

(2) INFORMATION FOR SEQ ID NO:873:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..122
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568201
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:
Met Phe Asp Tyr His Arg Gln His Gly Ile Glu Ile Arg Ile Ala Arg
1 5 10 15
Ile Phe Asn Thr Tyr Gly Pro Arg Met Asn Ile Asp Asp Gly Arg Val
 20 25 30
Val Ser Asn Phe Ile Ala Gln Ala Leu Arg Gly Glu Ala Leu Thr Val
 35 40 45
Gln Lys Pro Gly Thr Gln Thr Arg Ser Phe Cys Tyr Val Ser Asp Met
50 55 60
Val Asp Gly Leu Met Arg Leu Met Glu Gly Asp Asp Thr Gly Pro Ile
65 70 75 80
Asn Ile Gly Asn Pro Gly Glu Phe Thr Met Val Glu Leu Ala Glu Thr
 85 90 95
Val Lys Glu Leu Ile Asn Pro Ser Ile Glu Ile Lys Met Val Glu Asn
 100 105 110

Thr Pro Asp Asp Pro Arg Gln Arg Lys Pro
115 120

(2) INFORMATION FOR SEQ ID NO:874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

Met	Asn	Ile	Asp	Asp	Gly	Arg	Val	Val	Ser	Asn	Phe	Ile	Ala	Gln	Ala
1			5						10				15		
Leu	Arg	Gly	Glu	Ala	Leu	Thr	Val	Gln	Lys	Pro	Gly	Thr	Gln	Thr	Arg
		20						25				30			
Ser	Phe	Cys	Tyr	Val	Ser	Asp	Met	Val	Asp	Gly	Leu	Met	Arg	Leu	Met
		35					40				45				
Glu	Gly	Asp	Asp	Thr	Gly	Pro	Ile	Asn	Ile	Gly	Asn	Pro	Gly	Glu	Phe
		50				55					60				
Thr	Met	Val	Glu	Leu	Ala	Glu	Thr	Val	Lys	Glu	Leu	Ile	Asn	Pro	Ser
		65				70				75				80	
Ile	Glu	Ile	Lys	Met	Val	Glu	Asn	Thr	Pro	Asp	Asp	Pro	Arg	Gln	Arg
			85						90					95	

Lys Pro

(2) INFORMATION FOR SEQ ID NO:875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2350
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

tccaatcccc	tttttttttt	cgtttcgtcg	tttgcgtgtt	ttctctatcg	ctctcgttca	60
tctacgcgaat	ctctctcact	aggtacagtt	ttaaatgggt	aagaagaagt	cagacgagag	120
tgctgctacc	acaaagtgga	agccaagtgg	gaaagatgct	tcgaaagatt	ctaaaaaaga	180
gaaattgtca	gtctcggcta	tgcttgacgg	catggatcag	aaagatgata	aaccgaagaa	240
gggctcatca	ctagaaccca	aggtcgtccc	gaaatctaca	tcttacactg	atggcataga	300
tcttctctct	tctgatgaag	aagacgacgg	tgaatctgat	gaggaagaga	gacagaagga	360
agctaggagg	aagctgaaga	gtgaacaaag	gcaccttgag	atatctgtga	ctgataaagga	420
acaaaagaag	cgagaggcga	aagaaaagatt	agctcttcag	gctgcagagt	cggcaagagag	480
ggaggctatg	aaggacgac	atgatgcatt	cacggttgtt	attggaagca	agacctcagt	540
gcttgaagg	gacgacatgg	ctgatgcaaa	tggttaaggat	attaccatag	aatctttttc	600
tgatctcgt	cgaggtaaag	agcttttgaa	gaatgcttct	gtcaggattt	cacatggtaa	660
aaggtatggg	ttgatcgggc	caaacggaa	gggaaggtct	acactgttaa	agcttttagc	720
ttggaggaag	attccagtcg	caaaaatat	tgatgttctt	cttgttgagc	aagaggtggg	780
tggtgatgaa	aagagtgtct	tgaatgcagt	tgctctcgcc	aatgaagaat	tggttaagct	840
acgtgaagag	gctgaagctc	tgacagaagtc	gtctcttgga	gctgatggag	aaaatgttga	900
tggtgaggat	gatgatgata	ctggagaaaa	gcttgctgaa	ctgtatgaca	ggctgcagat	960
tttaggtcca	gatgctgctg	aagcacagcc	atccaaaatt	cttgcggggg	taggtttcac	1020
aaaAgaat	agcaagtgcg	gcgactcagt	ccttcagttg	tggtcggagg	atgcgaatat	1080
cattagctag	acgtctcttc	gtgcacaccta	cccttttgct	gttagatgaa	cccaactaac	1140
atcttgacct	gagagctgtt	ctatgggttag	aggagatttt	gtgtcgctgg	aagaagacac	1200
tagttgttgt	ttcacatgac	cgggacttcc	tcaacacagt	ctgcacggag	ataatacatc	1260

tccatgacca	gaatctccac	ttctaccgtg	gtaatttcga	tggtttttgaa	agcgatatg	1320
acgacgcgtcg	caaggagatg	aacaaaaaat	ttgatgtcta	cgacaaacag	atgaaagcag	1380
cgaagaggacg	tggaaccggg	ggctcaacagg	agaaggtaaa	ggacagggcc	aagtttactg	1440
ctgcaaaaaga	agcatcccaag	agtaagtcaa	agggcgaagac	agtggaatgaa	gaaggcccaag	1500
caccagaagc	tccaaggaag	tggagagatt	acagtgtggg	gttccacttc	ccagaaccac	1560
ctgagctcac	tctctctctt	ctgcagttaa	ttgaggttag	cttcagctat	cccaacaggg	1620
cagattttcag	actctcgaat	gttgatgtag	gtatcgatat	ggggacacgg	gttgcgatag	1680
ttgggccttaa	cggagcagga	aagtccactc	tattaaatct	tcttgcggga	gattttagttc	1740
caacagaggg	tgaaatgaga	agaagccaga	agctgaggat	tggcaggtat	tctcagcatt	1800
ttgttgacct	tttaacaaat	ggggaaacac	cggttcagta	tctccttcgt	cttcattcctg	1860
accaagaggg	atttagcaag	caagaggcag	tgcgcgcgaa	gctaggcaag	tttgggctac	1920
caagtccaaa	tcaacttatc	ccaattgcga	aattgtctag	aggacaaaag	gctagggttg	1980
tgttcacctc	gatctcaatg	tcaaaaccac	acattttgct	cctggacagag	ctacaaaatc	2040
acttagacat	gcagagtata	gatgccttgg	cggatgcact	agatgagttc	acaggtggag	2100
ttgtgttggg	gagtcacgag	tgcgagacta	tatcacgtgt	atgtgcggaa	gaggagaaga	2160
gtcgaatttg	ggttgtagaa	gacggaacag	tgaatttctt	cccaggcaca	tttgaagagt	2220
acaaagaaga	tctccaaaga	gaatatcaag	cagaagttag	ttagtgaaat	ttgtttgtta	2280
gctcttaagg	taaactcaaa	ctcctttatg	ttttataaca	aactcaaaaa	gttttggaca	2340
attttatttt						

(2) INFORMATION FOR SEQ ID NO:876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..331

(D) OTHER INFORMATION: / Ceres Seq. ID 1568214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

Met	Gly	Lys	Lys	Lys	Ser	Asp	Glu	Ser	Ala	Ala	Thr	Thr	Lys	Val	Lys
1				5						10				15	
Pro	Ser	Gly	Lys	Asp	Ala	Ser	Lys	Asp	Ser	Lys	Lys	Glu	Lys	Leu	Ser
			20					25					30		
Val	Ser	Ala	Met	Leu	Ala	Gly	Met	Asp	Gln	Lys	Asp	Asp	Lys	Pro	Lys
			35				40					45			
Lys	Gly	Ser	Ser	Ser	Arg	Thr	Lys	Ala	Ala	Pro	Lys	Ser	Thr	Ser	Tyr
			50				55					60			
Thr	Asp	Gly	Ile	Asp	Leu	Pro	Pro	Ser	Asp	Glu	Glu	Asp	Asp	Gly	Glu
65					70				75					80	
Ser	Asp	Glu	Glu	Glu	Arg	Gln	Lys	Glu	Ala	Arg	Arg	Lys	Leu	Lys	Ser
					85				90				95		
Glu	Gln	Arg	His	Leu	Glu	Ile	Ser	Val	Thr	Asp	Lys	Glu	Gln	Lys	Lys
			100					105					110		
Arg	Glu	Ala	Lys	Glu	Arg	Leu	Ala	Leu	Gln	Ala	Ala	Glu	Ser	Ala	Lys
			115				120					125			
Arg	Glu	Ala	Met	Lys	Asp	Asp	His	Asp	Ala	Phe	Thr	Val	Val	Ile	Gly
			130				135				140				
Ser	Lys	Thr	Ser	Val	Leu	Glu	Gly	Asp	Asp	Met	Ala	Asp	Ala	Asn	Val
145					150					155				160	
Lys	Asp	Ile	Thr	Ile	Glu	Ser	Phe	Ser	Val	Ser	Ala	Arg	Gly	Lys	Glu
			165						170					175	
Leu	Leu	Lys	Asn	Ala	Ser	Val	Arg	Ile	Ser	His	Gly	Lys	Arg	Tyr	Gly
			180					185					190		
Leu	Ile	Gly	Pro	Asn	Gly	Met	Gly	Lys	Ser	Thr	Leu	Glu	Lys	Leu	Leu
			195				200					205			
Ala	Trp	Arg	Lys	Ile	Pro	Val	Pro	Lys	Asn	Ile	Asp	Val	Leu	Leu	Val
			210				215					220			
Glu	Gln	Glu	Val	Val	Gly	Asp	Glu	Lys	Ser	Ala	Leu	Asn	Ala	Val	Val
225					230					235				240	

Ser Ala Asn Glu Glu Leu Val Lys Leu Arg Glu Glu Ala Glu Ala Leu
245 250 255
Gln Lys Ser Ser Ser Gly Ala Asp Gly Glu Asn Val Asp Gly Glu Asp
260 265 270
Asp Asp Asp Thr Gly Glu Lys Leu Ala Glu Leu Tyr Asp Arg Leu Gln
275 280 285
Ile Leu Gly Ser Asp Ala Ala Glu Ala Gln Ala Ser Lys Ile Leu Ala
290 295 300
Gly Leu Gly Phe Thr Lys Arg Tyr Ala Ser Cys Asp Ser Val Leu
305 310 315 320
Gln Trp Trp Leu Glu Asp Ala Asn Ile Ile Ser
325 330

(2) INFORMATION FOR SEQ ID NO:877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..412
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

Met Gln Val Arg Ala Thr Gln Ser Phe Ser Gly Gly Trp Arg Met Arg
1 5 10 15
Ile Ser Leu Ala Arg Ala Leu Phe Val Gln Pro Thr Leu Leu Leu Leu
20 25 30
Asp Glu Pro Thr Asn His Leu Asp Leu Arg Ala Val Leu Trp Leu Glu
35 40 45
Glu Tyr Leu Cys Arg Trp Lys Lys Thr Leu Val Val Val Ser His Asp
50 55 60
Arg Asp Phe Leu Asn Thr Val Cys Thr Glu Ile Ile His Leu His Asp
65 70 75 80
Gln Asn Leu His Phe Tyr Arg Gly Asn Phe Asp Gly Phe Glu Ser Gly
85 90 95
Tyr Glu Gln Arg Arg Lys Glu Met Asn Lys Lys Phe Asp Val Tyr Asp
100 105 110
Lys Gln Met Lys Ala Ala Lys Arg Thr Gly Asn Arg Gly Gln Gln Glu
115 120 125
Lys Val Lys Asp Arg Ala Lys Phe Thr Ala Ala Lys Glu Ala Ser Lys
130 135 140
Ser Lys Ser Lys Gly Lys Thr Val Asp Glu Glu Gly Pro Ala Pro Glu
145 150 155 160
Ala Pro Arg Lys Trp Arg Asp Tyr Ser Val Val Phe His Phe Pro Glu
165 170 175
Pro Thr Glu Leu Thr Pro Pro Leu Leu Gln Leu Ile Glu Val Ser Phe
180 185 190
Ser Tyr Pro Asn Arg Pro Asp Phe Arg Leu Ser Asn Val Asp Val Gly
195 200 205
Ile Asp Met Gly Thr Arg Val Ala Ile Val Gly Pro Asn Gly Ala Gly
210 215 220
Lys Ser Thr Leu Leu Asn Leu Leu Ala Gly Asp Leu Val Pro Thr Glu
225 230 235 240
Gly Glu Met Arg Arg Ser Gln Lys Leu Arg Ile Gly Arg Tyr Ser Gln
245 250 255
His Phe Val Asp Leu Leu Thr Met Gly Glu Thr Pro Val Gln Tyr Leu
260 265 270
Leu Arg Leu His Pro Asp Gln Glu Gly Phe Ser Lys Gln Glu Ala Val
275 280 285
Arg Ala Lys Leu Gly Lys Phe Gly Leu Pro Ser His Asn His Leu Ser

290	295	300
Pro Ile Ala Lys Leu Ser Arg Gly Gln Lys Ala Arg Val Val Phe Thr		
305	310	315
Ser Ile Ser Met Ser Lys Pro His Ile Leu Leu Leu Asp Glu Pro Thr		
	325	330
Asn His Leu Asp Met Gln Ser Ile Asp Ala Leu Ala Asp Ala Leu Asp		
	340	345
Glu Phe Thr Gly Gly Val Val Leu Val Ser His Asp Ser Arg Leu Ile		
	355	360
Ser Arg Val Cys Ala Glu Glu Glu Lys Ser Gln Ile Trp Val Val Glu		
	370	375
Asp Gly Thr Val Asn Phe Phe Pro Gly Thr Phe Glu Glu Tyr Lys Glu		
385	390	395
Asp Leu Gln Arg Glu Ile Lys Ala Glu Val Asp Glu		
	405	410

(2) INFORMATION FOR SEQ ID NO:878:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..398

(D) OTHER INFORMATION: / Ceres Seq. ID 1568216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

Met Arg Ile Ser Leu Ala Arg Ala Leu Phe Val Gln Pro Thr Leu Leu	
1	5
Leu Leu Asp Glu Pro Thr Asn His Leu Asp Leu Arg Ala Val Leu Trp	
	20
Leu Glu Glu Tyr Leu Cys Arg Trp Lys Lys Thr Leu Val Val Val Ser	
	35
His Asp Arg Asp Phe Leu Asn Thr Val Cys Thr Glu Ile Ile His Leu	
	50
His Asp Gln Asn Leu His Phe Tyr Arg Gly Asn Phe Asp Gly Phe Glu	
	65
Ser Gly Tyr Glu Gln Arg Arg Lys Glu Met Asn Lys Lys Phe Asp Val	
	85
Tyr Asp Lys Gln Met Lys Ala Ala Lys Arg Thr Gly Asn Arg Gly Gln	
	100
Gln Glu Lys Val Lys Asp Arg Ala Lys Phe Thr Ala Ala Lys Glu Ala	
	115
Ser Lys Ser Lys Ser Lys Gly Lys Thr Val Asp Glu Glu Gly Pro Ala	
	130
Pro Glu Ala Pro Arg Lys Trp Arg Asp Tyr Ser Val Val Phe His Phe	
	145
Pro Glu Pro Thr Glu Leu Thr Pro Pro Leu Leu Gln Leu Ile Glu Val	
	165
Ser Phe Ser Tyr Pro Asn Arg Pro Asp Phe Arg Leu Ser Asn Val Asp	
	180
Val Gly Ile Asp Met Gly Thr Arg Val Ala Ile Val Gly Pro Asn Gly	
	195
Ala Gly Lys Ser Thr Leu Leu Asn Leu Leu Ala Gly Asp Leu Val Pro	
	210
Thr Glu Gly Glu Met Arg Arg Ser Gln Lys Leu Arg Ile Gly Arg Tyr	
	225
Ser Gln His Phe Val Asp Leu Leu Thr Met Gly Glu Thr Pro Val Gln	
	245
Tyr Leu Leu Arg Leu His Pro Asp Gln Glu Gly Phe Ser Lys Gln Glu	
	260

Ala Val Arg Ala Lys Leu Gly Lys Phe Gly Leu Pro Ser His Asn His
275 280 285
Leu Ser Pro Ile Ala Lys Leu Ser Arg Gly Gln Lys Ala Arg Val Val
290 295 300
Phe Thr Ser Ile Ser Met Ser Lys Pro His Ile Leu Leu Leu Asp Glu
305 310 315 320
Pro Thr Asn His Leu Asp Met Gln Ser Ile Asp Ala Leu Ala Asp Ala
325 330 335
Leu Asp Glu Phe Thr Gly Gly Val Val Leu Val Ser His Asp Ser Arg
340 345 350
Leu Ile Ser Arg Val Cys Ala Glu Glu Glu Lys Ser Gln Ile Trp Val
355 360 365
Val Glu Asp Gly Thr Val Asn Phe Phe Pro Gly Thr Phe Glu Glu Tyr
370 375 380
Lys Glu Asp Leu Gln Arg Glu Ile Lys Ala Glu Val Asp Glu
385 390 395

(2) INFORMATION FOR SEQ ID NO:879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 919 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..919
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

aaaagaaga	aaaaaatgcc	ttcttttgc	tttgatctc	atcaccattt	ggcgaatcct	60
acagactgc	cqccgtactc	cgtcgaaatt	agcatcgacg	gtgactcttc	cgacttggat	120
ttctttgtc	aggtcgattt	agagtcgagg	ggtgtaccgg	cgccggagaa	acagctacat	180
tccggtgta	agaagaggag	aactaggagg	agaagaggga	ggaagaagaa	gaagaagaag	240
aaaggtgaa	gagattgcag	gatctgcat	cttcctttag	agactaacaa	agaagctgaa	300
gatgaagtg	aagaagaaga	agatgattct	gatgatgatg	aagatgaaga	agatgaagaa	360
gaagaagaag	aagaagaaga	atattatggt	ttgcctttgc	aattaggttg	ctcttgtaaa	420
ggtgatttg	gtgtgtctca	tagtaagttg	gctgagactt	ggtttaagat	caaaggaaac	480
atgacatgtg	agatatgcgg	cgcaatggct	ctaaAcgtgg	ctgggtgaaca	atctaaNtcc	540
ggagagcact	gcttctacac	attcacaagc	agctgcggga	caatctctaa	ctcagacaga	600
gccacagagg	atctggcatg	gtcgccctgt	tatgaacttc	ttacttgtct	ctatggtctt	660
cgctcttcgt	gtttcttgcc	tttttcaact	caaagtccct	aagtgaacag	ttttccattc	720
ctctctctct	ctctcttttcg	cccccccgca	cgagctcact	cttctcctgt	tcttgagccg	780
cttgcacatg	ctgaatacat	ccctcctgtt	gcttgattat	tcacacgttt	tgtagctgta	840
aaaaattggg	agtgttttag	ttgttgtaac	ttgtgagatt	tacattttgt	ataatatigt	900
ctctctgtcc	ggctctgtg					

(2) INFORMATION FOR SEQ ID NO:880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..271
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

Lys Arg Lys Lys Lys Met Pro Ser Phe Ala Phe Gly Ser His His His	
1 5 10	15
Leu Ala Asn Pro Thr Asp Ser Pro Pro Tyr Ser Val Glu Ile Ser Ile	
20 25 30	
Asp Gly Asp Ser Ser Asp Leu Asp Ser Leu Ser Gln Val Asp Leu Glu	

Ser	Gly		35						40				45				
Lys	Arg	Arg	Thr	Arg	Arg	Arg	Lys	Arg	His	Lys	Lys	Lys	Lys	Lys	Lys	Lys	80
Lys	Gly	Gly	Arg	Asp	Cys	Arg	Ile	Cys	His	Leu	Pro	Leu	Glu	Thr	Asn		
Lys	Glu	Ala	Glu	Asp	Glu	Asp	Glu	Glu	Glu	Glu	Asp	Asp	Ser	Asp	Asp		
Asp	Glu	Asp	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Tyr		
Tyr	Gly	Leu	Pro	Leu	Gln	Leu	Gly	Cys	Ser	Cys	Lys	Gly	Asp	Leu	Gly		
Val	Ala	His	Ser	Lys	Cys	Ala	Glu	Thr	Trp	Phe	Lys	Ile	Lys	Gly	Asn		
Met	Thr	Cys	Glu	Ile	Cys	Gly	Ala	Met	Ala	Leu	Asn	Val	Ala	Gly	Glu		
Gln	Ser	Xaa	Ser	Gly	Glu	His	Cys	Phe	Tyr	Thr	Phe	Thr	Ser	Ser	Cys		
Gly	Thr	Ile	Ser	Asn	Ser	Asp	Arg	Ala	Thr	Arg	Asn	Leu	Ala	Trp	Ser		
Pro	Cys	Tyr	Glu	Leu	Leu	Thr	Cys	Cys	Tyr	Gly	Leu	Arg	Leu	Arg	Cys		
Phe	Leu	Ala	Phe	Ser	Leu	Gln	Ser	Pro	Gln	Val	Lys	Arg	Phe	Pro	Ser		
Leu	Ser	Leu	Ser	Leu	Phe	Arg	Pro	Pro	Ala	Arg	Ala	His	Ser	Ser	Pro		
Val	Leu	Glu	Pro	Leu	Ala	Ile	Ala	Glu	Ser	Ile	Pro	Pro	Val	Ala			

(2) INFORMATION FOR SEQ ID NO:881:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..266

(D) OTHER INFORMATION: / Ceres Seq. ID 1568219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

Met	Pro	Ser	Phe	Ala	Phe	Gly	Ser	His	His	His	Leu	Ala	Asn	Pro	Thr
1				5					10					15	
Asp	Ser	Pro	Pro	Tyr	Ser	Val	Glu	Ile	Ser	Ile	Asp	Gly	Asp	Ser	Ser
			20					25					30		
Asp	Leu	Asp	Ser	Leu	Ser	Gln	Val	Asp	Leu	Glu	Ser	Gly	Gly	Val	Pro
		35					40					45			
Ala	Pro	Glu	Lys	Gln	Leu	His	Ser	Gly	Gly	Lys	Lys	Arg	Arg	Thr	Arg
	50					55				60					
Arg	Arg	Lys	Arg	Arg	Lys	Lys	Lys	Lys	Lys	Lys	Gly	Gly	Arg	Asp	
65				70					75					80	
Cys	Arg	Ile	Cys	His	Leu	Pro	Leu	Glu	Thr	Asn	Lys	Glu	Ala	Glu	Asp
			85					90						95	
Glu	Asp	Glu	Glu	Glu	Glu	Asp	Asp	Ser	Asp	Asp	Asp	Glu	Asp	Glu	Glu
		100					105					110			
Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Tyr	Tyr	Gly	Leu	Pro	Leu
		115				120						125			
Gln	Leu	Gly	Gly	Ser	Cys	Lys	Gly	Asp	Leu	Glu	Val	Ala	His	Ser	Lys
	130					135				140					
Cys	Ala	Glu	Thr	Trp	Phe	Lys	Ile	Lys	Gly	Asn	Met	Thr	Cys	Glu	Ile
145					150					155				160	

Cys Gly Ala Met Ala Leu Asn Val Ala Gly Glu Gln Ser Xaa Ser Gly
165 170 175
Glu His Cys Phe Tyr Thr Phe Thr Ser Ser Cys Gly Thr Ile Ser Asn
180 185 190
Ser Asp Arg Ala Thr Arg Asn Leu Ala Trp Ser Pro Cys Tyr Glu Leu
195 200 205
Leu Thr Cys Cys Tyr Gly Leu Arg Leu Arg Cys Phe Leu Ala Phe Ser
210 215 220
Leu Gln Ser Pro Gln Val Lys Arg Phe Pro Ser Leu Ser Leu Ser Leu
225 230 235 240
Phe Arg Pro Pro Ala Arg Ala His Ser Ser Pro Val Leu Glu Pro Leu
245 250 255
Ala Ile Ala Glu Ser Ile Pro Pro Val Ala
260 265

(2) INFORMATION FOR SEQ ID NO:882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1475
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

aaaatagaga	cctttcttta	acacagagaa	agagcctgag	agacaagtga	gaaacgcaac	60
aacaacacgc	aaagagagag	tcacaattcg	aaagagaaaa	agaatcaaat	tcctttcttc	120
tccttttttt	attttcaatt	attactttaa	tcttctttcc	cgctctctat	tcttctcttc	180
cttttagatc	aatacccggt	tagctttctt	cccatacgtc	tctccgttta	cgaccagtat	240
acagaggctg	gagctgggga	agaaaaggat	tgctatgga	gggagacgtc	ggaatagggt	300
tggtatgcc	gaataactatg	gatgggaagg	cgagtaattg	aaatggttta	gagaagactg	360
taccttcttg	ttgccttaag	gctatggcat	gtttactctga	ggaatgatct	aaagtgtcat	420
ccactgttgt	ttctgggtgg	ttttcggaac	ctcaccctcg	ctctgggaaa	aaaggcggca	480
aagcagtcct	tttcaacaac	ccatgtggc	caggagaagc	acactcactg	aaagtggaga	540
aagttctgtt	caaagacaag	tcggattttc	aggaagtctc	agtgttcgag	tcagccaagt	600
acggaaagg	gcttgttcta	gatgggatcg	tacagctgac	cgaaaaagat	gaatgtgc	660
atcaggagat	gatagcccat	ctgcttttat	gctctatata	ttccccataa	aatgttcttg	720
ttgttggtgg	aggtgatggg	gtgtgtcttc	gagagatttc	tcgccatagt	tctgttgagg	780
ttattgatat	ctgtgagata	gacaagatgg	ttatagatgt	gtctaagaag	ttcttccccg	840
agtttagcgt	tggttttgac	gatctctgtg	ttcaacttca	catgttgtag	gctgtgaggt	900
tcctccgtga	atccccgtga	gggaagtatg	atgccatcat	tgattgattc	tcagatcccc	960
taggtctctg	ctttgcgctt	gttgagaagc	ctttcttcga	gacactggct	agagcgttga	1020
agcctggggg	agttctttgt	aacatggcag	aaagtattgt	gctccatact	catcttattg	1080
aaatatatgt	ctccattttg	cgtaaaacal	tcaaaagtgt	tcactatgag	tgagcagcgt	1140
tcctccacata	tcacaagcgc	gtgattgggt	tgctctttgt	ctctactgaa	ggaccagcgt	1200
ttgacttcaa	gaacccaatc	aacctatttg	agaaactaga	cggtgcgatg	accocataaa	1260
gagaaatgaa	gttctataac	cttgatattc	acagagcccg	attgttgatt	cccaatttcc	1320
tcggcgagaga	agtatgttca	cttctgggtt	cttgacttct	gtttggctct	accataatcc	1380
tcataatcaa	cttttagaaa	ctttgaaga	ggaataataa	atcattgaag	gctttgtatc	1440
tcataagtta	ctcttttata	aaaagactta	tatttt			

(2) INFORMATION FOR SEQ ID NO:883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..359

(D) OTHER INFORMATION: / Ceres Seq. ID 1568231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:

Met	Glu	Gly	Asp	Val	Gly	Ile	Gly	Leu	Val	Cys	Gln	Asn	Thr	Met	Asp
1				5				10						15	
Gly	Lys	Ala	Ser	Asn	Gly	Asn	Gly	Leu	Glu	Lys	Thr	Val	Pro	Ser	Cys
				20				25					30		
Cys	Leu	Lys	Ala	Met	Ala	Cys	Leu	Pro	Glu	Asp	Asp	Ala	Lys	Cys	His
				35			40					45			
Ser	Thr	Val	Val	Ser	Gly	Trp	Phe	Ser	Glu	Pro	His	Pro	Arg	Ser	Gly
				50			55				60				
Lys	Lys	Gly	Gly	Lys	Ala	Val	Tyr	Phe	Asn	Asn	Pro	Met	Trp	Pro	Gly
65				70					75					80	
Glu	Ala	His	Ser	Leu	Lys	Val	Glu	Lys	Val	Leu	Phe	Lys	Asp	Lys	Ser
				85				90					95		
Asp	Phe	Gln	Glu	Val	Leu	Val	Phe	Glu	Ser	Ala	Thr	Tyr	Gly	Lys	Val
				100				105					110		
Leu	Val	Leu	Asp	Gly	Ile	Val	Gln	Leu	Thr	Glu	Lys	Asp	Glu	Cys	Ala
				115			120					125			
Tyr	Gln	Glu	Met	Ile	Ala	His	Leu	Pro	Leu	Cys	Ser	Ile	Ser	Ser	Pro
				130			135				140				
Lys	Asn	Val	Leu	Val	Val	Gly	Gly	Asp	Gly	Gly	Val	Leu	Arg	Glu	
145				150				155					160		
Ile	Ser	Arg	His	Ser	Ser	Val	Glu	Val	Ile	Asp	Ile	Cys	Glu	Ile	Asp
				165				170					175		
Lys	Met	Val	Ile	Asp	Val	Ser	Lys	Lys	Phe	Phe	Pro	Glu	Leu	Ala	Val
				180			185					190			
Gly	Phe	Asp	Asp	Pro	Arg	Val	Gln	Leu	His	Ile	Gly	Asp	Ala	Ala	Glu
				195			200					205			
Phe	Leu	Arg	Lys	Ser	Pro	Glu	Gly	Lys	Tyr	Asp	Ala	Ile	Ile	Val	Asp
				210			215					220			
Ser	Ser	Asp	Pro	Val	Gly	Pro	Ala	Leu	Ala	Leu	Val	Glu	Lys	Pro	Phe
225				230				235						240	
Phe	Glu	Thr	Leu	Ala	Arg	Ala	Leu	Lys	Pro	Gly	Gly	Val	Leu	Cys	Asn
				245				250					255		
Met	Ala	Glu	Ser	Met	Trp	Leu	His	Thr	His	Leu	Ile	Glu	Asp	Met	Ile
				260				265					270		
Ser	Ile	Cys	Arg	Gln	Thr	Phe	Lys	Ser	Val	His	Tyr	Ala	Trp	Ser	Ser
				275			280					285			
Val	Pro	Thr	Tyr	Pro	Ser	Gly	Val	Ile	Gly	Phe	Val	Leu	Cys	Ser	Thr
				290			295				300				
Glu	Gly	Pro	Ala	Val	Asp	Phe	Lys	Asn	Pro	Ile	Asn	Pro	Ile	Glu	Lys
305				310				315					320		
Leu	Asp	Gly	Ala	Met	Thr	His	Lys	Arg	Glu	Leu	Lys	Phe	Tyr	Asn	Ser
				325				330					335		
Asp	Met	His	Arg	Ala	Ala	Phe	Ala	Leu	Pro	Thr	Phe	Leu	Arg	Arg	Glu
				340			345					350			
Val	Ala	Ser	Leu	Leu	Ala	Ser									
				355											

(2) INFORMATION FOR SEQ ID NO:884:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..345

(D) OTHER INFORMATION: / Ceres Seq. ID 1568232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

Met Asp Gly Lys Ala Ser Asn Gly Asn Gly Leu Glu Lys Thr Val Pro

```

1           5           10           15
Ser Cys Cys Leu Lys Ala Met Ala Cys Leu Pro Glu Asp Asp Ala Lys
20           25           30
Cys His Ser Thr Val Val Ser Gly Trp Phe Ser Glu Pro His Pro Arg
35           40           45
Ser Gly Lys Lys Gly Gly Lys Ala Val Tyr Phe Asn Asn Pro Met Trp
50           55           60
Pro Gly Glu Ala His Ser Leu Lys Val Glu Lys Val Leu Phe Lys Asp
65           70           75
Lys Ser Asp Phe Gln Glu Val Leu Val Phe Glu Ser Ala Thr Tyr Gly
85           90           95
Lys Val Leu Val Leu Asp Gly Ile Val Gln Leu Thr Glu Lys Asp Glu
100          105          110
Cys Ala Tyr Gln Glu Met Ile Ala His Leu Pro Leu Cys Ser Ile Ser
115          120          125
Ser Pro Lys Asn Val Leu Val Val Gly Gly Gly Asp Gly Gly Val Leu
130          135          140
Arg Glu Ile Ser Arg His Ser Ser Val Glu Val Ile Asp Ile Cys Glu
145          150          155
Ile Asp Lys Met Val Ile Asp Val Ser Lys Lys Phe Phe Pro Glu Leu
165          170          175
Ala Val Gly Phe Asp Asp Pro Arg Val Gln Leu His Ile Gly Asp Ala
180          185          190
Ala Glu Phe Leu Arg Lys Ser Pro Glu Gly Lys Tyr Asp Ala Ile Ile
195          200          205
Val Asp Ser Ser Asp Pro Val Gly Pro Ala Leu Ala Leu Val Glu Lys
210          215          220
Pro Phe Phe Glu Thr Leu Ala Arg Ala Leu Lys Pro Gly Gly Val Leu
225          230          235
Cys Asn Met Ala Glu Ser Met Trp Leu His Thr His Leu Ile Glu Asp
245          250          255
Met Ile Ser Ile Cys Arg Gln Thr Phe Lys Ser Val His Tyr Ala Trp
260          265          270
Ser Ser Val Pro Thr Tyr Pro Ser Gly Val Ile Gly Phe Val Leu Cys
275          280          285
Ser Thr Glu Gly Pro Ala Val Asp Phe Lys Asn Pro Ile Asn Pro Ile
290          295          300
Glu Lys Leu Asp Gly Ala Met Thr His Lys Arg Glu Leu Lys Phe Tyr
305          310          315
Asn Ser Asp Met His Arg Ala Ala Phe Ala Leu Pro Thr Phe Leu Arg
325          330          335
Arg Glu Val Ala Ser Leu Leu Ala Ser
340          345

```

(2) INFORMATION FOR SEQ ID NO:885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..323

(D) OTHER INFORMATION: / Ceres Seq. ID 1568233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

```

Met Ala Cys Leu Pro Glu Asp Asp Ala Lys Cys His Ser Thr Val Val
1           5           10           15
Ser Gly Trp Phe Ser Glu Pro His Pro Arg Ser Gly Lys Lys Gly Gly
20           25           30
Lys Ala Val Tyr Phe Asn Asn Pro Met Trp Pro Gly Glu Ala His Ser
35           40           45

```

```

Leu Lys Val Glu Lys Val Leu Phe Lys Asp Lys Ser Asp Phe Gln Glu
50 55 60
Val Leu Val Phe Glu Ser Ala Thr Tyr Gly Lys Val Leu Val Leu Asp
65 70 75 80
Gly Ile Val Gln Leu Thr Glu Lys Asp Glu Cys Ala Tyr Gln Glu Met
85 90 95
Ile Ala His Leu Pro Leu Cys Ser Ile Ser Ser Pro Lys Asn Val Leu
100 105 110
Val Val Gly Gly Gly Asp Gly Gly Val Leu Arg Glu Ile Ser Arg His
115 120 125
Ser Ser Val Glu Val Ile Asp Ile Cys Glu Ile Asp Lys Met Val Ile
130 135 140
Asp Val Ser Lys Lys Phe Phe Pro Glu Leu Ala Val Gly Phe Asp Asp
145 150 155 160
Pro Arg Val Gln Leu His Ile Gly Asp Ala Ala Glu Phe Leu Arg Lys
165 170 175
Ser Pro Glu Gly Lys Tyr Asp Ala Ile Ile Val Asp Ser Ser Asp Pro
180 185 190
Val Gly Pro Ala Leu Ala Leu Val Glu Lys Pro Phe Phe Glu Thr Leu
195 200 205
Ala Arg Ala Leu Lys Pro Gly Gly Val Leu Cys Asn Met Ala Glu Ser
210 215 220
Met Trp Leu His Thr His Leu Ile Glu Asp Met Ile Ser Ile Cys Arg
225 230 235 240
Gln Thr Phe Lys Ser Val His Tyr Ala Trp Ser Ser Val Pro Thr Tyr
245 250 255
Pro Ser Gly Val Ile Gly Phe Val Leu Cys Ser Thr Glu Gly Pro Ala
260 265 270
Val Asp Phe Lys Asn Pro Ile Asn Pro Ile Glu Lys Leu Asp Gly Ala
275 280 285
Met Thr His Lys Arg Glu Leu Lys Phe Tyr Asn Ser Asp Met His Arg
290 295 300
Ala Ala Phe Ala Leu Pro Thr Phe Leu Arg Arg Glu Val Ala Ser Leu
305 310 315 320
Leu Ala Ser

```

(2) INFORMATION FOR SEQ ID NO:886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..439
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

```

cacaattcca gaagaaCaag aacagagaaa acagaggaag aggtgagatg gaggaacttg      60
tagggcttct gagaatccga gtgaagagag ggaatcaatct tgctcagcga gacactctaa      120
gcagcgaccc ttttgtgtgc ataaccatgg gatcacagaa gctgaagact cgtgttgtgg      180
aaaataactg caaccctgag tggaacgagg aattaacctt tgcgttaaga catcccgatg      240
aacctgtgaa tctgatagtgt tatgataaag atacattcac atcgcacgac aagatgggag      300
atgcaaaagt agatattaaa ccatttctgg aggttcacaa aatgggtttg caagaacttc      360
cagatggaac agagatcaag agagttgtga taactttgat ggatagtgtt ctgaaatcac      420
tcttttttgt ttggagccc

```

(2) INFORMATION FOR SEQ ID NO:887:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..145
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568235
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:
Gln Ile Gln Lys Asn Lys Asn Arg Glu Asn Arg Gly Arg Gly Glu Met
1 5 10 15
Glu Glu Leu Val Gly Leu Leu Arg Ile Arg Val Lys Arg Gly Ile Asn
 20 25 30
Leu Ala Gln Arg Asp Thr Leu Ser Ser Asp Pro Phe Val Val Ile Thr
 35 40 45
Met Gly Ser Gln Lys Leu Lys Thr Arg Val Val Glu Asn Asn Cys Asn
 50 55 60
Pro Glu Trp Asn Glu Glu Leu Thr Leu Ala Leu Arg His Pro Asp Gly
65 70 75 80
Pro Val Asn Leu Ile Val Tyr Asp Lys Asp Thr Phe Thr Ser His Asp
 85 90 95
Lys Met Gly Asp Ala Lys Ile Asp Ile Lys Pro Phe Leu Glu Val His
 100 105 110
Lys Met Gly Leu Gln Glu Leu Pro Asp Gly Thr Glu Ile Lys Arg Val
 115 120 125
Val Ile Thr Leu Met Asp Ser Val Leu Lys Ser Leu Phe Leu Val Trp
130 135 140

Ser
145

(2) INFORMATION FOR SEQ ID NO:888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

Met Glu Glu Leu Val Gly Leu Leu Arg Ile Arg Val Lys Arg Gly Ile
1 5 10 15
Asn Leu Ala Gln Arg Asp Thr Leu Ser Ser Asp Pro Phe Val Val Ile
 20 25 30
Thr Met Gly Ser Gln Lys Leu Lys Thr Arg Val Val Glu Asn Asn Cys
 35 40 45
Asn Pro Glu Trp Asn Glu Glu Leu Thr Leu Ala Leu Arg His Pro Asp
 50 55 60
Glu Pro Val Asn Leu Ile Val Tyr Asp Lys Asp Thr Phe Thr Ser His
65 70 75 80
Asp Lys Met Gly Asp Ala Lys Ile Asp Ile Lys Pro Phe Leu Glu Val
 85 90 95
His Lys Met Gly Leu Gln Glu Leu Pro Asp Gly Thr Glu Ile Lys Arg
 100 105 110
Val Val Ile Thr Leu Met Asp Ser Val Leu Lys Ser Leu Phe Leu Val
115 120 125

Trp Ser
130

(2) INFORMATION FOR SEQ ID NO:889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..97
(D) OTHER INFORMATION: / Ceres Seq. ID 1568237
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:
Met Gly Ser Gln Lys Leu Lys Thr Arg Val Glu Asn Asn Cys Asn
1 5 10 15
Pro Glu Trp Asn Glu Glu Leu Thr Leu Ala Leu Arg His Pro Asp Glu
20 25 30
Pro Val Asn Leu Ile Val Tyr Asp Lys Asp Thr Phe Thr Ser His Asp
35 40 45
Lys Met Gly Asp Ala Lys Ile Asp Ile Lys Pro Phe Leu Glu Val His
50 55 60
Lys Met Gly Leu Gln Glu Leu Pro Asp Gly Thr Glu Ile Lys Arg Val
65 70 75 80
Val Ile Thr Leu Met Asp Ser Val Leu Lys Ser Leu Phe Leu Val Trp
85 90 95
Ser

(2) INFORMATION FOR SEQ ID NO:890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..602
(D) OTHER INFORMATION: / Ceres Seq. ID 1568263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

aacaagagcg tccttttgatt ggttttggat tttgttgtgt tcctctcaaa atgacaaaaac 60
tatggacttc tctctctgct ctctattccc tcgctggacc cgtggtgatg ctgctctatc 120
cgtttatatgc gtccgtgata gcaatagaga gcccatcaaa agtagatgac gagcaatggc 180
ttgcttatgtg gattctctat tctttcctta ctctatcaga actcatcctt caatctctcc 240
tagagtggat accgatatgg tacacggcga aGctagtgtt tgtggcatgg ttggttttac 300
cacaaatttag agggagctgct tttatataca acaaagtcgt gaggggaacag ttcaagaagt 360
acggcatcct caaacctaag gtagagcatc aggcgtgagtg agtcaaaaag aggaggggagc 420
acaagagggc ttcaactgttg gggtctccag tttctaatct ctttttgctt thctattttt 480
gtcttataac tcttttgata tacggaaaaa tggggtagtt ctattattga gcctctgctt 540
gaatgtatgt gaagaagacct tttattcgac gttaaaatat tatattagag attataaaatt 600
tt

(2) INFORMATION FOR SEQ ID NO:891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..132
(D) OTHER INFORMATION: / Ceres Seq. ID 1568264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

Gln Glu Arg Pro Leu Ile Gly Phe Gly Phe Cys Cys Val Pro Leu Lys
1 5 10 15
Met Thr Lys Leu Trp Thr Ser Leu Ser Ala Leu His Ser Leu Ala Gly
20 25 30

Pro Val Val Met Leu Leu Tyr Pro Leu Tyr Ala Ser Val Ile Ala Ile
35 40 45
Glu Ser Pro Ser Lys Val Asp Asp Glu Gln Trp Leu Ala Tyr Trp Ile
50 55 60
Leu Tyr Ser Phe Leu Thr Leu Ser Glu Leu Ile Leu Gln Ser Leu Leu
65 70 75 80
Glu Trp Ile Pro Ile Trp Tyr Thr Ala Lys Leu Val Phe Val Ala Trp
85 90 95
Leu Val Leu Pro Gln Phe Arg Gly Ala Ala Phe Ile Tyr Asn Lys Val
100 105 110
Val Arg Glu Gln Phe Lys Lys Tyr Gly Ile Leu Lys Pro Lys Val Glu
115 120 125
His Gln Ala Glu
130

(2) INFORMATION FOR SEQ ID NO:892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

Met Thr Lys Leu Trp Thr Ser Leu Ser Ala Leu His Ser Leu Ala Gly
1 5 10 15
Pro Val Val Met Leu Leu Tyr Pro Leu Tyr Ala Ser Val Ile Ala Ile
20 25 30
Glu Ser Pro Ser Lys Val Asp Asp Glu Gln Trp Leu Ala Tyr Trp Ile
35 40 45
Leu Tyr Ser Phe Leu Thr Leu Ser Glu Leu Ile Leu Gln Ser Leu Leu
50 55 60
Glu Trp Ile Pro Ile Trp Tyr Thr Ala Lys Leu Val Phe Val Ala Trp
65 70 75 80
Leu Val Leu Pro Gln Phe Arg Gly Ala Ala Phe Ile Tyr Asn Lys Val
85 90 95
Val Arg Glu Gln Phe Lys Lys Tyr Gly Ile Leu Lys Pro Lys Val Glu
100 105 110
His Gln Ala Glu
115

(2) INFORMATION FOR SEQ ID NO:893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

Met Leu Leu Tyr Pro Leu Tyr Ala Ser Val Ile Ala Ile Glu Ser Pro
1 5 10 15
Ser Lys Val Asp Asp Glu Gln Trp Leu Ala Tyr Trp Ile Leu Tyr Ser
20 25 30
Phe Leu Thr Leu Ser Glu Leu Ile Leu Gln Ser Leu Leu Glu Trp Ile
35 40 45
Pro Ile Trp Tyr Thr Ala Lys Leu Val Phe Val Ala Trp Leu Val Leu

50	55	60	
Pro Gln Phe Arg Gly	Ala Ala Phe Ile Tyr Asn Lys Val Val Arg Glu		
65	70	75	80
Gln Phe Lys Lys Tyr	Gly Ile Leu Lys Pro Lys Val Glu His Gln Ala		
	85	90	95

Glu

(2) INFORMATION FOR SEQ ID NO:894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1969
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

aaaggctttt	aatattttat	catcttcagg	cttattcgat	ttctcttcaga	tttgaaatgg	60
tgctgtctcaa	ggctctctctc	gtctctactt	cgctatttga	tgccagaaaa	ccaggaaactt	120
ctggactccg	taagaagggtg	aaagtgttta	agcaaccaaa	ttaccttgaa	aattttgtcc	180
aggcaacggt	caatgctctt	actacagaga	aagttaaagg	tgcgacactt	gtgtttctctg	240
gtgatgggtcg	ttattattca	gagcaagcta	ttcagattat	agtaaagatg	gcagcagcta	300
atgggtgttag	acgtgtgtgg	gttgggtcaa	acagtcctgt	atcaactcct	gcagtatcag	360
ctattatttcg	tgaaaagata	ggggctgatg	gatctaaagc	cacaggagca	tttatcttaa	420
cagcaagctca	taactctggt	ggcccaactg	aggatttcgg	aattaaagac	aatatggaaa	480
atgggtggacc	agctcctgaa	tcaatcactg	ataagattta	cgagaacaca	aagacaactaa	540
aggagtacc	aatagcggaa	gatctacc	gggttgatat	ttctactatt	ggtataacca	600
gctttgaagg	acctgaagga	aagtttgacg	togaagtgtt	tgattctgca	gatgatacga	660
ttaaactaat	gaagtcaatc	ttcgactttg	aatccatcaa	gaaatttgcta	tcctatccaa	720
aattttacttt	ctgctatgat	cgattgcgat	gagtggtctg	agcatatgca	catcgcatct	780
ttgtcgaaga	actaggtgca	ccagaaaagt	cggtgttgaa	ctgtgtacc	aaggaggact	840
ttggaggggg	ccaccgggat	cccaatctta	cctatgctaa	ggagctcggt	gcacgcacgt	900
gattgagtaa	aactgatgat	gctgggtggc	agcctccaga	gtttggcgcc	gctgtgatg	960
gtgatgcaga	ccgaaacatg	atcctcggtt	aaaggttttt	cgtaactcct	tcggattcac	1020
ttgtcttaat	tgctgcaaat	gctgttgggg	ccataccata	cttcagctct	ggtttaaaaa	1080
gtgtgtctag	gagcatgcgc	acctcagctg	cacttgatgt	cggttgcaaaa	aacttggggt	1140
tgaagttctt	tgaggttcca	acaggctgga	aattctttgg	caatctaagt	gatgctggga	1200
gtgtctctgt	atgcggagaa	gaaggttttg	gaaccgggtc	ggatcatatc	cgtagaagaa	1260
atgggactctg	ggcaggttctt	ctttggctat	caatactggc	tcacaagaac	agggaacc	1320
ttgatgggaa	tgcaaaactg	gtgacgggtg	aagacattgt	ccgccagcac	tggtgtacat	1380
atggccgctca	ctattacatc	gcatacgact	atgagacgt	acgcgaact	tcagataaag	1440
aaactcatggg	acttttgggt	aagttgcaat	cttcacttcc	cgaggtcaac	aagattataa	1500
agggaattcca	tcagagggtg	gcaaatgttg	caagcccgaga	tgagttcgag	tacaaagatc	1560
cagtagatgg	ctctgtttcca	aagcaccaag	ggatccgata	cttattcgag	gatgatacac	1620
gacttgtggt	ccgtctctctg	ggaactggct	cagaaggagc	aacaataaag	ctatacattg	1680
aacaatacaga	gaaggagacc	tcaaaagatg	gcgcagatgc	tcaggatgct	cttgggtccc	1740
tggtgtgatg	tgcatataaag	ctgtcgaaaa	tgcaagagtt	caccggccga	tcataccaaa	1800
ctgtattacc	ataagacacg	tttcagaaga	cgctgtctcc	aataactact	tcattccaac	1860
ttcatttctt	atgaatttgg	gttttgcttt	tttctgttta	ctgttatct	tacacaagta	1920
tacttcaakA	catataatct	taattgaaata	tacattaggt	tgccaattg		

(2) INFORMATION FOR SEQ ID NO:895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..417

(D) OTHER INFORMATION: / Ceres Seq. ID 1568268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

```

Arg Leu Leu Ile Phe Tyr His Leu Gln Ala Tyr Ser Ile Phe Phe Arg
1      5      10      15
Phe Glu Met Val Ser Phe Lys Val Ser Leu Val Ser Thr Ser Pro Ile
20      25      30
Asp Gly Gln Lys Pro Gly Thr Ser Gly Leu Arg Lys Lys Val Lys Val
35      40      45
Phe Lys Gln Pro Asn Tyr Leu Glu Asn Phe Val Gln Ala Thr Phe Asn
50      55      60
Ala Leu Thr Thr Glu Lys Val Lys Gly Ala Thr Leu Val Val Ser Gly
65      70      75      80
Asp Gly Arg Tyr Tyr Ser Glu Gln Ala Ile Gln Ile Ile Val Lys Met
85      90      95
Ala Ala Ala Asn Gly Val Arg Arg Val Trp Val Gly Gln Asn Ser Leu
100     105     110
Leu Ser Thr Pro Ala Val Ser Ala Ile Ile Arg Glu Arg Val Gly Ala
115     120     125
Asp Gly Ser Lys Ala Thr Gly Ala Phe Ile Leu Thr Ala Ser His Asn
130     135     140
Pro Gly Gly Pro Thr Glu Asp Phe Gly Ile Lys Tyr Asn Met Glu Asn
145     150     155     160
Gly Gly Pro Ala Pro Glu Ser Ile Thr Asp Lys Ile Tyr Glu Asn Thr
165     170     175
Lys Thr Ile Lys Glu Tyr Pro Ile Ala Glu Asp Leu Pro Arg Val Asp
180     185     190
Ile Ser Thr Ile Gly Ile Thr Ser Phe Glu Gly Pro Glu Gly Lys Phe
195     200     205
Asp Val Glu Val Phe Asp Ser Ala Asp Asp Tyr Val Lys Leu Met Lys
210     215     220
Ser Ile Phe Asp Phe Glu Ser Ile Lys Lys Leu Leu Ser Tyr Pro Lys
225     230     235     240
Phe Thr Phe Cys Tyr Asp Ala Leu His Gly Val Ala Gly Ala Tyr Ala
245     250     255
His Arg Ile Phe Val Glu Glu Leu Gly Ala Pro Glu Ser Ser Leu Leu
260     265     270
Asn Cys Val Pro Lys Glu Asp Phe Gly Gly Gly His Pro Asp Pro Asn
275     280     285
Leu Thr Tyr Ala Lys Glu Leu Val Ala Arg Met Gly Leu Ser Lys Thr
290     295     300
Asp Asp Ala Gly Gly Glu Pro Pro Glu Phe Gly Ala Ala Ala Asp Gly
305     310     315     320
Asp Ala Asp Arg Asn Met Ile Leu Gly Lys Arg Phe Phe Val Thr Pro
325     330     335
Ser Asp Ser Val Ala Ile Ile Ala Ala Asn Ala Val Gly Ala Ile Pro
340     345     350
Tyr Phe Ser Ser Gly Leu Lys Gly Val Ala Arg Ser Met Pro Thr Ser
355     360     365
Ala Ala Leu Asp Val Val Ala Lys Asn Leu Gly Leu Lys Phe Phe Glu
370     375     380
Val Pro Thr Gly Trp Lys Phe Phe Gly Asn Leu Met Asp Ala Gly Met
385     390     395     400
Cys Ser Val Cys Gly Glu Glu Ser Phe Gly Thr Gly Ser Asp His Ile
405     410     415

```

Arg

(2) INFORMATION FOR SEQ ID NO:896:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..399
(D) OTHER INFORMATION: / Ceres Seq. ID 1568269
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

Met	Val	Ser	Phe	Lys	Val	Ser	Leu	Val	Ser	Thr	Ser	Pro	Ile	Asp	Gly
1				5						10				15	
Gln	Lys	Pro	Gly	Thr	Ser	Gly	Leu	Arg	Lys	Lys	Val	Lys	Val	Phe	Lys
			20					25					30		
Gln	Pro	Asn	Tyr	Leu	Glu	Asn	Phe	Val	Gln	Ala	Thr	Phe	Asn	Ala	Leu
		35					40					45			
Thr	Thr	Glu	Lys	Val	Lys	Gly	Ala	Thr	Leu	Val	Val	Ser	Gly	Asp	Gly
	50					55					60				
Arg	Tyr	Tyr	Ser	Glu	Gln	Ala	Ile	Gln	Ile	Ile	Val	Lys	Met	Ala	Ala
	65				70					75				80	
Ala	Asn	Gly	Val	Arg	Arg	Val	Trp	Val	Gly	Gln	Asn	Ser	Leu	Leu	Ser
			85						90				95		
Thr	Pro	Ala	Val	Ser	Ala	Ile	Ile	Arg	Glu	Arg	Val	Gly	Ala	Asp	Gly
		100						105					110		
Ser	Lys	Ala	Thr	Gly	Ala	Phe	Ile	Leu	Thr	Ala	Ser	His	Asn	Pro	Gly
		115						120				125			
Gly	Pro	Thr	Glu	Asp	Phe	Gly	Ile	Lys	Tyr	Asn	Met	Glu	Asn	Gly	Gly
		130				135						140			
Pro	Ala	Pro	Glu	Ser	Ile	Thr	Asp	Lys	Ile	Tyr	Glu	Asn	Thr	Lys	Thr
	145				150					155				160	
Ile	Lys	Glu	Tyr	Pro	Ile	Ala	Glu	Asp	Leu	Pro	Arg	Val	Asp	Ile	Ser
			165						170					175	
Thr	Ile	Gly	Ile	Thr	Ser	Phe	Glu	Gly	Pro	Glu	Gly	Lys	Phe	Asp	Val
		180						185					190		
Glu	Val	Phe	Asp	Ser	Ala	Asp	Asp	Tyr	Val	Lys	Leu	Met	Lys	Ser	Ile
		195					200					205			
Phe	Asp	Phe	Glu	Ser	Ile	Lys	Lys	Leu	Leu	Ser	Tyr	Pro	Lys	Phe	Thr
		210				215						220			
Phe	Cys	Tyr	Asp	Ala	Leu	His	Gly	Val	Ala	Gly	Ala	Tyr	Ala	His	Arg
		225				230				235				240	
Ile	Phe	Val	Glu	Glu	Leu	Gly	Ala	Pro	Glu	Ser	Ser	Leu	Leu	Asn	Cys
			245						250					255	
Val	Pro	Lys	Glu	Asp	Phe	Gly	Gly	Gly	His	Pro	Asp	Pro	Asn	Leu	Thr
		260						265					270		
Tyr	Ala	Lys	Glu	Leu	Val	Ala	Arg	Met	Gly	Leu	Ser	Lys	Thr	Asp	Asp
		275					280						285		
Ala	Gly	Gly	Glu	Pro	Pro	Glu	Phe	Gly	Ala	Ala	Ala	Asp	Gly	Asp	Ala
		290				295						300			
Asp	Arg	Asn	Met	Ile	Leu	Gly	Lys	Arg	Phe	Phe	Val	Thr	Pro	Ser	Asp
		305			310					315				320	
Ser	Val	Ala	Ile	Ile	Ala	Ala	Asn	Ala	Val	Gly	Ala	Ile	Pro	Tyr	Phe
			325						330					335	
Ser	Ser	Gly	Leu	Lys	Gly	Val	Ala	Arg	Ser	Met	Pro	Thr	Ser	Ala	Ala
			340					345					350		
Leu	Asp	Val	Val	Ala	Lys	Asn	Leu	Gly	Leu	Lys	Phe	Phe	Glu	Val	Pro
		355					360					365			
Thr	Gly	Trp	Lys	Phe	Phe	Gly	Asn	Leu	Met	Asp	Ala	Gly	Met	Cys	Ser
		370				375							380		
Val	Cys	Gly	Glu	Glu	Ser	Phe	Gly	Thr	Gly	Ser	Asp	His	Ile	Arg	
		385				390				395					

- (2) INFORMATION FOR SEQ ID NO:897:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 amino acids

[illegible]

```
(2) INFORMATION FOR SEQ ID NO:898:
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1445 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: DNA (genomic)
  (ix) FEATURE:
      (A) NAME/KEY: -
      (B) LOCATION: 1..1445
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1568286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

gcacaaacac	cgccgtat	ccacggcg	cttatcaccg	gcaacaaccc	taggtttttg	60
ttttccgtcg	cgatggaggt	ggataagaag	gacgagagag	aggtcgaatc	ttcggagcaa	120
gtggtgaatc	catgggaagt	gtccgccaaa	gacggcgga	agatcgatta	cgacaagcct	180
attgacaaat	ttggatgta	aaggcttgac	gagtcactga	ttgatcgtgt	tcagagactg	240
actctctgct	aaccacacgt	gttccctccg	cgtagtgtct	tcttcgccca	Cggggatttc	300
aatgagattt	tggaagctta	tgagagagga	gacaagtctt	atctctacac	tggaagagga	360
ccttcacacg	aagcattgca	tttggggcct	ttgattcctt	tcatgtttac	caaataactg	420
caagaagcct	tcaaggttcc	ccttggtata	cagctcacgg	atgatgaaaa	aagatatatg	480
aagaacttat	cggtggagga	aagtcaaaag	cttgccagag	aaaatgcgaa	agatatattt	540
gctgtgggat	tcgatgtaac	aaagaccttc	attttctcgg	acttcgacta	gttgccgggt	600
gctttctata	aaaatatggt	gaaggttggc	aagtcggtta	cacttaataa	ggctatggga	660
atctttggct	tttccgggtg	agatcctatc	gcgaaactca	gtttccctcc	gtgcaggga	720
gttccatctt	ttcctagctc	attcccacat	ttgttccctg	gcaaggacaa	tctccgctgc	780
ttgattcctt	gtgctattgt	ccaggatcct	tattttagaa	tgactcgtga	tgctgcaccc	840
cggttgaggc	atagcaagcc	cgccctgatt	gagtcacacat	tttttccctg	gttgccaggga	900
gagaatggaa	aaatgtctgc	tagtgatcca	aattctgcta	tctatgtgac	tgattccgca	960
aaggacatta	aaaacaagat	aaacagatat	cggttttagt	gtgggcaaga	ctccattgag	1020
aagcacccag	aacttggagc	aaatctcgag	gttgacatac	ccgtcaagta	tctgagtttc	1080
ttcctcgaag	acgattctga	actagaacac	attaaaaagg	aatatggaga	aggaagaatg	1140
ctaacaggag	aagttaaaag	gagacttacg	gaagtgttga	cagaatattg	ggagaaacac	1200
cgcagggttc	gagctgctgt	tactgatgag	atggttgatg	cgctcatggc	ggtgagacct	1260
ctcccaagca	agttcgaaat	gaaaaagtca	gaaacccctt	ttggctctct	agcaacttca	1320
caTcYactcc	gtttgatttg	gatcagaca	tctttgggtg	tctattgata	gatttgatcc	1380
ttgaaattga	accatacttg	ttagttaaaa	tttcatatt	tacatttatt	tatgaatcac	1440
attct						

(2) INFORMATION FOR SEQ ID NO:899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..426
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

Ala	Lys	Pro	Pro	Pro	Tyr	Ile	His	Gly	Arg	Leu	Ile	Thr	Gly	Asn	Asn
1			5					10					15		
Arg	Arg	Phe	Leu	Phe	Ser	Val	Ala	Met	Glu	Val	Asp	Lys	Lys	Asp	Glu
			20					25					30		
Arg	Glu	Ala	Glu	Ser	Ser	Glu	Gln	Val	Val	Asn	Pro	Trp	Glu	Val	Ser
			35					40				45			
Ala	Lys	Asp	Gly	Gly	Lys	Ile	Asp	Tyr	Asp	Lys	Leu	Ile	Asp	Lys	Phe
			50					55				60			
Gly	Cys	Gln	Arg	Leu	Asp	Glu	Ser	Leu	Ile	Asp	Arg	Val	Gln	Arg	Leu
			70					75				80			
Thr	Ser	Arg	Gln	Pro	His	Val	Phe	Leu	Arg	Arg	Ser	Val	Phe	Phe	Ala
			85					90				95			
His	Arg	Asp	Phe	Asn	Glu	Ile	Leu	Asp	Ala	Tyr	Glu	Arg	Gly	Asp	Lys
			100					105				110			
Phe	Tyr	Leu	Tyr	Thr	Gly	Arg	Gly	Pro	Ser	Ser	Glu	Ala	Leu	His	Leu
			115					120				125			
Gly	His	Leu	Ile	Pro	Phe	Met	Phe	Thr	Lys	Tyr	Leu	Gln	Glu	Ala	Phe
			130					135				140			
Lys	Val	Pro	Leu	Val	Ile	Gln	Leu	Thr	Asp	Asp	Glu	Lys	Ser	Ile	Trp
			145					150				155			
Lys	Asn	Leu	Ser	Val	Glu	Glu	Ser	Gln	Arg	Leu	Ala	Arg	Glu	Asn	Ala
			165					170						175	

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Lys Asp Ile Ile Ala Cys Gly Phe Asp Val Thr Lys Thr Phe Ile Phe
180 185 190
Ser Asp Phe Asp Tyr Val Gly Gly Ala Phe Tyr Lys Asn Met Val Lys
195 200 205
Val Gly Lys Cys Val Thr Leu Asn Lys Ala Met Gly Ile Phe Gly Phe
210 215 220
Ser Gly Glu Asp Pro Ile Ala Lys Leu Ser Phe Pro Pro Val Gln Ala
225 230 235 240
Val Pro Ser Phe Pro Ser Ser Phe Pro His Leu Phe Pro Gly Lys Asp
245 250 255
Asn Leu Arg Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe
260 265 270
Arg Met Thr Arg Asp Val Ala Pro Arg Leu Gly Tyr Ser Lys Pro Ala
275 280 285
Leu Ile Glu Ser Thr Phe Phe Pro Ala Leu Gln Gly Glu Asn Gly Lys
290 295 300
Met Ser Ala Ser Asp Pro Asn Ser Ala Ile Tyr Val Thr Asp Ser Ala
305 310 315 320
Lys Asp Ile Lys Asn Lys Ile Asn Arg Tyr Ala Phe Ser Gly Gly Gln
325 330 335
Asp Ser Ile Glu Lys His Arg Glu Leu Gly Ala Asn Leu Glu Val Asp
340 345 350
Ile Pro Val Lys Tyr Leu Ser Phe Phe Leu Glu Asp Asp Ser Glu Leu
355 360 365
Glu His Ile Lys Lys Glu Tyr Gly Glu Gly Arg Met Leu Thr Gly Glu
370 375 380
Val Lys Lys Arg Leu Thr Glu Val Leu Thr Glu Ile Val Glu Lys His
385 390 395 400
Arg Arg Ala Arg Ala Ala Val Thr Asp Glu Met Val Asp Ala Phe Met
405 410 415
Ala Val Arg Pro Leu Pro Ser Lys Phe Glu
420 425

(2) INFORMATION FOR SEQ ID NO:900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..402
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

Met Glu Val Asp Lys Lys Asp Glu Arg Glu Ala Glu Ser Ser Glu Gln
1 5 10 15
Val Val Asn Pro Trp Glu Val Ser Ala Lys Asp Gly Gly Lys Ile Asp
20 25 30
Tyr Asp Lys Leu Ile Asp Lys Phe Gly Cys Gln Arg Leu Asp Glu Ser
35 40 45
Leu Ile Asp Arg Val Gln Arg Leu Thr Ser Arg Gln Pro His Val Phe
50 55 60
Leu Arg Arg Ser Val Phe Phe Ala His Arg Asp Phe Asn Glu Ile Leu
65 70 75 80
Asp Ala Tyr Glu Arg Gly Asp Lys Phe Tyr Leu Tyr Thr Gly Arg Gly
85 90 95
Pro Ser Ser Glu Ala Leu His Leu Gly His Leu Ile Pro Phe Met Phe
100 105 110
Thr Lys Tyr Leu Gln Glu Ala Phe Lys Val Pro Leu Val Ile Gln Leu
115 120 125
Thr Asp Asp Glu Lys Ser Ile Trp Lys Asn Leu Ser Val Glu Glu Ser

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(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 amino acids

(C) STRANDEDNESS:

MOLECULE TYPE: peptid

(A) NAME/KEY: peptid

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO: 901:
 Ser Lys Tyr Leu Gln Glu Ala Phe Lys Val Pro Leu

5 10
Ile Met Ser Ser Gly Lys Ser Ile Trp Lys A

Gln Leu Thr Asp Asp Glu Lys Ser Ile Trp Lys Asn Leu Ser Val Glu

20 25 30

Glu Ser Gln Arg Leu Ala Arg Glu Asn Ala Lys Asp Ile Ile Ala Cys

35 40 45

Gly Phe Asp Val Thr Lys Thr Phe Ile Phe Ser Asp Phe Asp Tyr Val

50 55 60

Gly Gly Ala Phe Tyr Lys Asn Met Val Lys Val Gly Lys Cys Val Thr

65 70 75 80

Leu Asn Lys Ala Met Gly Ile Phe Gly Phe Ser Gly Glu Asp Pro Ile

85 90 95

Ala Lys Leu Ser Phe Pro Pro Val Gln Ala Val Pro Ser Phe Pro Ser

100	105	110
-----	-----	-----

Ser Phe Pro His Leu Phe Pro Gly Lys Asp Asn Leu Arg Cys Leu Ile
115 120 125
Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr Arg Asp Val
130 135 140
Ala Pro Arg Leu Gly Tyr Ser Lys Pro Ala Leu Ile Glu Ser Thr Phe
145 150 155 160
Phe Pro Ala Leu Gln Gly Glu Asn Gly Lys Met Ser Ala Ser Asp Pro
165 170 175
Asn Ser Ala Ile Tyr Val Thr Asp Ser Ala Lys Asp Ile Lys Asn Lys
180 185 190
Ile Asn Arg Tyr Ala Phe Ser Gly Gly Gln Asp Ser Ile Glu Lys His
195 200 205
Arg Glu Leu Gly Ala Asn Leu Glu Val Asp Ile Pro Val Lys Tyr Leu
210 215 220
Ser Phe Phe Leu Glu Asp Asp Ser Glu Leu Glu His Ile Lys Lys Glu
225 230 235 240
Tyr Gly Glu Gly Arg Met Leu Thr Gly Glu Val Lys Lys Arg Leu Thr
245 250 255
Glu Val Leu Thr Glu Ile Val Glu Lys His Arg Arg Ala Arg Ala Ala
260 265 270
Val Thr Asp Glu Met Val Asp Ala Phe Met Ala Val Arg Pro Leu Pro
275 280 285
Ser Lys Phe Glu
290

(2) INFORMATION FOR SEQ ID NO:902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..904
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

ctttttttcg	agaaaaacgA	agttttctga	gctaaactag	atcagctatg	gcgacccggtg	60
gtgctgcggc	ggatttggaa	gatgttcaga	cggtggatct	catgtcggag	ctctcccgcc	120
gcctcaagtg	ttctcagaag	ccgcacaaac	gcctcatctt	catgtgacct	ccagggtcag	180
ggaagaggtac	tcaatctcca	gtagtgaagg	atgagtattg	cttggtgcac	ttatccactg	240
gagacatggt	aagagctgct	gttgcttcta	agacccctct	tggtgtcaag	gctaaagaag	300
ctatggaaaa	aggagagctc	gtctctgatg	atttggtgtg	tggtataatt	gatgaagcca	360
tgaaacagcc	aaaatgcca	aaaggattta	tcttgatGg	gttccccagg	actgttactc	420
aggcagagaa	agctgatgag	atgcttaaga	ggcgaggaa	tgaaattgac	aaagtcttca	480
actttgtcat	tgatgacgca	atcttggagg	aaagaataac	cgggcgatgg	atccaccat	540
cgagtggcag	gagttaccac	accaaatttg	ctctcccaa	aaccctgga	gttgatgata	600
ttactggaga	gcctctgac	caacgtaaag	atgataacg	tgatgttcta	aaagtcgaggc	660
tttcagcttt	ccacagtcga	actcaaccgg	tgattgatta	ctacgcaaa	aggccgcttc	720
tcacaaacat	ccaggccgag	agggtctccc	aagaagttac	atcagaggtt	aaaaaagcat	780
tgctatgac	aaagactcct	caagcaaatc	atctcctctg	gttagaatcc	attcttttcc	840
ttactacaag	agagagacac	atctatataa	tccactcatc	tgcggaatga	cagttttttc	900
tttt						

(2) INFORMATION FOR SEQ ID NO:903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..246

(D) OTHER INFORMATION: / Ceres Seq. ID 1568301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

```
Met Ala Thr Gly Gly Ala Ala Ala Asp Leu Glu Asp Val Gln Thr Val
1      5      10
Asp Leu Met Ser Glu Leu Leu Arg Arg Leu Lys Cys Ser Gln Lys Pro
20      25      30
Asp Lys Arg Leu Ile Phe Ile Gly Pro Pro Gly Ser Gly Lys Gly Thr
35      40      45
Gln Ser Pro Val Val Lys Asp Glu Tyr Cys Leu Cys His Leu Ser Thr
50      55      60
Gly Asp Met Leu Arg Ala Ala Val Ala Ser Lys Thr Pro Leu Gly Val
65      70      75      80
Lys Ala Lys Glu Ala Met Glu Lys Gly Glu Leu Val Ser Asp Asp Leu
85      90      95
Val Val Gly Ile Ile Asp Glu Ala Met Asn Lys Pro Lys Cys Gln Lys
100      105      110
Gly Phe Ile Leu Asp Gly Phe Pro Arg Thr Val Thr Gln Ala Glu Lys
115      120      125
Leu Asp Glu Met Leu Lys Arg Arg Gly Thr Glu Ile Asp Lys Val Leu
130      135      140
Asn Phe Ala Ile Asp Asp Ala Ile Leu Glu Glu Arg Ile Thr Gly Arg
145      150      155      160
Trp Ile His Pro Ser Ser Gly Arg Ser Tyr His Thr Lys Phe Ala Pro
165      170      175
Pro Lys Thr Pro Gly Val Asp Asp Ile Thr Gly Glu Pro Leu Ile Gln
180      185      190
Arg Lys Asp Asp Asn Ala Asp Val Leu Lys Ser Arg Leu Ala Ala Phe
195      200      205
His Ser Gln Thr Gln Pro Val Ile Asp Tyr Tyr Ala Lys Lys Ala Val
210      215      220
Leu Thr Asn Ile Gln Ala Glu Lys Ala Pro Gln Glu Val Thr Ser Glu
225      230      235      240
Val Lys Lys Ala Leu Ser
245
```

(2) INFORMATION FOR SEQ ID NO:904:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..228

(D) OTHER INFORMATION: / Ceres Seq. ID 1568302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

```
Met Ser Glu Leu Leu Arg Arg Leu Lys Cys Ser Gln Lys Pro Asp Lys
1      5      10      15
Arg Leu Ile Phe Ile Gly Pro Pro Gly Ser Gly Lys Gly Thr Gln Ser
20      25      30
Pro Val Val Lys Asp Glu Tyr Cys Leu Cys His Leu Ser Thr Gly Asp
35      40      45
Met Leu Arg Ala Ala Val Ala Ser Lys Thr Pro Leu Gly Val Lys Ala
50      55      60
Lys Glu Ala Met Glu Lys Gly Glu Leu Val Ser Asp Asp Leu Val Val
65      70      75      80
Gly Ile Ile Asp Glu Ala Met Asn Lys Pro Lys Cys Gln Lys Gly Phe
85      90      95
Ile Leu Asp Gly Phe Pro Arg Thr Val Thr Gln Ala Glu Lys Leu Asp
100      105      110
```

Glu Met Leu Lys Arg Arg Gly Thr Glu Ile Asp Lys Val Leu Asn Phe
115 120 125
Ala Ile Asp Asp Ala Ile Leu Glu Glu Arg Ile Thr Gly Arg Trp Ile
130 135 140
His Pro Ser Ser Gly Arg Ser Tyr His Thr Lys Phe Ala Pro Pro Lys
145 150 155 160
Thr Pro Gly Val Asp Asp Ile Thr Gly Glu Pro Leu Ile Gln Arg Lys
165 170 175
Asp Asp Asn Ala Asp Val Leu Lys Ser Arg Leu Ala Ala Phe His Ser
180 185 190
Gln Thr Gln Pro Val Ile Asp Tyr Tyr Ala Lys Lys Ala Val Leu Thr
195 200 205
Asn Ile Gln Ala Glu Lys Ala Pro Gln Glu Val Thr Ser Glu Val Lys
210 215 220
Lys Ala Leu Ser
225

(2) INFORMATION FOR SEQ ID NO:905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

Met Leu Arg Ala Ala Val Ala Ser Lys Thr Pro Leu Gly Val Lys Ala
1 5 10 15
Lys Glu Ala Met Glu Lys Gly Glu Leu Val Ser Asp Asp Leu Val Val
20 25 30
Gly Ile Ile Asp Glu Ala Met Asn Lys Pro Lys Cys Gln Lys Gly Phe
35 40 45
Ile Leu Asp Gly Phe Pro Arg Thr Val Thr Gln Ala Glu Lys Leu Asp
50 55 60
Glu Met Leu Lys Arg Arg Gly Thr Glu Ile Asp Lys Val Leu Asn Phe
65 70 75 80
Ala Ile Asp Asp Ala Ile Leu Glu Glu Arg Ile Thr Gly Arg Trp Ile
85 90 95
His Pro Ser Ser Gly Arg Ser Tyr His Thr Lys Phe Ala Pro Pro Lys
100 105 110
Thr Pro Gly Val Asp Asp Ile Thr Gly Glu Pro Leu Ile Gln Arg Lys
115 120 125
Asp Asp Asn Ala Asp Val Leu Lys Ser Arg Leu Ala Ala Phe His Ser
130 135 140
Gln Thr Gln Pro Val Ile Asp Tyr Tyr Ala Lys Lys Ala Val Leu Thr
145 150 155 160
Asn Ile Gln Ala Glu Lys Ala Pro Gln Glu Val Thr Ser Glu Val Lys
165 170 175
Lys Ala Leu Ser
180

(2) INFORMATION FOR SEQ ID NO:906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..1303

(D) OTHER INFORMATION: / Ceres Seq. ID 1568304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

aaagctcaga	tatctgaata	actcgcttgc	gtgcctctct	ctctctaaaa	gcccatctct	60
ttctctctct	ctctctccat	tgaagaagaa	acctacottc	gtaatatatt	ctcaattacg	120
atacatggta	atgttaaaag	gtcaacccaa	aaatogaatc	ttgatcgatt	cottcattgc	180
ttgtggcatt	tagtgccacc	ccaatctctc	cccaagacgg	agattagaac	cctaaatcga	240
ttgtggcatt	catgggagag	acaaaaggtt	gagtttttca	ggttgagtga	ttttggggat	300
tgttatgatg	aatggagcgc	ttatggagct	agcgtttcta	ttcatgttac	caacgggaga	360
ttctttgttc	aatactatgt	tccttatctc	ttcgccatcc	agattttcac	cttctattcc	420
ttctttgatcc	gcttaagggga	agagctctgaa	gatgggggaat	gtgagggtag	agatccggtt	480
agcgattcag	gtacggatga	gagtgctctc	gaggaaggac	ttgagaacaa	caacgctttg	540
catccaagtg	atcgttttgg	ttatctttat	ctccaatact	ttgagagatc	agctccttat	600
accagagttc	ctctgatgga	taagatcaat	gaattggctc	aaagataccc	gggattgatg	660
tcgtttgaga	gcgttgatct	ttctccagct	agttggatgt	cagtagcatg	gtacccgatt	720
taccatatac	caatgggaag	aaccattaaa	gacttatcca	cgtgtttcct	cacttatcac	780
actctttcct	cttcttttca	agatatggaa	ccgggaagaaa	atgggtgggga	caaggagaga	840
gtgcggaggg	aagggggaaga	tataactctg	ctcccathtt	ggatgggtac	ttacaagatg	900
caaggcgatg	tttggctttc	gcaggaccac	gatgatcaag	agagattggc	ttcgtctttac	960
agtggttggg	attcttggct	taaacagctc	aggggtccaac	atcatgactt	caactacttc	1020
tgcaatatgt	caatgaactca	tcgtggctaa	acctcggttg	gatgacacca	tgatgtttgc	1080
ttgttttctc	atatatagtc	taattcttgc	tttgttctgg	aaccgcttgc	gttttgaata	1140
acgcatagga	gcgattcgct	ttgcagtggt	ttggttagaa	tagcgttttc	agttctctaa	1200
ccctttgagag	agtatatgtc	gtatatagag	ttttgttgct	tgttgaaaca	gagtacaatt	1260
gttgttgctt	gtataaaaca	gagtgattgt	ttcttataag	ttg		

(2) INFORMATION FOR SEQ ID NO:907:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..308

(D) OTHER INFORMATION: / Ceres Seq. ID 1568305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

Met	Val	Asn	Val	Lys	Gly	Ser	Thr	Lys	Lys	Ser	Asn	Leu	Asp	Arg	Phe
1			5					10					15		
Leu	His	Cys	Ile	Thr	Pro	Leu	Val	Pro	Pro	Gln	Ser	Leu	Pro	Lys	Thr
			20					25					30		
Glu	Ile	Arg	Thr	Leu	Asn	Arg	Leu	Trp	His	Pro	Trp	Glu	Arg	Gln	Lys
			35				40					45			
Val	Glu	Phe	Phe	Arg	Leu	Ser	Asp	Leu	Trp	Asp	Cys	Tyr	Asp	Glu	Trp
			50				55				60				
Ser	Ala	Tyr	Gly	Ala	Ser	Val	Pro	Ile	His	Val	Thr	Asn	Gly	Glu	Ser
			65			70			75					80	
Leu	Val	Gln	Tyr	Tyr	Val	Pro	Tyr	Leu	Ser	Ala	Ile	Gln	Ile	Phe	Thr
			85					90					95		
Ser	His	Ser	Ser	Leu	Ile	Arg	Leu	Arg	Glu	Ser	Glu	Asp	Gly	Gly	Glu
			100				105					110			
Cys	Glu	Gly	Arg	Asp	Pro	Phe	Ser	Asp	Ser	Gly	Ser	Asp	Glu	Ser	Val
			115				120					125			
Ser	Glu	Gly	Leu	Glu	Asn	Asn	Thr	Leu	Leu	His	Pro	Ser	Ser	Asp	Arg
			130			135				140					
Leu	Gly	Tyr	Leu	Tyr	Leu	Gln	Tyr	Phe	Glu	Arg	Ser	Ala	Pro	Tyr	Thr
			145			150			155					160	
Arg	Val	Pro	Leu	Met	Asp	Lys	Ile	Asn	Glu	Leu	Ala	Gln	Arg	Tyr	Pro
			165					170						175	
Gly	Leu	Met	Ser	Leu	Arg	Ser	Val	Asp	Leu	Ser	Pro	Ala	Ser	Trp	Met
			180					185						190	

Ser Val Ala Trp Tyr Pro Ile Tyr His Ile Pro Met Gly Arg Thr Ile
195 200 205
Lys Asp Leu Ser Thr Cys Phe Leu Thr Tyr His Thr Leu Ser Ser Ser
210 215 220
Phe Gln Asp Met Glu Pro Glu Glu Asn Gly Gly Asp Lys Glu Arg Val
225 230 235 240
Arg Arg Glu Gly Glu Asp Ile Thr Leu Leu Pro Phe Gly Met Ala Thr
245 250 255
Tyr Lys Met Gln Gly Asp Val Trp Leu Ser Gln Asp His Asp Asp Gln
260 265 270
Glu Arg Leu Ala Ser Leu Tyr Ser Val Ala Asp Ser Trp Leu Lys Gln
275 280 285
Leu Arg Val Gln His His Asp Phe Asn Tyr Phe Cys Asn Met Ser Met
290 295 300
Thr His Arg Gly

(2) INFORMATION FOR SEQ ID NO:908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1963 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1963
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

atttaattggc	aaagccggaa	aatgacgtca	tcttaaccga	gaaacaaaca	tggagcacat	60
gggaagagct	tctctcgcgc	tgccgcgtac	accgtcacgg	taccgaatca	tggaaactctg	120
tttccgcgtga	aatccagaaa	ctgagtcoca	acctctgttc	cctcacgcgc	tcgcgttgcc	180
gccacaagta	ctctgacctc	aaaagccggt	tcactcaaga	gctggccgta	ccggaatccg	240
tcgctgcgat	ctcaaacgct	ccttggttag	aggagttaag	gaagctccgc	gtcgaatgagc	300
tcgctgcgga	agttgaacag	tacgatttat	ccatctcaac	gttgcatcgc	aaggtggaagc	360
aaattggaaga	agagagagag	atgagtttca	ttaaaccgga	cacggaaaac	gagaatttag	420
atctagagag	gaagaaagag	cgtagCGatG	tccggtgaac	cagtcocaaa	ccgcgcgggt	480
cagctaattga	acgaaaccat	ttctccagat	cccaaagaaa	tcggatcggg	aaacacggag	540
agggaggagg	aaatggccgc	aagcgcgcgc	ggagaatcga	agcttgccgc	agaggattct	600
tgtagaggaa	gctgtgaaag	tgtggagaag	gaactgacga	cgaactcggg	gagagttgaa	660
ccggtgagtg	tgaccagagt	gatagagtcg	gaggacggag	cgaagtcgtg	agaggagagt	720
actagtatg	tgacagagtc	gcgagccttg	ccaagaaagg	gaacgtcggg	gccggataag	780
gaagatcaat	ctccgacgag	cgccaaagat	ttcacccgtg	aatcacagcc	gttgattagt	840
tttgcgaga	tctctctctc	tcacccctgt	ggttcccaat	tttcgcccgc	actcgaactgt	900
caggaaacaa	ttgagtgatc	tacaataatt	agagagcacg	tagattttga	gataattcgc	960
aagcgagtcg	aaggaggctt	gtacaaaagt	tggaggatca	actctttctg	tgatttgcgt	1020
ctacttgtta	ataatgcaag	agtgttttat	cagagaagat	cttcagaggt	taaattttgt	1080
gagcagcttc	accaactcgt	caagaaacag	atgactacta	ctctcaaggg	acttagtaat	1140
agagatgaga	tctcaactct	accaccaaaa	gaagaagtgt	ttgcaatccc	ttcatcaaa	1200
ccgtgtttct	ctaaaccagg	aatgtctgtt	cctaattatg	tagcttgtcg	gaaacgtagt	1260
gccttggctg	ctaaaccttt	gctattattg	cctcctggac	cagataaaaa	ggccaaagaa	1320
acagatcatg	ttgtggacta	tgatgagaag	cgggtttcac	acaaggtatg	tgaagcctct	1380
gggaagacgc	atgatgactc	tctgattgtg	aagataataa	ctagaggaag	aacctcctcg	1440
acgggaaaag	tagctaacag	gaacgtcaag	aaccgtgact	ccagtttgaa	tgttgatgat	1500
agcaaaagata	aggttaagaa	aactgatgaa	gagaagaaag	gtggctcgaa	aaagaaaggg	1560
gtgcgaggtt	ttctcaggag	aatgaaaagt	ggactcttcg	atgacacatt	gaagcgtagc	1620
ttctgtctgc	attcttctac	tacgggaaaa	ggaggaggag	cggaaacagag	gaagaataac	1680
agcaacaaag	ctgataattac	gaaaacacgc	ataccaaagg	taagacaaga	aaataagaaa	1740
gcaagctctg	tgaagagaag	caataatggt	cgaaactcag	aaagagaagc	tgctccatct	1800
tactctattc	tagcaaaagc	aagcagagaa	gctggtgaaa	aagaggagcg	gtctttctat	1860
tcaccacgat	tgaagaaacg	tgcaaggagg	tgatgtagtt	gttgactaac	ttatataact	1920
taacttgaga	tgaaaatcag	aaactaataa	attccaaaga	gtc		

(2) INFORMATION FOR SEQ ID NO:909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..481
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

Met	Ser	Gly	Glu	Pro	Val	Pro	Asn	Pro	Pro	Val	Gln	Leu	Met	Asn	Glu
1			5					10						15	
Thr	Ile	Ser	Pro	Asp	Pro	Lys	Glu	Ile	Gly	Ser	Glu	Asn	Thr	Glu	Arg
			20					25					30		
Glu	Glu	Glu	Met	Ala	Gly	Ser	Gly	Gly	Gly	Glu	Ser	Lys	Leu	Ala	Gly
			35				40					45			
Glu	Asp	Ser	Cys	Arg	Gly	Ser	Cys	Glu	Ser	Val	Glu	Lys	Glu	Leu	Thr
			50			55					60				
Thr	Asn	Ser	Glu	Arg	Val	Glu	Pro	Val	Ser	Val	Thr	Glu	Leu	Ile	Glu
65				70					75					80	
Ser	Glu	Asp	Gly	Ala	Ser	Arg	Gly	Glu	Glu	Ile	Thr	Ser	Asp	Val	Gln
			85					90						95	
Ser	Ser	Ala	Ser	Leu	Pro	Arg	Lys	Gly	Thr	Ser	Glu	Pro	Asp	Lys	Glu
			100				105						110		
Asp	Gln	Ser	Pro	Thr	Ser	Ala	Lys	Asp	Phe	Thr	Val	Glu	Ser	Gln	Pro
			115				120						125		
Leu	Ile	Ser	Phe	Val	Glu	Ile	Leu	Leu	Ser	His	Pro	Cys	Gly	Ser	His
			130			135					140				
Phe	Ser	Arg	Arg	Leu	Glu	Arg	Gln	Glu	Thr	Ile	Glu	Tyr	Gly	Thr	Ile
145				150					155					160	
Ile	Arg	Glu	His	Val	Asp	Phe	Glu	Ile	Ile	Arg	Lys	Arg	Val	Glu	Gly
			165					170						175	
Gly	Leu	Tyr	Lys	Ser	Trp	Arg	Ile	Asn	Phe	Phe	Arg	Asp	Leu	Leu	Leu
			180				185						190		
Leu	Val	Asn	Asn	Ala	Arg	Val	Phe	Tyr	His	Arg	Gly	Ser	Ser	Glu	Phe
			195				200					205			
Lys	Phe	Ala	Glu	Gln	Leu	His	Gln	Leu	Val	Lys	Lys	Gln	Met	Thr	Thr
			210			215					220				
Thr	Leu	Lys	Gly	Leu	Ser	Asn	Arg	Asp	Glu	Ile	Ser	Ile	Ser	Pro	Pro
225				230					235					240	
Lys	Glu	Glu	Val	Val	Ala	Ile	Pro	Ser	Ser	Lys	Pro	Val	Ser	Ser	Lys
			245						250					255	
Pro	Arg	Met	Ser	Val	Pro	Asn	Ile	Val	Ala	Cys	Arg	Lys	Arg	Ser	Ala
			260				265						270		
Leu	Ala	Ala	Lys	Pro	Leu	Leu	Leu	Leu	Pro	Pro	Gly	Pro	Asp	Lys	Lys
			275				280					285			
Ala	Lys	Lys	Thr	Asp	His	Val	Val	Asp	Tyr	Asp	Glu	Lys	Pro	Val	Ser
			290			295					300				
Asp	Lys	Asp	Gly	Glu	Ala	Ser	Gly	Lys	Asp	Asp	Asp	Asp	Ser	Leu	Ile
305				310					315					320	
Val	Lys	Ile	Ile	Thr	Arg	Gly	Arg	Thr	Ser	Ser	Thr	Gly	Lys	Val	Ala
			325						330					335	
Asn	Arg	Asn	Val	Lys	Asn	Arg	Asp	Ser	Ser	Leu	Asn	Val	Asp	Asp	Ser
			340				345							350	
Lys	Asp	Lys	Val	Lys	Lys	Thr	Asp	Glu	Glu	Lys	Lys	Gly	Gly	Ser	Lys
			355				360					365			
Lys	Lys	Gly	Ala	Ala	Ser	Phe	Leu	Arg	Arg	Met	Lys	Val	Gly	Ser	Ser
			370			375					380				
Asp	Asp	Thr	Leu	Lys	Arg	Ser	Ser	Ala	Ala	Asp	Ser	Ser	Thr	Thr	Gly

385		390		395		400
Lys Gly Gly Gly Ala Glu Gln Arg Lys Asn Asn Ser Asn Lys Ala Asp		405		410		415
Asn Lys Lys Thr Pro Ile Pro Arg Ile Arg Gln Thr Asn Lys Lys Ala		420		425		430
Ser Pro Val Lys Arg Ser Asn Asn Gly Arg Asn Ser Glu Arg Glu Ala		435		440		445
Ala Pro Ser Tyr Pro Ile Leu Ala Lys Arg Ser Arg Glu Ala Gly Glu		450		455		460
Lys Glu Glu Ala Ser Ser Tyr Ser Pro Arg Leu Lys Lys Arg Ala Arg		465		470		475
Arg						480

(2) INFORMATION FOR SEQ ID NO:910:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 468 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..468

(D) OTHER INFORMATION: / Ceres Seq. ID 1568311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

Met Asn Glu Thr Ile Ser Pro Asp Pro Lys Glu Ile Gly Ser Glu Asn	
1 5 10 15	
Thr Glu Arg Glu Glu Met Ala Gly Ser Gly Gly Glu Ser Lys	
20 25 30	
Leu Ala Gly Glu Asp Ser Cys Arg Gly Ser Cys Glu Ser Val Glu Lys	
35 40 45	
Glu Leu Thr Thr Asn Ser Glu Arg Val Glu Pro Val Ser Val Thr Glu	
50 55 60	
Leu Ile Glu Ser Glu Asp Gly Ala Ser Arg Gly Glu Glu Ile Thr Ser	
65 70 75	
Asp Val Gln Ser Ser Ala Ser Leu Pro Arg Lys Gly Thr Ser Glu Pro	
85 90 95	
Asp Lys Glu Asp Gln Ser Pro Thr Ser Ala Lys Asp Phe Thr Val Glu	
100 105 110	
Ser Gln Pro Leu Ile Ser Phe Val Glu Ile Leu Leu Ser His Pro Cys	
115 120 125	
Gly Ser His Phe Ser Arg Arg Leu Glu Arg Gln Glu Thr Ile Glu Tyr	
130 135 140	
Gly Thr Ile Ile Arg Glu His Val Asp Phe Glu Ile Ile Arg Lys Arg	
145 150 155	
Val Glu Gly Gly Leu Tyr Lys Ser Trp Arg Ile Asn Phe Phe Arg Asp	
165 170 175	
Leu Leu Leu Leu Val Asn Asn Ala Arg Val Phe Tyr His Arg Gly Ser	
180 185 190	
Ser Glu Phe Lys Phe Ala Glu Gln Leu His Gln Leu Val Lys Lys Gln	
195 200 205	
Met Thr Thr Thr Leu Lys Gly Leu Ser Asn Arg Asp Glu Ile Ser Ile	
210 215 220	
Ser Pro Pro Lys Glu Glu Val Val Ala Ile Pro Ser Ser Lys Pro Val	
225 230 235	
Ser Ser Lys Pro Arg Met Ser Val Pro Asn Ile Val Ala Cys Arg Lys	
245 250 255	
Arg Ser Ala Leu Ala Ala Lys Pro Leu Leu Leu Leu Pro Gly Pro	
260 265 270	
Asp Lys Lys Ala Lys Lys Thr Asp His Val Val Asp Tyr Asp Glu Lys	
275 280 285	

Pro Val Ser Asp Lys Asp Gly Glu Ala Ser Gly Lys Asp Asp Asp Asp
290 295 300
Ser Leu Ile Val Lys Ile Ile Thr Arg Gly Arg Thr Ser Ser Thr Gly
305 310 315 320
Lys Val Ala Asn Arg Asn Val Lys Asn Arg Asp Ser Ser Leu Asn Val
325 330 335
Asp Asp Ser Lys Asp Lys Val Lys Lys Thr Asp Glu Glu Lys Lys Gly
340 345 350
Gly Ser Lys Lys Lys Gly Ala Ala Ser Phe Leu Arg Arg Met Lys Val
355 360 365
Gly Ser Ser Asp Asp Thr Leu Lys Arg Ser Ser Ala Ala Asp Ser Ser
370 375 380
Thr Thr Gly Lys Gly Gly Gly Ala Glu Gln Arg Lys Asn Asn Ser Asn
385 390 395 400
Lys Ala Asp Asn Lys Lys Thr Pro Ile Pro Arg Ile Arg Gln Thr Asn
405 410 415
Lys Lys Ala Ser Pro Val Lys Arg Ser Asn Asn Gly Arg Asn Ser Glu
420 425 430
Arg Glu Ala Ala Pro Ser Tyr Pro Ile Leu Ala Lys Arg Ser Arg Glu
435 440 445
Ala Gly Glu Lys Glu Glu Ala Ser Tyr Ser Pro Arg Leu Lys Lys
450 455 460
Arg Ala Arg Arg
465

(2) INFORMATION FOR SEQ ID NO:911:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 446 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..446

(D) OTHER INFORMATION: / Ceres Seq. ID 1568312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

Met Ala Gly Ser Gly Gly Gly Glu Ser Lys Leu Ala Gly Glu Asp Ser
1 5 10 15
Cys Arg Gly Ser Cys Glu Ser Val Glu Lys Glu Leu Thr Thr Asn Ser
20 25 30
Glu Arg Val Glu Pro Val Ser Val Thr Glu Leu Ile Glu Ser Glu Asp
35 40 45
Gly Ala Ser Arg Gly Glu Glu Ile Thr Ser Asp Val Gln Ser Ser Ala
50 55 60
Ser Leu Pro Arg Lys Gly Thr Ser Glu Pro Asp Lys Glu Asp Gln Ser
65 70 75 80
Pro Thr Ser Ala Lys Asp Phe Thr Val Glu Ser Gln Pro Leu Ile Ser
85 90 95
Phe Val Glu Ile Leu Leu Ser His Pro Cys Gly Ser His Phe Ser Arg
100 105 110
Arg Leu Glu Arg Gln Glu Thr Ile Glu Tyr Gly Thr Ile Ile Arg Glu
115 120 125
His Val Asp Phe Glu Ile Ile Arg Lys Arg Val Glu Gly Gly Leu Tyr
130 135 140
Lys Ser Trp Arg Ile Asn Phe Phe Arg Asp Leu Leu Leu Val Asn
145 150 155 160
Asn Ala Arg Val Phe Tyr His Arg Gly Ser Ser Glu Phe Lys Phe Ala
165 170 175
Glu Gln Leu His Gln Leu Val Lys Lys Gln Met Thr Thr Thr Leu Lys
180 185 190
Gly Leu Ser Asn Arg Asp Glu Ile Ser Ile Ser Pro Pro Lys Glu Glu

195	200	205
Val Val Ala Ile Pro Ser Ser Lys Pro Val Ser Ser Lys Pro Arg Met		
210	215	220
Ser Val Pro Asn Ile Val Ala Cys Arg Lys Arg Ser Ala Leu Ala Ala		
225	230	235
Lys Pro Leu Leu Leu Leu Pro Pro Gly Pro Asp Lys Lys Ala Lys Lys		
245	250	255
Thr Asp His Val Val Asp Tyr Asp Glu Lys Pro Val Ser Asp Lys Asp		
260	265	270
Gly Glu Ala Ser Gly Lys Asp Asp Asp Ser Leu Ile Val Lys Ile		
275	280	285
Ile Thr Arg Gly Arg Thr Ser Ser Thr Gly Lys Val Ala Asn Arg Asn		
290	295	300
Val Lys Asn Arg Asp Ser Ser Leu Asn Val Asp Ser Lys Asp Lys		
305	310	315
Val Lys Lys Thr Asp Glu Glu Lys Lys Gly Ser Lys Lys Lys Gly		
325	330	335
Ala Ala Ser Phe Leu Arg Arg Met Lys Val Gly Ser Ser Asp Asp Thr		
340	345	350
Leu Lys Arg Ser Ser Ala Ala Asp Ser Ser Thr Thr Gly Lys Gly Gly		
355	360	365
Gly Ala Glu Gln Arg Lys Asn Asn Ser Asn Lys Ala Asp Asn Lys Lys		
370	375	380
Thr Pro Ile Pro Arg Ile Arg Gln Thr Asn Lys Lys Ala Ser Pro Val		
385	390	395
Lys Arg Ser Asn Asn Gly Arg Asn Ser Glu Arg Glu Ala Ala Pro Ser		
405	410	415
Tyr Pro Ile Leu Ala Lys Arg Ser Arg Glu Ala Gly Glu Lys Glu Glu		
420	425	430
Ala Ser Ser Tyr Ser Pro Arg Leu Lys Lys Arg Ala Arg Arg		
435	440	445

(2) INFORMATION FOR SEQ ID NO:912:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..635
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

ttacagtcoc	atgatccgtg	cttggTttga	tcctcaccat	catcaccaat	ccatctccac	60
cgacgatctc	aaccaccacc	atcaccttcc	tcacccggtt	caccaatcag	caatcccgg	120
aatcggtattc	gocctcagggt	aattatcttc	gggttttcgc	ataccagcac	ggtttcagg	180
ccaagaagag	gagcagcacg	acggtctcac	tcacaagcgc	tcctctgctt	ctctatattc	240
tcgccattga	caatcgaaac	taatcctcta	agtttcagg	ctgtgtacg	ttccatgcac	300
attgaagctt	gacttagatt	gtccggaaca	gggaagggtg	tctcggtttg	tgtagtcaat	360
ggcctgaatc	tagaanaacg	aaggaaatga	agaaagaaca	acagtttcag	gttcttcttc	420
ttcttcttcc	aatattcttaa	cttgcgcgat	tgtaattttt	catattttca	ccagtttagac	480
caacgttctt	ctgtagctca	attatggtta	gattocaagg	ttctgtcttg	ttgtgttatg	540
tttgtAactt	tgtatcatca	tcacCotatt	gttactgctc	cctgttttta	ttgtgttaact	600
ccgtggatgt	tctaataaag	ctgaaactt	tctctc			

(2) INFORMATION FOR SEQ ID NO:913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1568314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

Tyr	Ser	Pro	Met	Ile	Arg	Ala	Trp	Phe	Asp	Pro	His	His	His	Gln
1			5						10				15	
Ser	Ile	Ser	Thr	Asp	Asp	Leu	Asn	His	His	His	His	Leu	Pro	Pro
			20					25				30		
Val	His	Gln	Ser	Ala	Ile	Pro	Gly	Ile	Gly	Phe	Ala	Ser	Gly	Leu
		35				40					45			
Ser	Ser	Gly	Phe	Arg	Ile	Pro	Ala	Arg	Phe	Gln	Gly	Gln	Glu	Glu
		50			55				60					
Gln	His	Asp	Gly	Leu	Thr	His	Lys	Pro	Ser	Ser	Ala	Ser	Ile	Ser
65				70					75				80	
Arg	His													

(2) INFORMATION FOR SEQ ID NO:914:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1568315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

Met	Ile	Arg	Ala	Trp	Phe	Asp	Pro	His	His	His	His	Gln	Ser	Ile	Ser
1			5						10					15	
Thr	Asp	Asp	Leu	Asn	His	His	His	His	Leu	Pro	Pro	Pro	Val	His	Gln
			20					25					30		
Ser	Ala	Ile	Pro	Gly	Ile	Gly	Phe	Ala	Ser	Gly	Glu	Leu	Ser	Ser	Gly
		35				40					45				
Phe	Arg	Ile	Pro	Ala	Arg	Phe	Gln	Gly	Gln	Glu	Glu	Glu	Gln	His	Asp
		50			55					60					
Gly	Leu	Thr	His	Lys	Pro	Ser	Ser	Ala	Ser	Ser	Ile	Ser	Arg	His	
65				70					75						

(2) INFORMATION FOR SEQ ID NO:915:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..44

(D) OTHER INFORMATION: / Ceres Seq. ID 1568316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

Met	Val	Arg	Phe	Gln	Gly	Phe	Val	Leu	Leu	Cys	Tyr	Val	Cys	Asn	Phe
1			5						10					15	
Val	Ser	Ser	Ser	Ser	Tyr	Cys	Tyr	Cys	Ser	Leu	Phe	Leu	Leu	Cys	Asn
			20				25						30		
Ser	Val	Asp	Val	Leu	Ile	Lys	Ser	Glu	Thr	Phe	Ser				
		35				40									

(2) INFORMATION FOR SEQ ID NO:916:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 407 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..407
(D) OTHER INFORMATION: / Ceres Seq. ID 1568321
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:
tttggggttg gttgagatga tgaagggaag agagagagtg tgggaggaga tggttaagga 60
gaatcaattg caagagaaga agcttgagga agttgggttg tgggtggttg ctgatgttat 120
actttggaggg attgcgactg tggcttgggt tttcttttac actttcttcg cggagacgca 180
agggaggatg cttgaggata tggatgagct tttcagtggt ttcaggtgga gagattccaa 240
gagtaagcct aagggttaacc ccgagaagac ggtaccgaat cccgaggttg agattggatc 300
aaacaagcag tggaaaggaag gagacacaca aagttcgtag gaaattttgat catgatgtga 360
atttgtatgg tatgGtgggt ttaatgataa aacgaacaaa ttagcgt

(2) INFORMATION FOR SEQ ID NO:917:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..112
(D) OTHER INFORMATION: / Ceres Seq. ID 1568322
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:
Leu Gly Leu Val Glu Met Met Lys Gly Lys Glu Arg Val Trp Glu Glu
1 5 10 15
Met Val Lys Glu Asn Gln Leu Gln Glu Lys Lys Leu Glu Glu Val Gly
20 25 30
Val Trp Trp Phe Ala Asp Val Ile Leu Gly Gly Ile Ala Thr Val Ala
35 40 45
Trp Val Phe Phe Tyr Thr Phe Leu Pro Glu Thr Gln Gly Arg Met Leu
50 55 60
Glu Asp Met Asp Glu Leu Phe Ser Gly Phe Arg Trp Arg Asp Ser Lys
65 70 75 80
Ser Lys Pro Lys Gly Asn Pro Glu Lys Thr Val Pro Asn Pro Glu Val
85 90 95
Glu Ile Gly Ser Asn Lys Gln Trp Lys Glu Gly Asp Thr Gln Ser Ser
100 105 110

(2) INFORMATION FOR SEQ ID NO:918:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..107
(D) OTHER INFORMATION: / Ceres Seq. ID 1568323
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:
Met Met Lys Gly Lys Glu Arg Val Trp Glu Glu Met Val Lys Glu Asn
1 5 10 15
Gln Leu Gln Glu Lys Lys Leu Glu Glu Val Gly Val Trp Trp Phe Ala
20 25 30
Asp Val Ile Leu Gly Gly Ile Ala Thr Val Ala Trp Val Phe Phe Tyr
35 40 45

Thr Phe Leu Pro Glu Thr Gln Gly Arg Met Leu Glu Asp Met Asp Glu
50 55 60
Leu Phe Ser Gly Phe Arg Trp Arg Asp Ser Lys Ser Lys Pro Lys Gly
65 70 75 80
Asn Pro Glu Lys Thr Val Pro Asn Pro Glu Val Glu Ile Gly Ser Asn
85 90 95
Lys Gln Trp Lys Glu Gly Asp Thr Gln Ser Ser
100 105

(2) INFORMATION FOR SEQ ID NO:919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1568324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

Met Lys Gly Lys Glu Arg Val Trp Glu Glu Met Val Lys Glu Asn Gln
1 5 10 15
Leu Gln Glu Lys Lys Leu Glu Glu Val Gly Val Trp Trp Phe Ala Asp
20 25 30
Val Ile Leu Gly Gly Ile Ala Thr Val Ala Trp Val Phe Phe Tyr Thr
35 40 45
Phe Leu Pro Glu Thr Gln Gly Arg Met Leu Glu Asp Met Asp Glu Leu
50 55 60
Phe Ser Gly Phe Arg Trp Arg Asp Ser Lys Ser Lys Pro Lys Gly Asn
65 70 75 80
Pro Glu Lys Thr Val Pro Asn Pro Glu Val Glu Ile Gly Ser Asn Lys
85 90 95
Gln Trp Lys Glu Gly Asp Thr Gln Ser Ser
100 105

(2) INFORMATION FOR SEQ ID NO:920:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..821

(D) OTHER INFORMATION: / Ceres Seq. ID 1568333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

aaaaaaaggga gaaagcttga aacgcgcgctt cttcttcttc tctgtcgttc tctctgtaaa 60
tcgcttcttc aatcatctct gtggatttgt ctctattcat aacttgggtga agaagatggt 120
gacggaagag gagctcaaaa gattgtacag aatccagaag acgttgtatgc agatgttaag 180
ggatcgttga tattttatcg cggattctga acttacgatg actaaacaac agtttattag 240
gaaacatggt gataacatga aaagagagga tcttgttact ctaagagcta agcgaatga 300
taatagtgat cagctctata tattcttccc tgatgaggcg aaagtgtggtg tgaagacgat 360
gaaaatgtac acgaacacga tgaatcaga gaatgtgttc agagctattt tggttgtgcA 420
acagaaacttg accccggttg ctcgaaacttg cattagttag atctcttcta aGgtttcatc 480
tggaagtctt ccaGggaggg ggaatgcta gtgaacata aagaacatgt tcttgttctc 540
gagcatcaag ttcttaccac tgaagagaag aaaactttac tggagagata cacagtgaag 600
gagacacagc ttccaaggat caaagtgact gatccaatcg caagataact ttgactaaaa 660
cgtgggcaag tcgtgaagat cattcgtccg agtgaacagg ctggtcgcta tgttaacctat 720
cgttatgttg tataagccaa agcaaaaggc ttttgtggat tgtaatgcga attgaacgct 780
gagagtgttg aaacataaga gtaatgcttt tgtactaaac c

(2) INFORMATION FOR SEQ ID NO:921:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 169 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..169
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568334
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

Lys	Lys	Gly	Glu	Ser	Leu	Lys	Arg	Arg	Phe	Phe	Phe	Phe	Ser	Val	Val
1				5					10					15	
Leu	Ser	Val	Asn	Arg	Phe	Phe	Asn	His	Leu	Cys	Gly	Phe	Val	Ser	Ile
			20				25						30		
His	Asn	Leu	Val	Lys	Lys	Met	Leu	Thr	Glu	Glu	Glu	Leu	Lys	Arg	Leu
			35				40					45			
Tyr	Arg	Ile	Gln	Lys	Thr	Leu	Met	Gln	Met	Leu	Arg	Asp	Arg	Gly	Tyr
			50				55					60			
Phe	Ile	Ala	Asp	Ser	Glu	Leu	Thr	Met	Thr	Lys	Gln	Gln	Phe	Ile	Arg
65					70					75				80	
Lys	His	Gly	Asp	Asn	Met	Lys	Arg	Glu	Asp	Leu	Val	Thr	Leu	Lys	Ala
				85						90				95	
Lys	Arg	Asn	Asp	Asn	Ser	Asp	Gln	Leu	Tyr	Ile	Phe	Phe	Pro	Asp	Glu
			100					105						110	
Ala	Lys	Val	Gly	Val	Lys	Thr	Met	Lys	Met	Tyr	Thr	Asn	Arg	Met	Lys
			115				120					125			
Ser	Glu	Asn	Val	Phe	Arg	Ala	Ile	Leu	Val	Val	Gln	Gln	Asn	Leu	Thr
			130			135						140			
Pro	Phe	Ala	Arg	Thr	Cys	Ile	Ser	Glu	Ile	Ser	Ser	Lys	Val	Ser	Ser
145				150					155					160	
Gly	Ser	Phe	Pro	Gly	Arg	Arg	Lys	Cys							
				165											

(2) INFORMATION FOR SEQ ID NO:922:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..131
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568335
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

Met	Leu	Thr	Glu	Glu	Leu	Lys	Arg	Leu	Tyr	Arg	Ile	Gln	Lys	Thr
1					5				10				15	
Leu	Met	Gln	Met	Leu	Arg	Asp	Arg	Gly	Tyr	Phe	Ile	Ala	Asp	Ser
			20					25					30	
Leu	Thr	Met	Thr	Lys	Gln	Gln	Phe	Ile	Arg	Lys	His	Gly	Asp	Asn
			35				40					45		Met
Lys	Arg	Glu	Asp	Leu	Val	Thr	Leu	Lys	Ala	Lys	Arg	Asn	Asp	Asn
			50				55				60			Ser
Asp	Gln	Leu	Tyr	Ile	Phe	Phe	Pro	Asp	Glu	Ala	Lys	Val	Gly	Val
65					70				75					80
Thr	Met	Lys	Met	Tyr	Thr	Asn	Arg	Met	Lys	Ser	Glu	Asn	Val	Phe
			85					90					95	Arg
Ala	Ile	Leu	Val	Val	Gln	Gln	Asn	Leu	Thr	Pro	Phe	Ala	Arg	Thr
			100				105					110		Cys
Ile	Ser	Glu	Ile	Ser	Ser	Lys	Val	Ser	Ser	Gly	Ser	Phe	Pro	Gly
			115				120					125		Arg

Arg Lys Cys
130

(2) INFORMATION FOR SEQ ID NO:923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

Met	Gln	Met	Leu	Arg	Asp	Arg	Gly	Tyr	Phe	Ile	Ala	Asp	Ser	Glu	Leu
1			5					10					15		
Thr	Met	Thr	Lys	Gln	Gln	Phe	Ile	Arg	Lys	His	Gly	Asp	Asn	Met	Lys
			20					25					30		
Arg	Glu	Asp	Leu	Val	Thr	Leu	Lys	Ala	Lys	Arg	Asn	Asp	Asn	Ser	Asp
			35				40					45			
Gln	Leu	Tyr	Ile	Phe	Phe	Pro	Asp	Glu	Ala	Lys	Val	Gly	Val	Lys	Thr
			50			55					60				
Met	Lys	Met	Tyr	Thr	Asn	Arg	Met	Lys	Ser	Glu	Asn	Val	Phe	Arg	Ala
					70					75				80	
Ile	Leu	Val	Val	Gln	Gln	Asn	Leu	Thr	Pro	Phe	Ala	Arg	Thr	Cys	Ile
				85				90						95	
Ser	Glu	Ile	Ser	Ser	Lys	Val	Ser	Ser	Gly	Ser	Phe	Pro	Gly	Arg	Arg
			100				105						110		

Lys Cys

(2) INFORMATION FOR SEQ ID NO:924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1264
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

aatggattac	ttttcttcca	cacatatata	acttaactct	ctctttttct	cttttgcctt	60
aaccctccca	aagaaaagat	aagagccttt	taaaagtttt	ttttttacct	tcctctcatg	120
gacttgtctg	tacttgatag	gcttaagtgg	ctgcaacagc	aacaaaatgt	ttcaactgag	180
tttcttcaga	tacttggctc	agatggggaga	gaagagctca	aaagagtga	gagttacttg	240
ggaaaAcaac	aatgatgagc	tgacagattt	cagacatttt	ccggaattcg	gaccggatta	300
tgatactact	gatggctgca	tttctaggac	aagttagcttc	catatggagc	cagtgaagaa	360
taatggacac	agcagagcca	ttaccttgca	gaacaagaga	aaaccagagg	gtaagacaga	420
aaagagagag	aagaagaaga	tcaaaagcaga	ggatgaaaca	gagccaaagca	tgaaggggaa	480
atcaaacatg	agtaacRoag	agacatcttc	agaaattcag	aaaccagatt	acattcatgt	540
tagggctaga	cgaggtgaag	ccacogacag	acatagctta	gcagagaggg	caagaagaga	600
aaagataagc	aagaagatga	aatgtctaca	agatatgttt	cctggatgca	acaaagttac	660
tggaataagc	ggatgtcttg	atgagatcat	caactatgtc	caatctctcg	accaacaagt	720
cgaattcttg	tcgatgaaac	ttctgtcat	aaatccagaa	cttgagtgtc	atatcgatga	780
ttatcccgca	aaacagtttc	aggcttactt	cacaggtcct	ccagaagggt	actcgaagca	840
gtcaatcatg	gcggattttc	ggcttttttc	attacatcag	caaggatctt	tagattactc	900
agtcataaac	tcagaccaca	ccacatctct	cggcgctaaa	gatcatatcat	catcaagctg	960
ggaaactcac	tcacagtgtc	tttacaacag	cttgagaacc	gattcttttt	ccaatttttt	1020
cagcctcaag	taaaaaaatt	agggatagcc	tcattaaaaa	aatcgcggtt	ttttgtgttt	1080
gtcttatcca	tttatctatc	tattctgaaa	tttgaaccag	aaagacagag	gaaaccaatc	1140

caaagatctt tctcaatcta ttatcttcat acaaatatag tgattttacat atattccagg 1200
ggatatgtat atgtgtagaa gaaagagaaa aaactcttgt ggcatagca attccttttt 1260
ttgt

(2) INFORMATION FOR SEQ ID NO:925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..276

(D) OTHER INFORMATION: / Ceres Seq. ID 1568358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

Met	Gly	Glu	Lys	Ser	Ser	Lys	Glu	Leu	Arg	Val	Thr	Trp	Glu	Asn	Asn
1			5				10						15		
Asn	Asp	Glu	Leu	Gln	Ser	Phe	Arg	His	Phe	Pro	Glu	Phe	Gly	Pro	Asp
			20				25						30		
Tyr	Asp	Thr	Thr	Asp	Gly	Cys	Ile	Ser	Arg	Thr	Ser	Ser	Phe	His	Met
			35				40						45		
Glu	Pro	Val	Lys	Asn	Asn	Gly	His	Ser	Arg	Ala	Ile	Thr	Leu	Gln	Asn
			50				55						60		
Lys	Arg	Lys	Pro	Glu	Gly	Lys	Thr	Glu	Lys	Arg	Glu	Lys	Lys	Lys	Ile
							70						75		
Lys	Ala	Glu	Asp	Glu	Thr	Glu	Pro	Ser	Met	Lys	Gly	Lys	Ser	Asn	Met
							85						90		
Ser	Asn	Xaa	Glu	Thr	Ser	Ser	Glu	Ile	Gln	Lys	Pro	Asp	Tyr	Ile	His
													100		
Val	Arg	Ala	Arg	Arg	Gly	Glu	Ala	Thr	Asp	Arg	His	Ser	Leu	Ala	Glu
													110		
Arg	Ala	Arg	Arg	Glu	Lys	Ile	Ser	Lys	Lys	Met	Lys	Cys	Leu	Gln	Asp
													120		
Ile	Val	Pro	Gly	Cys	Asn	Lys	Val	Thr	Gly	Lys	Ala	Gly	Met	Leu	Asp
													130		
Glu	Ile	Ile	Asn	Tyr	Val	Gln	Ser	Leu	Gln	Gln	Val	Glu	Phe	Leu	
													140		
Ser	Met	Lys	Leu	Ser	Val	Ile	Asn	Pro	Glu	Leu	Glu	Cys	His	Ile	Asp
													150		
Asp	Leu	Ser	Ala	Lys	Gln	Phe	Gln	Ala	Tyr	Phe	Thr	Gly	Pro	Pro	Glu
													160		
Gly	Asp	Ser	Lys	Gln	Ser	Ile	Met	Ala	Asp	Phe	Arg	Ser	Phe	Pro	Leu
													170		
His	Gln	Gln	Gly	Ser	Leu	Asp	Tyr	Ser	Val	Ile	Asn	Ser	Asp	His	Thr
													180		
Thr	Ser	Leu	Gly	Ala	Lys	Asp	His	Thr	Ser	Ser	Ser	Trp	Glu	Thr	His
													190		
Ser	Gln	Cys	Leu	Tyr	Asn	Ser	Leu	Arg	Thr	Asp	Ser	Ile	Ser	Asn	Phe
													200		
Phe	Ser	Leu	Lys										210		
													220		
													230		
													240		
													250		
													260		
													270		
													275		

(2) INFORMATION FOR SEQ ID NO:926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..229

(D) OTHER INFORMATION: / Ceres Seq. ID 1568359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

Met Glu Pro Val Lys Asn Asn Gly His Ser Arg Ala Ile Thr Leu Gln
1 5 10 15
Asn Lys Arg Lys Pro Glu Gly Lys Thr Glu Lys Arg Glu Lys Lys
20 25 30
Ile Lys Ala Glu Asp Glu Thr Glu Pro Ser Met Lys Gly Lys Ser Asn
35 40 45
Met Ser Asn Xaa Glu Thr Ser Ser Glu Ile Gln Lys Pro Asp Tyr Ile
50 55 60
His Val Arg Ala Arg Arg Gly Glu Ala Thr Asp Arg His Ser Leu Ala
65 70 75 80
Glu Arg Ala Arg Arg Glu Lys Ile Ser Lys Lys Met Lys Cys Leu Gln
85 90 95
Asp Ile Val Pro Gly Cys Asn Lys Val Thr Gly Lys Ala Gly Met Leu
100 105 110
Asp Glu Ile Ile Asn Tyr Val Gln Ser Leu Gln Gln Gln Val Glu Phe
115 120 125
Leu Ser Met Lys Leu Ser Val Ile Asn Pro Glu Leu Glu Cys His Ile
130 135 140
Asp Asp Leu Ser Ala Lys Gln Phe Gln Ala Tyr Phe Thr Gly Pro Pro
145 150 155 160
Glu Gly Asp Ser Lys Gln Ser Ile Met Ala Asp Phe Arg Ser Phe Pro
165 170 175
Leu His Gln Gln Gly Ser Leu Asp Tyr Ser Val Ile Asn Ser Asp His
180 185 190
Thr Thr Ser Leu Gly Ala Lys Asp His Thr Ser Ser Ser Trp Glu Thr
195 200 205
His Ser Gln Cys Leu Tyr Asn Ser Leu Arg Thr Asp Ser Ile Ser Asn
210 215 220
Phe Phe Ser Leu Lys
225

(2) INFORMATION FOR SEQ ID NO:927:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1568360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

Met Lys Gly Lys Ser Asn Met Ser Asn Xaa Glu Thr Ser Ser Glu Ile
1 5 10 15
Gln Lys Pro Asp Tyr Ile His Val Arg Ala Arg Arg Gly Glu Ala Thr
20 25 30
Asp Arg His Ser Leu Ala Glu Arg Ala Arg Arg Glu Lys Ile Ser Lys
35 40 45
Lys Met Lys Cys Leu Gln Asp Ile Val Pro Gly Cys Asn Lys Val Thr
50 55 60
Gly Lys Ala Gly Met Leu Asp Glu Ile Ile Asn Tyr Val Gln Ser Leu
65 70 75 80
Gln Gln Gln Val Glu Phe Leu Ser Met Lys Leu Ser Val Ile Asn Pro
85 90 95
Glu Leu Glu Cys His Ile Asp Asp Leu Ser Ala Lys Gln Phe Gln Ala
100 105 110
Tyr Phe Thr Gly Pro Pro Glu Gly Asp Ser Lys Gln Ser Ile Met Ala
115 120 125
Asp Phe Arg Ser Phe Pro Leu His Gln Gln Gly Ser Leu Asp Tyr Ser

Met	Ala	Thr	Ser	5	Ser	Met	Lys	Ser	Ile	Pro	Met	Ala	Ile	Pro	Ser	Phe
1										10					15	
Ser	Met	Cys	His	Lys	Leu	Glu	Leu	Lys	Glu	Gly	Lys	Thr	Arg	Asp		
			20				25					30				
Val	Pro	Lys	Ala	Glu	Glu	Asp	Glu	Gly	Leu	Ser	Cys	Glu	Phe	Gln	Glu	
		35					40					45				
Met	Leu	Asp	Ser	Leu	Pro	Lys	Glu	Arg	Gly	Trp	Arg	Thr	Arg	Tyr	Leu	
	50					55					60					

Tyr Leu Phe Gln Gly Phe Trp Cys Gln Ala Lys Glu Ile Gln Ala Ile
65 70 75 80
Met Ser Phe Gln Lys His Phe Gln Ser Leu Glu Asn Asp Val Val Leu
85 90 95
Ala Thr Ile Pro Lys Ser Gly Thr Thr Trp Leu Lys Ala Leu Thr Phe
100 105 110
Thr Ile Leu Asn Arg His Arg Phe Asp Pro Val Ala Ser Ser Thr Asn
115 120 125
His Pro Leu Phe Thr Ser Asn Pro His Asp Leu Val Pro Phe Phe Glu
130 135 140
Tyr Lys Leu Tyr Ala Asn Gly Asp Val Pro Asp Leu Ser Gly Leu Ala
145 150 155 160
Ser Pro Arg Thr Phe Ala Thr His Leu Pro Phe Gly Ser Leu Lys Glu
165 170 175
Thr Ile Glu Lys Pro Gly Val Lys Val Val Tyr Leu Cys Arg Asn Pro
180 185 190
Phe Asp Thr Phe Ile Ser Ser Trp His Tyr Thr Asn Asn Ile Lys Ser
195 200 205
Glu Ser Val Ser Pro Val Leu Leu Asp Gln Ala Phe Asp Leu Tyr Cys
210 215 220
Arg Gly Val Ile Gly Phe Gly Pro Phe Trp Glu His Met Leu Gly Tyr
225 230 235 240
Trp Arg Glu Ser Leu Lys Arg Pro Glu Lys Val Phe Phe Leu Arg Tyr
245 250 255
Glu Asp Leu Lys Asp Asp Ile Glu Thr Asn Leu Lys Arg Leu Ala Thr
260 265 270
Phe Leu Glu Leu Pro Phe Thr Glu Glu Glu Arg Lys Gly Val Val
275 280 285
Lys Ala Ile Ala Glu Leu Cys Ser Phe Glu Asn Leu Lys Lys Leu Glu
290 295 300
Val Asn Lys Ser Asn Lys Ser Ile Lys Asn Phe Glu Asn Arg Phe Leu
305 310 315 320
Phe Arg Lys Gly Glu Val Ser Asp Trp Val Asn Tyr Leu Ser Pro Ser
325 330 335
Gln Val Glu Arg Leu Ser Ala Leu Val Asp Asp Lys Leu Gly Gly Ser
340 345 350
Gly Leu Thr Phe Arg Leu Ser
355

(2) INFORMATION FOR SEQ ID NO:930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..354
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

Met Lys Ser Ile Pro Met Ala Ile Pro Ser Phe Ser Met Cys His Lys
1 5 10 15
Leu Glu Leu Leu Lys Glu Gly Lys Thr Arg Asp Val Pro Lys Ala Glu
20 25 30
Glu Asp Glu Gly Leu Ser Cys Glu Phe Gln Glu Met Leu Asp Ser Leu
35 40 45
Pro Lys Glu Arg Gly Trp Arg Thr Arg Tyr Leu Tyr Leu Phe Gln Gly
50 55 60
Phe Trp Cys Gln Ala Lys Glu Ile Gln Ala Ile Met Ser Phe Gln Lys
65 70 75 80
His Phe Gln Ser Leu Glu Asn Asp Val Val Leu Ala Thr Ile Pro Lys

	85		90		95
Ser Gly Thr Thr Trp Leu Lys Ala Leu Thr Phe Thr Ile Leu Asn Arg	100		105		110
His Arg Phe Asp Pro Val Ala Ser Ser Thr Asn His Pro Leu Phe Thr	115		120		125
Ser Asn Pro His Asp Leu Val Pro Phe Phe Glu Tyr Lys Leu Tyr Ala	130		135		140
Asn Gly Asp Val Pro Asp Leu Ser Gly Leu Ala Ser Pro Arg Thr Phe	145		150		155
Ala Thr His Leu Pro Phe Gly Ser Leu Lys Glu Thr Ile Glu Lys Pro	165		170		175
Gly Val Lys Val Val Tyr Leu Cys Arg Asn Pro Phe Asp Thr Phe Ile	180		185		190
Ser Ser Trp His Tyr Thr Asn Asn Ile Lys Ser Glu Ser Val Ser Pro	195		200		205
Val Leu Leu Asp Gln Ala Phe Asp Leu Tyr Cys Arg Gly Val Ile Gly	210		215		220
Phe Gly Pro Phe Trp Glu His Met Leu Gly Tyr Trp Arg Glu Ser Leu	225		230		235
Lys Arg Pro Glu Lys Val Phe Phe Leu Arg Tyr Glu Asp Leu Lys Asp	245		250		255
Asp Ile Glu Thr Asn Leu Lys Arg Leu Ala Thr Phe Leu Glu Leu Pro	260		265		270
Phe Thr Glu Glu Glu Glu Arg Lys Gly Val Val Lys Ala Ile Ala Glu	275		280		285
Leu Cys Ser Phe Glu Asn Leu Lys Lys Leu Glu Val Asn Lys Ser Asn	290		295		300
Lys Ser Ile Lys Asn Phe Glu Asn Arg Phe Leu Phe Arg Lys Gly Glu	305		310		315
Val Ser Asp Trp Val Asn Tyr Leu Ser Pro Ser Gln Val Glu Arg Leu	325		330		335
Ser Ala Leu Val Asp Asp Lys Leu Gly Gly Ser Gly Leu Thr Phe Arg	340		345		350
Leu Ser					

(2) INFORMATION FOR SEQ ID NO:931:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 349 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..349

(D) OTHER INFORMATION: / Ceres Seq. ID 1568368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:

Met Ala Ile Pro Ser Phe Ser Met Cys His Lys Leu Glu Leu Leu Lys	
1	5 10 15
Glu Gly Lys Thr Arg Asp Val Pro Lys Ala Glu Glu Asp Glu Gly Leu	
20	25 30
Ser Cys Glu Phe Gln Glu Met Leu Asp Ser Leu Pro Lys Glu Arg Gly	
35	40 45
Trp Arg Thr Arg Tyr Leu Tyr Leu Phe Gln Gly Phe Trp Cys Gln Ala	
50	55 60
Lys Glu Ile Gln Ala Ile Met Ser Phe Gln Lys His Phe Gln Ser Leu	
65	70 75
Glu Asn Asp Val Val Leu Ala Thr Ile Pro Lys Ser Gly Thr Thr Trp	
	85 90 95
Leu Lys Ala Leu Thr Phe Thr Ile Leu Asn Arg His Arg Phe Asp Pro	
	100 105 110

```

Val Ala Ser Ser Thr Asn His Pro Leu Phe Thr Ser Asn Pro His Asp
      115              120              125
Leu Val Pro Phe Phe Glu Tyr Lys Leu Tyr Ala Asn Gly Asp Val Pro
      130              135              140
Asp Leu Ser Gly Leu Ala Ser Pro Arg Thr Phe Ala Thr His Leu Pro
      145              150              155
Phe Gly Ser Leu Lys Glu Thr Ile Glu Lys Pro Gly Val Lys Val Val
      165              170              175
Tyr Leu Cys Arg Asn Pro Phe Asp Thr Phe Ile Ser Ser Trp His Tyr
      180              185              190
Thr Asn Asn Ile Lys Ser Glu Ser Val Ser Pro Val Leu Leu Asp Gln
      195              200              205
Ala Phe Asp Leu Tyr Cys Arg Gly Val Ile Gly Phe Gly Pro Phe Trp
      210              215              220
Glu His Met Leu Gly Tyr Trp Arg Glu Ser Leu Lys Arg Pro Glu Lys
      225              230              235
Val Phe Phe Leu Arg Tyr Glu Asp Leu Lys Asp Asp Ile Glu Thr Asn
      245              250              255
Leu Lys Arg Leu Ala Thr Phe Leu Glu Leu Pro Phe Thr Glu Glu Glu
      260              265              270
Glu Arg Lys Gly Val Val Lys Ala Ile Ala Glu Leu Cys Ser Phe Glu
      275              280              285
Asn Leu Lys Lys Leu Glu Val Asn Lys Ser Asn Lys Ser Ile Lys Asn
      290              295              300
Phe Glu Asn Arg Phe Leu Phe Arg Lys Gly Glu Val Ser Asp Trp Val
      305              310              315
Asn Tyr Leu Ser Pro Ser Gln Val Glu Arg Leu Ser Ala Leu Val Asp
      325              330              335
Asp Lys Leu Gly Gly Ser Gly Leu Thr Phe Arg Leu Ser
      340              345

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(2) INFORMATION FOR SEQ ID NO:932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..797

(D) OTHER INFORMATION: / Ceres Seq. ID 1568376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:

```

aaattcgcat agcttgcaaa taacgctgac aaaaaaagaa acagtgaaga agaaaaaaaaa    60
aaaaggtcat ttctattttc tccatttgat ttttgccgac cggagaaaaa atcttctttgc    120
cgtctctctc ttcatttcac caggaaacttt tatttgaaat cggtttgatt tagccatggc    180
aaacgcggca tcgggaatgg ctgtgcatga tgattgcaag ctgaaattta tggaaactgaa    240
ggcgaaaaaga acattccgta ccatagttcta caagattgag gataagcaag tgattgtaga    300
gaaactcggg gaacctgaac aatcatatga tgactttgca gctagtcttc cagctgatga    360
tgcccgatatt tgcattttacg atttogaactt tGgtcactgc ggagaactgc cagaagagca    420
agatcttctt cattgcatgg tctccggaca ctgccaaaagt gagagacaag atgattttacg    480
cgagctctaa agatagggttc aagagagaaac tagatggaat tcaagtggaa cttcaagcta    540
ctgatccaac agaaatgggt ctgtatgttt tcaaaagccg caccaactaa gtaaaaaaaaa    600
accctgtaag ggcatttgaa taagtttggg ttctggagtg aatatgtttc ctctgactgt    660
tatgaaaact ttttaaaccc ttcaacttca ttctacttgg tattattgta tgcctttgat    720
gtgttatgtg tgcctttgta tggttttcaa ttagttttac atgtacaata cttgaaatca    780
gattgttgct aagcttc

```

(2) INFORMATION FOR SEQ ID NO:933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..104
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568377
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:
Met Ala Asn Ala Ala Ser Gly Met Ala Val His Asp Asp Cys Lys Leu
1 5 10 15
Lys Phe Met Glu Leu Lys Ala Lys Arg Thr Phe Arg Thr Ile Val Tyr
 20 25 30
Lys Ile Glu Asp Lys Gln Val Ile Val Glu Lys Leu Gly Glu Pro Glu
 35 40 45
Gln Ser Tyr Asp Asp Phe Ala Ala Ser Leu Pro Ala Asp Asp Cys Arg
 50 55 60
Tyr Cys Ile Tyr Asp Phe Asp Phe Gly His Cys Gly Glu Leu Pro Glu
65 70 75 80
Glu Gln Asp Leu Leu His Cys Met Val Ser Gly His Cys Gln Ser Glu
 85 90 95
Arg Gln Asp Asp Leu Arg Glu Leu
 100

(2) INFORMATION FOR SEQ ID NO:934:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..97
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568378
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:
Met Ala Val His Asp Asp Cys Lys Leu Lys Phe Met Glu Leu Lys Ala
1 5 10 15
Lys Arg Thr Phe Arg Thr Ile Val Tyr Lys Ile Glu Asp Lys Gln Val
 20 25 30
Ile Val Glu Lys Leu Gly Glu Pro Glu Gln Ser Tyr Asp Asp Phe Ala
 35 40 45
Ala Ser Leu Pro Ala Asp Asp Cys Arg Tyr Cys Ile Tyr Asp Phe Asp
 50 55 60
Phe Gly His Cys Gly Glu Leu Pro Glu Glu Gln Asp Leu Leu His Cys
65 70 75 80
Met Val Ser Gly His Cys Gln Ser Glu Arg Gln Asp Asp Leu Arg Glu
 85 90 95
Leu

(2) INFORMATION FOR SEQ ID NO:935:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..87
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568379
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:
Met Met Thr Leu Gln Leu Val Phe Gln Leu Met Ile Ala Asp Ile Ala
1 5 10 15

Phe Thr Ile Ser Thr Leu Val Thr Ala Glu Asn Cys Gln Lys Ser Lys
20 25 30
Ile Phe Phe Ile Ala Trp Ser Pro Asp Thr Ala Lys Val Arg Asp Lys
35 40 45
Met Ile Tyr Ala Ser Ser Lys Asp Arg Phe Lys Arg Glu Leu Asp Gly
50 55 60
Ile Gln Val Glu Leu Gln Ala Thr Asp Pro Thr Glu Met Gly Leu Asp
65 70 75 80
Val Phe Lys Ser Arg Thr Asn
85

(2) INFORMATION FOR SEQ ID NO:936:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1327 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1327

(D) OTHER INFORMATION: / Ceres Seq. ID 1568405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

actgggtcgt	ctctttcttc	gatttctctt	tctatctggg	ttccattttc	gtctcgtttg	60
tgtttcgtgt	gggtttgttt	gtctctgttc	ttctatttgt	ggcgttattc	atcgtgtcaa	120
ttgtcatctt	catcgttttc	gtcgtgttat	ttgggttttc	tcgtttgggt	cttctgaaca	180
ttcttcatct	ttctcttttt	gggtttgtct	cccacgaaca	ggtagattga	tgaaaagcaa	240
ccatggatga	cctacatgga	agcaatgctc	gaatgcacat	tagagaagct	caagatccaa	300
tgcatgtgca	atttgaacat	catgctttgc	atcacatcca	caatggaagc	ggtaggtgtg	360
atgaccaggc	tgatgatggc	aatgctgggt	ggatgagtga	gggtgtggaa	acagacattc	420
cttctcacc	tggaagtgtg	actgacaatc	gtgggtgaag	ggtcgaccgt	ggtagtgaac	480
aaggagatga	gttaacattg	tcttttcagg	gccaaagtct	cggttttgac	agtgtcttgc	540
ctgagaaggt	tcaagctgtg	cttctattat	tgggtgtgtg	tgaattacct	cagcagcccc	600
tcctggccta	ggatcacctc	atcagaacaa	cagagtatcg	agtttacctg	gtactcctca	660
aagggttagt	attccgcagc	gatttagctt	tttggtcaga	tttcgagaga	aacggaagg	720
aaggaaattt	gataagaaga	ttcgttatac	agtcgccaa	gaggtagctt	tgaggatgca	780
acgcaataaa	ggtcagttca	catctgccaa	gtcaaaacat	gatgaagctg	catctgctgg	840
atctagctgg	gggtcgaaac	aaacctgggc	catagaaaat	agtgaagctc	agcatcaaga	900
gatctcatgt	ggcagctgtg	gaattggcga	gaagtcaact	ccaatgatgc	gacgtggacc	960
tgccggccca	agaaacattt	gcaatgcatg	tggcacttat	tgggcaaaac	aggggtgctt	1020
tagggagcta	tccaagacct	ctcctcaaac	agcccagaat	cttcttttaa	ataagaatga	1080
agatgcaaat	cttgagactg	atcatcaaat	aatgataaca	gtggccaagt	acataagcaa	1140
ctcacagtga	gggcatgttg	gtcttcccca	ttacaagcaa	gagaagagat	tcaacagagt	1200
ttgcattccc	tcaggttttg	tagctttatc	attccotttg	aaagaatctg	actcagattt	1260
ggttatcagg	atttgatcta	tgacaatgta	atctgagtga	taatgatctg	caatgttttg	1320
ctctcttc						

(2) INFORMATION FOR SEQ ID NO:937:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1568406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

Met Asp Asp Leu His Gly Ser Asn Ala Arg Met His Ile Arg Glu Ala			
1 5 10 15			
Gln Asp Pro Met His Val Gln Phe Glu His His Ala Leu His His Ile			
20 25 30			

His Asn Gly Ser Gly Met Val Asp Asp Gln Ala Asp Asp Gly Asn Ala
35 40 45
Gly Gly Met Ser Glu Gly Val Glu Thr Asp Ile Pro Ser His Pro Gly
50 55 60
Asn Val Thr Asp Asn Arg Gly Glu Val Val Asp Arg Gly Ser Glu Gln
65 70 75 80
Gly Asp Gln Leu Thr Leu Ser Phe Gln Gly Gln Val Tyr Val Phe Asp
85 90 95
Ser Val Leu Pro Glu Lys Val Gln Ala Val Leu Leu Leu Leu Gly Gly
100 105 110
Arg Glu Leu Pro Gln Gln Pro Leu Leu Ala
115 120

(2) INFORMATION FOR SEQ ID NO:938:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

Met His Ile Arg Glu Ala Gln Asp Pro Met His Val Gln Phe Glu His
1 5 10 15
His Ala Leu His His Ile His Asn Gly Ser Gly Met Val Asp Asp Gln
20 25 30
Ala Asp Asp Gly Asn Ala Gly Gly Met Ser Glu Gly Val Glu Thr Asp
35 40 45
Ile Pro Ser His Pro Gly Asn Val Thr Asp Asn Arg Gly Glu Val Val
50 55 60
Asp Arg Gly Ser Glu Gln Gly Asp Gln Leu Thr Leu Ser Phe Gln Gly
65 70 75 80
Gln Val Tyr Val Phe Asp Ser Val Leu Pro Glu Lys Val Gln Ala Val
85 90 95
Leu Leu Leu Leu Gly Gly Arg Glu Leu Pro Gln Gln Pro Leu Leu Ala
100 105 110

(2) INFORMATION FOR SEQ ID NO:939:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:

Met Gln Arg Asn Lys Gly Gln Phe Thr Ser Ala Lys Ser Asn Asn Asp
1 5 10 15
Glu Ala Ala Ser Ala Gly Ser Ser Trp Gly Ser Asn Gln Thr Trp Ala
20 25 30
Ile Glu Ser Ser Glu Ala Gln His Gln Glu Ile Ser Cys Arg His Cys
35 40 45
Gly Ile Gly Glu Lys Ser Thr Pro Met Met Arg Arg Gly Pro Ala Gly
50 55 60
Pro Arg Thr Leu Cys Asn Ala Cys Gly Leu Met Trp Ala Asn Lys Gly

65	70	75	80
Ala Phe Arg Asp Leu Ser Lys Ala Ser	Pro Gln Thr Ala Gln Asn Leu		
	85	90	95
Pro Leu Asn Lys Asn Glu Asp Ala Asn	Leu Glu Thr Asp His Gln Ile		
	100	105	110
Met Ile Thr Val Ala Asn Asp Ile Ser	Asn Ser Gln		
	115	120	

(2) INFORMATION FOR SEQ ID NO:940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1289
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

actaattaaa	tctctctataa	aacataagag	agtctaaaca	ctgtggtaga	aaaaaatata	60
gactttttaga	tatgtgtagt	aaaataacat	tagtgtaa	tttattttcc	agttatttca	120
tatcaacaga	tgtgtggaat	ggatcatttc	ctgcgctttt	ggctttttgga	gattcaattc	180
tgcatactgg	caacaacaa	tttctctga	cttttatgaa	agaaataatc	tgccatattg	240
gaaggagttt	cagcatgaga	agggcgacag	gaagattttg	aaatggaaga	gttttctctg	300
atatagtttc	tgaaggttta	gggatcaaga	agattttacc	agcttatcgt	aagttgttca	360
attctccaag	tgaccttaga	actgggtgtt	gcttcgcatac	aggtggtgca	ggagttgacc	420
ctgtttacatc	caaatgtgct	agagttttaa	cgccaaagga	tcaagttaac	gattttcaag	480
ggtacataag	aaagctaaag	gccacagcag	gtccttcaag	agcaagtgt	atagtttcaa	540
atgcagtgtat	tctgttttct	caaggaaata	atgatattgg	aatctcatat	tttggaaact	600
caactgtctgc	tttccgagga	tttaactcca	atagataatac	caactaaacta	gctgtgttga	660
acaaacaggtt	tatgaaagaa	ttatacgtac	aaggagcgag	aaaattcgcg	gtaattggggg	720
tgataccgtt	gggatgtttt	cctatgacaa	gaattcttct	tggtgggttc	gtcatcacgt	780
gtaacttctt	cgcgaaataga	gtcgcagaa	agtaacacgg	aaaattgagg	agcggaacta	840
aaagtgtggg	acgtgaagca	ggttttaggg	gtacaaaatt	tgcttatgtc	gacatgtaca	900
acactcttat	ggatgttatt	aaaaattata	gaagatacgg	attttctaat	gagaaaaaatg	960
gggtgtgttg	tatgattacc	gctataatac	catgcgccaa	cccagataaa	tacgtctctt	1020
acgacttcgt	tcattccatc	gagaaaagctt	acagaacaat	ttctaaaaag	ctgtgccagg	1080
atatacaagaa	tggccttgcc	tgatttatta	tatatacaat	gctttatttt	aattttaata	1140
acagcctatc	ttataataag	aaatgagaag	acaaaaatca	tacatggcca	ttctctgttt	1200
ttctctatgt	taaagaatgt	ataatccagt	ttatgtattg	ttcactttat	ataatccacg	1260
aaacaacaaag	gagtttgttt	acaaCatgt				

(2) INFORMATION FOR SEQ ID NO:941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..343
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

Met Cys Ser Lys Ile Thr Leu Val Leu Thr Leu Phe Ser Ser Tyr Phe	
1	5
Ile Ser Thr Asp Ala Val Asn Gly Ser Phe Pro Ala Leu Leu Ala Phe	
	20
Gly Asp Ser Ile Leu Asp Thr Gly Asn Asn Asn Phe Leu Leu Thr Phe	
	35
Met Lys Gly Asn Ile Trp Pro Tyr Gly Arg Ser Phe Ser Met Arg Arg	
50	60

Ala Thr Gly Arg Phe Gly Asn Gly Arg Val Phe Ser Asp Ile Val Ala
65 70 75 80
Glu Gly Leu Gly Ile Lys Lys Ile Leu Pro Ala Tyr Arg Lys Leu Phe
85 90 95
Asn Ser Pro Ser Asp Leu Arg Thr Gly Val Cys Phe Ala Ser Gly Gly
100 105 110
Ala Gly Val Asp Pro Val Thr Ser Lys Leu Leu Arg Val Leu Thr Pro
115 120 125
Lys Asp Gln Val Asn Asp Phe Lys Gly Tyr Ile Arg Lys Leu Lys Ala
130 135 140
Thr Ala Gly Pro Ser Arg Ala Ser Ser Ile Val Ser Asn Ala Val Ile
145 150 155 160
Leu Val Ser Gln Gly Asn Asn Asp Ile Gly Ile Ser Tyr Phe Gly Thr
165 170 175
Pro Thr Ala Ala Phe Arg Gly Leu Thr Pro Asn Arg Tyr Thr Thr Lys
180 185 190
Leu Ala Gly Trp Asn Lys Gln Phe Met Lys Glu Leu Tyr Asp Gln Gly
195 200 205
Ala Arg Lys Phe Ala Val Met Gly Val Ile Pro Leu Gly Cys Leu Pro
210 215 220
Met Thr Arg Ile Phe Leu Gly Gly Phe Val Ile Thr Cys Asn Phe Phe
225 230 235 240
Ala Asn Arg Val Ala Glu Gln Tyr Asn Gly Lys Leu Arg Ser Gly Thr
245 250 255
Lys Ser Trp Gly Arg Glu Ala Gly Phe Arg Gly Thr Lys Phe Val Tyr
260 265 270
Val Asp Met Tyr Asn Thr Leu Met Asp Val Ile Lys Asn Tyr Arg Arg
275 280 285
Tyr Gly Phe Ser Asn Glu Lys Asn Gly Cys Cys Cys Met Ile Thr Ala
290 295 300
Ile Ile Pro Cys Pro Asn Pro Asp Lys Tyr Val Phe Tyr Asp Phe Val
305 310 315 320
His Pro Ser Glu Lys Ala Tyr Arg Thr Ile Ser Lys Lys Leu Val Gln
325 330 335
Asp Ile Lys Asn Gly Leu Ala
340

(2) INFORMATION FOR SEQ ID NO:942:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..295

(D) OTHER INFORMATION: / Ceres Seq. ID 1568411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

Met Lys Gly Asn Ile Trp Pro Tyr Gly Arg Ser Phe Ser Met Arg Arg
1 5 10 15
Ala Thr Gly Arg Phe Gly Asn Gly Arg Val Phe Ser Asp Ile Val Ala
20 25 30
Glu Gly Leu Gly Ile Lys Lys Ile Leu Pro Ala Tyr Arg Lys Leu Phe
35 40 45
Asn Ser Pro Ser Asp Leu Arg Thr Gly Val Cys Phe Ala Ser Gly Gly
50 55 60
Ala Gly Val Asp Pro Val Thr Ser Lys Leu Leu Arg Val Leu Thr Pro
65 70 75 80
Lys Asp Gln Val Asn Asp Phe Lys Gly Tyr Ile Arg Lys Leu Lys Ala
85 90 95
Thr Ala Gly Pro Ser Arg Ala Ser Ser Ile Val Ser Asn Ala Val Ile

100 105 110
Leu Val Ser Gln Gly Asn Asn Asp Ile Gly Ile Ser Tyr Phe Gly Thr
115 120 125
Pro Thr Ala Ala Phe Arg Gly Leu Thr Pro Asn Arg Tyr Thr Thr Lys
130 135 140
Leu Ala Gly Trp Asn Lys Gln Phe Met Lys Glu Leu Tyr Asp Gln Gly
145 150 155 160
Ala Arg Lys Phe Ala Val Met Gly Val Ile Pro Leu Gly Cys Leu Pro
165 170 175
Met Thr Arg Ile Phe Leu Gly Gly Phe Val Ile Thr Cys Asn Phe Phe
180 185 190
Ala Asn Arg Val Ala Glu Gln Tyr Asn Gly Lys Leu Arg Ser Gly Thr
195 200 205
Lys Ser Trp Gly Arg Glu Ala Gly Phe Arg Gly Thr Lys Phe Val Tyr
210 215 220
Val Asp Met Tyr Asn Thr Leu Met Asp Val Ile Lys Asn Tyr Arg Arg
225 230 235 240
Tyr Gly Phe Ser Asn Glu Lys Asn Gly Cys Cys Cys Met Ile Thr Ala
245 250 255
Ile Ile Pro Cys Pro Asn Pro Asp Lys Tyr Val Phe Tyr Asp Phe Val
260 265 270
His Pro Ser Glu Lys Ala Tyr Arg Thr Ile Ser Lys Lys Leu Val Gln
275 280 285
Asp Ile Lys Asn Gly Leu Ala
290 295

(2) INFORMATION FOR SEQ ID NO:943:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..282

(D) OTHER INFORMATION: / Ceres Seq. ID 1568412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

Met Arg Arg Ala Thr Gly Arg Phe Gly Asn Gly Arg Val Phe Ser Asp
1 5 10 15
Ile Val Ala Glu Gly Leu Gly Ile Lys Lys Ile Leu Pro Ala Tyr Arg
20 25 30
Lys Leu Phe Asn Ser Pro Ser Asp Leu Arg Thr Gly Val Cys Phe Ala
35 40 45
Ser Gly Gly Ala Gly Val Asp Pro Val Thr Ser Lys Leu Leu Arg Val
50 55 60
Leu Thr Pro Lys Asp Gln Val Asn Asp Phe Lys Gly Tyr Ile Arg Lys
65 70 75 80
Leu Lys Ala Thr Ala Gly Pro Ser Arg Ala Ser Ser Ile Val Ser Asn
85 90 95
Ala Val Ile Leu Val Ser Gln Gly Asn Asn Asp Ile Gly Ile Ser Tyr
100 105 110
Phe Gly Thr Pro Thr Ala Ala Phe Arg Gly Leu Thr Pro Asn Arg Tyr
115 120 125
Thr Thr Lys Leu Ala Gly Trp Asn Lys Gln Phe Met Lys Glu Leu Tyr
130 135 140
Asp Gln Gly Ala Arg Lys Phe Ala Val Met Gly Val Ile Pro Leu Gly
145 150 155 160
Cys Leu Pro Met Thr Arg Ile Phe Leu Gly Gly Phe Val Ile Thr Cys
165 170 175
Asn Phe Phe Ala Asn Arg Val Ala Glu Gln Tyr Asn Gly Lys Leu Arg
180 185 190

Ser Gly Thr Lys Ser Trp Gly Arg Glu Ala Gly Phe Arg Gly Thr Lys
195 200 205
Phe Val Tyr Val Asp Met Tyr Asn Thr Leu Met Asp Val Ile Lys Asn
210 215 220
Tyr Arg Arg Tyr Gly Phe Ser Asn Glu Lys Asn Gly Cys Cys Cys Met
225 230 235 240
Ile Thr Ala Ile Ile Pro Cys Pro Asn Pro Asp Lys Tyr Val Phe Tyr
245 250 255
Asp Phe Val His Pro Ser Glu Lys Ala Tyr Arg Thr Ile Ser Lys Lys
260 265 270
Leu Val Gln Asp Ile Lys Asn Gly Leu Ala
275 280

(2) INFORMATION FOR SEQ ID NO:944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..593
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

atcaaaatct	ttacaatatt	tatcatgtat	gattctatca	agtgagatgg	aacgggtatgc	60
aatttttccg	tttaataatg	tggtttcgct	tacagggttg	acaagtcact	ccagtagcac	120
tagagaagct	tgaggtagca	acaaagacac	tgaggagagac	agtggtggag	acagaggtga	180
cccaacagcc	ggaagaatcc	gtccccgcgc	tgacagaaca	aaaatccgaa	gcaccaattg	240
tagaaaacaa	cgaagaagtg	gttgtggaag	aggcagagaa	gaaagatgaa	gaaaccgaga	300
agaaaaacaga	ggagaagac	gagaagacag	aagtgtcac	ggaactccg	gtagttgagg	360
aggagagagaa	gaagctgag	gaagtgaacc	aaactccggc	ggttgtggag	gaggagaaga	420
agacagaggt	ggttgaggag	aaacagactg	aggttgccgc	tgctgaggaa	gtgccctgtg	480
agaagggcga	ggagtaaaga	ggaaggaaga	agctatatat	gacctttttt	ggtctcatat	540
cgttttctgt	ttattttatt	ttatcaaWca	tttcataagt	attttctatg	ttt	

(2) INFORMATION FOR SEQ ID NO:945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

Met	Gln	Phe	Phe	Arg	Leu	Ile	Met	Cys	Phe	Arg	Leu	Gln	Val	Glu	Gln
1			5					10				15			
Val	Thr	Pro	Val	Ala	Val	Glu	Asn	Val	Glu	Val	Pro	Thr	Lys	Thr	Val
			20					25				30			
Glu	Glu	Thr	Val	Val	Glu	Thr	Glu	Val	Thr	Gln	Gln	Pro	Glu	Glu	Ser
			35				40				45				
Val	Pro	Ala	Val	Thr	Glu	Gln	Lys	Ser	Glu	Ala	Pro	Ile	Val	Glu	Thr
			50				55				60				
Asn	Glu	Glu	Val	Val	Val	Glu	Glu	Ala	Glu	Lys	Lys	Asp	Glu	Glu	Thr
			65				70			75			80		
Glu	Lys	Lys	Thr	Glu	Glu	Lys	Asp	Glu	Lys	Thr	Glu	Val	Ile	Thr	Glu
			85				90				95				
Thr	Pro	Val	Val	Glu	Glu	Glu	Lys	Lys	Ala	Glu	Glu	Val	Thr	Glu	
			100				105				110				
Thr	Pro	Ala	Val	Val	Glu	Glu	Lys	Lys	Thr	Glu	Val	Val	Glu	Glu	

115 120 125
Lys Gln Thr Glu Val Ala Ala Glu Glu Val Ala Val Glu Lys Ala
130 135 140
Glu Glu
145

(2) INFORMATION FOR SEQ ID NO:946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

Met Cys Phe Arg Leu Gln Val Glu Gln Val Thr Pro Val Ala Val Glu
1 5 10 15
Asn Val Glu Val Pro Thr Lys Thr Val Glu Glu Thr Val Val Glu Thr
20 25 30
Glu Val Thr Gln Gln Pro Glu Glu Ser Val Pro Ala Val Thr Glu Gln
35 40 45
Lys Ser Glu Ala Pro Ile Val Glu Thr Asn Glu Glu Val Val Val Glu
50 55 60
Glu Ala Glu Lys Lys Asp Glu Glu Thr Glu Lys Lys Thr Glu Glu Lys
65 70 75 80
Asp Glu Lys Thr Glu Val Ile Thr Glu Thr Pro Val Val Glu Glu Glu
85 90 95
Glu Lys Lys Ala Glu Glu Val Thr Glu Thr Pro Ala Val Val Glu Glu
100 105 110
Glu Lys Lys Thr Glu Val Val Glu Glu Lys Gln Thr Glu Val Ala Ala
115 120 125
Ala Glu Glu Val Ala Val Glu Lys Ala Glu Glu
130 135

(2) INFORMATION FOR SEQ ID NO:947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

cgagatatat cgactccgcg accctccact actctgctga ctacacacac cacacacaaa 60
cacaaatcgcc ggcaacaatg gcgaagctca caetctctct ctctctctcc ttctctcatct 120
tctctctatc catcgctttc caatcagacg agctctctgt tgacgacgac gaatttggtc 180
tagaaggagc aaagcccgcc tccaccgatc ttcacacato ttctctctct tcgccacagc 240
agcagcaaca gactccaact attcggagaa gatactcaga tcttaccgat ttggattcaa 300
aagtccaatt tactctcgaa catgctctcg gtgactctga ttctctcccc gccggtactt 360
tctccgctcg tctcaaaaac tggagtcgat gcggaaaagc attaacgaag ctgcgattct 420
ctagaaatga tttttctgct gaagagaagc atgcatctca gaatctgctg aaaggagatg 480
gtctttatcg gattcggctt ccatctaatt tggttagctc accagggaga gagtttgtga 540
ttgcatcagt gagagctaga tgtctaccac gggatggctt ggaatgagat ttcattatag 600
acatgggaag tgcataacat ttggcgagta gttatggctt tcttggggcg tgtcaaatag 660
ctcgacaatt gaaccttcca gcaaaatggt cgtttaactc tcacacaatt ctgaaaaagca 720
gtgagcagcg gccaaagact ccaatattca ctgaggagat tctaggchdK tgagaatgta 780
gagggagaag ttgaaccacc accagagaga tcattttggg cgaaatattg gatgtatttg 840

ataccgctgg gactcgtagt gatgaatgcc gtgacacaag catcaaacat ggctgaagaa 900
cCtgcggggtg gacaggcagg aggtgcacaa gtgcaaccag ctgccaggag aagatgattc 960
cacttttact tctcccaaag caatgaaagc tgcagctggg tagagatgat gattcaacag 1020
atcttcatgt aaaccatctt gccatcattt ggtttttatgt aacctttaat tttaatcctc 1080
gatcggtgtg ttttagtact caccaatcgg gaaatcaaaa atcttgtctt catgacatat 1140
caagaacaaa gacattt

(2) INFORMATION FOR SEQ ID NO:948:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1568437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

Arg Tyr Ile Asp Ser Ala Thr Leu His Tyr Ser Ala Asp Leu His Thr
1 5 10 15
His Thr Gln Thr Gln Ser Pro Ala Thr Met Ala Lys Leu Thr Leu Leu
20 25 30
Phe Phe Leu Ser Phe Leu Ile Phe Ser Ser Ser Ile Ala Phe Gln Ser
35 40 45
Asp Glu Leu Leu Val Asp Asp Glu Phe Gly Leu Glu Gly Ala Lys
50 55 60
Pro Arg Ser Thr Asp Leu His Thr Ser Ser Ser Ser Pro Gln Gln
65 70 75 80
Gln Gln Gln Thr Pro Thr Ile Arg Arg Arg Tyr Ser Asp Pro Thr Asp
85 90 95
Leu Asp Ser Lys Val Gln Phe Thr Leu Glu His Ala Phe Gly Asp Ser
100 105 110
Asp Phe Ser Pro Ala Gly Thr Phe Ser Ala Arg Leu Lys Thr Trp Ser
115 120 125
His Gly Gly Lys Thr Leu Thr Lys Leu Arg Phe Ser Arg Asn Asp Phe
130 135 140
Ser Ala Glu Glu Lys Asp Ala Phe Lys Asn Leu Leu Lys Gly Asp Gly
145 150 155 160
Phe Tyr Arg Ile Arg Leu Pro Ser Asn Val Val Ser Pro Pro Gly Arg
165 170 175
Glu Phe Val Ile Ala Ser Val Arg Ala Arg Cys Leu Pro Arg Asp Gly
180 185 190
Leu Asp Glu His Phe Ile Ile His Met Glu Gly Ala Asn Ile Leu Ala
195 200 205
Val Ser Tyr Gly Ser Pro Gly Ala Cys Gln Tyr Pro Arg Gln Leu Lys
210 215 220
Leu Pro Ala Lys Trp Ser Phe Asn Ser His Thr Ile Leu Lys Ser Ser
225 230 235 240
Glu Gln Ala Pro Arg Thr Pro Ile Phe Thr Glu Glu Ile Leu Gly Xaa
245 250 255

(2) INFORMATION FOR SEQ ID NO:949:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1568438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

Met Ala Lys Leu Thr Leu Leu Phe Phe Leu Ser Phe Leu Ile Phe Ser
1 5 10 15
Ser Ser Ile Ala Phe Gln Ser Asp Glu Leu Leu Val Asp Asp Asp Glu
20 25 30
Phe Gly Leu Glu Gly Ala Lys Pro Arg Ser Thr Asp Leu His Thr Ser
35 40 45
Ser Ser Ser Ser Pro Gln Gln Gln Gln Thr Pro Thr Ile Arg Arg
50 55 60
Arg Tyr Ser Asp Pro Thr Asp Leu Asp Ser Lys Val Gln Phe Thr Leu
65 70 75 80
Glu His Ala Phe Gly Asp Ser Asp Phe Ser Pro Ala Gly Thr Phe Ser
85 90 95
Ala Arg Leu Lys Thr Trp Ser His Gly Gly Lys Thr Leu Thr Lys Leu
100 105 110
Arg Phe Ser Arg Asn Asp Phe Ser Ala Glu Glu Lys Asp Ala Phe Lys
115 120 125
Asn Leu Leu Lys Gly Asp Gly Phe Tyr Arg Ile Arg Leu Pro Ser Asn
130 135 140
Val Val Ser Pro Pro Gly Arg Glu Phe Val Ile Ala Ser Val Arg Ala
145 150 155 160
Arg Cys Leu Pro Arg Asp Gly Leu Asp Glu His Phe Ile Ile His Met
165 170 175
Glu Gly Ala Asn Ile Leu Ala Val Ser Tyr Gly Ser Pro Gly Ala Cys
180 185 190
Gln Tyr Pro Arg Gln Leu Lys Leu Pro Ala Lys Trp Ser Phe Asn Ser
195 200 205
His Thr Ile Leu Lys Ser Ser Glu Gln Ala Pro Arg Thr Pro Ile Phe
210 215 220
Thr Glu Glu Ile Leu Gly Xaa
225 230

(2) INFORMATION FOR SEQ ID NO:950:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 501 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..501

(D) OTHER INFORMATION: / Ceres Seq. ID 1568490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

atatacCttc ttcttcttca ccttatgcaa gataatggac aaagtattgat gaatgtcgtc 60
cgaaaaaggg gtgggttatat ttaccaagag ctctgttgtt ttgtcctatg cggttcaagt 120
ttctttccaa gatcttggtg ttaaccctaa gatccacgag attgataagg accttgaatg 180
ccgagagata gagaaggctc ttatgaggct aggggtgttca aagcccggtcc cagccgtctt 240
cattggtgac aagctcgttg gttcgaccaa cgaagtaatg tccatgcacc taagcagctc 300
gctcgttccc ctagtgaagc catatttatg ttaacaacaa acgaaggagt atttatgata 360
ttaattagct atgtatatgt tattcaataa ggaacaaaat tgagccaaat ctttgtaatg 420
tgttttttgg tattattatt gttgtataa cattgggaaa gtgtacgtat aattataaga 480
ctgttatatt gattcgaagg t

(2) INFORMATION FOR SEQ ID NO:951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1568491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

Tyr	Thr	Phe	Phe	Phe	Thr	Leu	Cys	Lys	Ile	Met	Asp	Lys	Val	Met
1				5					10				15	
Arg	Met	Ser	Ser	Glu	Lys	Gly	Val	Val	Ile	Phe	Thr	Lys	Ser	Ser
			20				25						30	Cys
Cys	Leu	Ser	Tyr	Ala	Val	Gln	Val	Leu	Phe	Gln	Asp	Leu	Gly	Val
		35				40					45			Asn
Pro	Lys	Ile	His	Glu	Ile	Asp	Lys	Asp	Pro	Glu	Cys	Arg	Glu	Ile
	50				55					60				Glu
Lys	Ala	Leu	Met	Arg	Leu	Gly	Cys	Ser	Lys	Pro	Val	Pro	Ala	Val
	65			70					75					80
Ile	Gly	Gly	Lys	Leu	Val	Gly	Ser	Thr	Asn	Glu	Val	Met	Ser	Met
			85						90				95	His
Leu	Ser	Ser	Ser	Leu	Val	Pro	Leu	Val	Lys	Pro	Tyr	Leu	Cys	
			100					105						110

(2) INFORMATION FOR SEQ ID NO:952:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1568492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

Met	Asp	Lys	Val	Met	Arg	Met	Ser	Ser	Glu	Lys	Gly	Val	Val	Ile
1				5					10					15
Thr	Lys	Ser	Ser	Cys	Cys	Leu	Ser	Tyr	Ala	Val	Gln	Val	Leu	Phe
			20				25						30	Gln
Asp	Leu	Gly	Val	Asn	Pro	Lys	Ile	His	Glu	Ile	Asp	Lys	Asp	Pro
	35				40						45			Glu
Cys	Arg	Glu	Ile	Glu	Lys	Ala	Leu	Met	Arg	Leu	Gly	Cys	Ser	Lys
	50				55					60				Pro
Val	Pro	Ala	Val	Phe	Ile	Gly	Gly	Lys	Leu	Val	Gly	Ser	Thr	Asn
	65			70					75					80
Val	Met	Ser	Met	His	Leu	Ser	Ser	Ser	Leu	Val	Pro	Leu	Val	Lys
			85						90				95	Pro
Tyr	Leu	Cys												

(2) INFORMATION FOR SEQ ID NO:953:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1568493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

Met	Arg	Met	Ser	Ser	Glu	Lys	Gly	Val	Val	Ile	Phe	Thr	Lys	Ser
1				5					10				15	
Cys	Cys	Leu	Ser	Tyr	Ala	Val	Gln	Val	Leu	Phe	Gln	Asp	Leu	Gly
		20					25						30	Val

Asn	Pro	Lys	Ile	His	Glu	Ile	Asp	Lys	Asp	Pro	Glu	Cys	Arg	Glu	Ile
		35				40					45				
Glu	Lys	Ala	Leu	Met	Arg	Leu	Gly	Cys	Ser	Lys	Pro	Val	Pro	Ala	Val
		50				55					60				
Phe	Ile	Gly	Gly	Lys	Leu	Val	Gly	Ser	Thr	Asn	Glu	Val	Met	Ser	Met
		65				70				75				80	
His	Leu	Ser	Ser	Ser	Leu	Val	Pro	Leu	Val	Lys	Pro	Tyr	Leu	Cys	
					85				90					95	

(2) INFORMATION FOR SEQ ID NO:954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1075 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1075
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

atgaaaccgg	atactcgaga	gtcgccggag	tgtccttccc	ttcttctatc	agctctgctt	60
ctcctttaga	aattagggtt	tttgaggag	acgagtattc	acttcttttc	accgtgaagc	120
gattgcttct	ttgttcaagg	agcaagcaaa	gctctcagct	tatcgagata	gaagattttc	180
aggaacacaa	gaggagtttg	atgaagcggt	aagggcagct	acacgcggtt	acattggcaa	240
ttgtgttttt	tacactactg	aagaacagct	ttacgagctt	ttctctagag	ctggagaaat	300
caaaaagatc	atcatggggtt	tggataagaa	cactaaaaca	ccttggtgct	ttgttttctg	360
cctgttctac	tctagagagg	atactgaaga	tgcagtcag	tatataaagt	ggGactattc	420
tcgatgaccg	gcctattcgt	gtggattttg	attggggatt	ccaagaagga	agacataagg	480
gacgttgtag	aagcggtggt	caggttctgt	atgaataccg	tacagattac	gatcctgtct	540
gaggttatgg	gaaatttagtt	cagaaggaac	tcgaagcaca	aagcgagctc	gtggattaac	600
gtactggctc	attgggagct	tatcctcaag	Ctgcgccaac	gaattattga	aatgggaagg	660
gtggtgagg	aaactatggt	caaggaggac	aaaatcgcca	tggaaagaga	ggagactacc	720
atcggaacg	acaaagagac	gatgatcgct	atggacgtga	taactcaaga	agaacacacg	780
atcatgagct	taggagagac	actgatagtg	acatgagacc	ggagaagaac	ccagatttcc	840
gtgagagcgg	tgactccgat	gacgatgggt	aagatgatcg	gaagagaaga	tcttaaaaca	900
aaactttaga	agttgtcaat	gttgctgaat	ggccaatgta	atcttttagt	tgatgatgtc	960
gaactcagtt	tggtttttct	agattttcat	tacaacggtt	cttaagtgtc	ttcgttcaat	1020
atcagtgtcc	tcattaacct	ttgctccttg	atcaacagat	atgtcattac	tagtt	

(2) INFORMATION FOR SEQ ID NO:955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

Glu	Thr	Gly	Tyr	Ser	Arg	Val	Ala	Gly	Val	Ser	Phe	Pro	Ser	Ser	Ile
1			5					10					15		
Ser	Ser	Ala	Ser	Pro	Leu	Glu	Ile	Arg	Val	Phe	Glu	Glu	Asp	Glu	Tyr
			20					25				30			
Ser	Leu	Leu	Phe	Thr	Val	Lys	Arg	Trp	Leu	Leu	Cys	Ser	Arg	Ser	Lys
			35				40				45				
Gln	Ser	Ser	Gln	Leu	Ile	Glu	Ile	Glu	Asp	Phe	Gln	Glu	His	Lys	Arg
			50			55				60					
Ser	Leu	Met	Lys	Arg											
			65												

(2) INFORMATION FOR SEQ ID NO:956:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..101
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568496
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:
Met Ala Ser Leu Phe Lys Glu Gln Ala Lys Leu Ser Ala Tyr Arg Asp
1 5 10 15
Arg Arg Phe Ser Gly Thr Gln Glu Phe Asp Glu Ala Leu Arg Ala
 20 25 30
Ser Thr Thr Val Tyr Ile Gly Asn Val Ser Phe Tyr Thr Thr Glu Glu
 35 40 45
Gln Leu Tyr Glu Leu Phe Ser Arg Ala Gly Glu Ile Lys Lys Ile Ile
 50 55 60
Met Gly Leu Asp Lys Asn Thr Lys Thr Pro Cys Gly Phe Cys Phe Val
65 70 75 80
Leu Phe Tyr Ser Arg Glu Asp Thr Glu Asp Ala Val Lys Tyr Ile Ser
 85 90 95
Gly Asp Tyr Ser Arg
 100

(2) INFORMATION FOR SEQ ID NO:957:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..56
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568497
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:
Met Glu Met Glu Gly Val Val Glu Glu Thr Met Val Lys Glu Asp Lys
1 5 10 15
Ile Ala Met Glu Glu Glu Glu Thr Thr Ile Gly Asn Asp Lys Glu Thr
 20 25 30
Met Ile Ala Met Asp Val Ile Thr Gln Glu Glu Thr Gln Ile Met Ser
 35 40 45
Leu Gly Glu Thr Leu Ile Val Thr
 50 55

(2) INFORMATION FOR SEQ ID NO:958:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1230 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1230
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568508
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:
acgtcaaaaaa ttcaaaaacc ccaaaacccct ataattctct atataaatat tcagccctag 60
atcttataat tcatcaatca aacaattctct tcaatcaaat ctcttcttca atcaaatctt 120
caaatccctt caaagatgcc ttcaatgcCa gaagagccgc tcctaaccac aacccagac 180
agattTctgt atgttcccaa ttcaactacc acagatctgg gaaatgtaca aaaaagccga 240

agcatcattc	tggaccgcgc	aagaagtaga	tctatcacaa	gacaaccgcg	actgggaaaa	300
cagttctaac	gcaggtgaac	gtcacttcat	caaacacgtc	ctcgtctttc	tcgctgcac	360
tgaacgaatc	gtactagaga	atctcgcttc	tcgcttcatg	tcgcatgttc	aaagtctcga	420
ggcgctgtct	ttctacggtt	tcagatgcgc	gattgaaaaa	atccactcgc	agatgtatag	480
tctctctctc	gatacttata	tcaaagataa	caaagagaga	gatcatctct	ttcgtgccat	540
tgaacaatc	ccttgcgtcg	ccaagaaagc	tcaatgggct	atgaaatgga	tcgacgggttc	600
tcagactttc	gcgcaacgaa	tcatcgcttt	cgcttgcgtc	gaaggtatct	tcttctccgc	660
aagcttttgt	tcaatctctc	ggctgaagaa	acggggactc	atgcctggat	taacattctc	720
aaacgaattg	atctctcgtg	acgaagggtt	acactgcgac	ttcgttgttc	tactctcac	780
gtactcaaaa	acaaagctta	gcgaagaacg	cgtgaaatca	aNtcGtctgc	gacgcggtcg	840
aaatcgagag	agagttttgt	tgcgacgcgc	ttcgtgcgcg	gttggttggg	atgacccgtg	900
atttgtagag	tcagtatatt	gagtttgttg	cgcataggct	tttggtgtacg	cttggtgtacg	960
ggaaggtgta	cggtgttact	aatccgtttg	attggatgga	acttatttcg	cttcaaggga	1020
aaacgaattt	cttcgagaaa	cgtgttgttg	attacaaaaa	ggcttcctgt	atgtctagcg	1080
ttaatggtaa	cgcgcgcttt	gataaccatg	tcttctctct	cgacgaagat	ttttaagag	1140
cggtttgttt	gatgctataa	ttacgattct	actcttctgt	tattaccgtg	tattatcctt	1200
ggtttttgaa	ttaatgaata	attagttgcc				

(2) INFORMATION FOR SEQ ID NO:959:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1568509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

Met	Phe	Pro	Ile	His	Tyr	Pro	Gln	Ile	Trp	Glu	Met	Tyr	Lys	Lys	Ala
1				5					10					15	
Glu	Ala	Ser	Phe	Trp	Thr	Ala	Glu	Glu	Val	Asp	Leu	Ser	Gln	Asp	Asn
		20						25					30		
Arg	Asp	Trp	Glu	Asn	Ser	Leu	Asn	Asp	Gly	Glu	Arg	His	Phe	Ile	Lys
		35					40				45				
His	Val	Leu	Ala	Phe	Phe	Ala	Ala	Ser	Asp	Gly	Ile	Val	Leu	Glu	Asn
		50				55				60					
Leu	Ala	Ser	Arg	Phe	Met	Ser	Asp	Val	Gln	Val	Ser	Glu	Ala	Arg	Ala
65				70					75					80	
Phe	Tyr	Gly	Phe	Gln	Ile	Ala	Ile	Glu	Asn	Ile	His	Ser	Glu	Met	Tyr
				85					90				95		
Ser	Leu	Leu	Leu	Asp	Thr	Tyr	Ile	Lys	Asp	Asn	Lys	Glu	Arg	Asp	His
		100						105					110		
Leu	Phe	Arg	Ala	Ile	Glu	Thr	Ile	Pro	Cys	Val	Ala	Lys	Lys	Ala	Gln
		115					120					125			
Trp	Ala	Met	Lys	Trp	Ile	Asp	Gly	Ser	Gln	Thr	Phe	Ala	Glu	Arg	Ile
		130				135					140				
Ile	Ala	Phe	Ala	Cys	Val	Glu	Gly	Ile	Phe	Phe	Ser	Gly	Ser	Phe	Cys
145				150					155					160	
Ser	Ile	Phe	Trp	Leu	Lys	Lys	Arg	Gly	Leu	Met	Pro	Gly	Leu	Thr	Phe
		165						170					175		
Ser	Asn	Glu	Leu	Ile	Ser	Arg	Asp	Glu	Gly	Leu	His	Cys	Asp	Phe	Ala
		180					185						190		
Cys	Leu	Leu	Tyr	Thr	Leu	Leu	Lys	Thr	Lys	Leu	Ser	Glu	Glu	Arg	Val
		195					200					205			
Lys	Ser	Xaa	Arg	Leu	Arg	Arg	Gly	Arg	Asn	Arg	Glu	Arg	Val	Cys	Val
		210					215					220			
Arg	Arg	Ala	Ser	Val	Arg	Val	Gly	Trp	Asp	Glu	Pro				
225				230					235						

(2) INFORMATION FOR SEQ ID NO:960:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..225
(D) OTHER INFORMATION: / Ceres Seq. ID 1568510
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:
Met Tyr Lys Lys Ala Glu Ala Ser Phe Trp Thr Ala Glu Glu Val Asp
1 5 10 15
Leu Ser Gln Asp Asn Arg Asp Trp Glu Asn Ser Leu Asn Asp Gly Glu
20 25 30
Arg His Phe Ile Lys His Val Leu Ala Phe Phe Ala Ala Ser Asp Gly
35 40 45
Ile Val Leu Glu Asn Leu Ala Ser Arg Phe Met Ser Asp Val Gln Val
50 55 60
Ser Glu Ala Arg Ala Phe Tyr Gly Phe Gln Ile Ala Ile Glu Asn Ile
65 70 75 80
His Ser Glu Met Tyr Ser Leu Leu Leu Asp Thr Tyr Ile Lys Asp Asn
85 90 95
Lys Glu Arg Asp His Leu Phe Arg Ala Ile Glu Thr Ile Pro Cys Val
100 105 110
Ala Lys Lys Ala Gln Trp Ala Met Lys Trp Ile Asp Gly Ser Gln Thr
115 120 125
Phe Ala Glu Arg Ile Ile Ala Phe Ala Cys Val Glu Gly Ile Phe Phe
130 135 140
Ser Gly Ser Phe Cys Ser Ile Phe Trp Leu Lys Lys Arg Gly Leu Met
145 150 155 160
Pro Gly Leu Thr Phe Ser Asn Glu Leu Ile Ser Arg Asp Glu Gly Leu
165 170 175
His Cys Asp Phe Ala Cys Leu Leu Tyr Thr Leu Leu Lys Thr Lys Leu
180 185 190
Ser Glu Glu Arg Val Lys Ser Xaa Arg Leu Arg Arg Gly Arg Asn Arg
195 200 205
Glu Arg Val Cys Val Arg Arg Ala Ser Val Arg Val Gly Trp Asp Glu
210 215 220

Pro
225

(2) INFORMATION FOR SEQ ID NO:961:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1568511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

Met Ser Asp Val Gln Val Ser Glu Ala Arg Ala Phe Tyr Gly Phe Gln
1 5 10 15
Ile Ala Ile Glu Asn Ile His Ser Glu Met Tyr Ser Leu Leu Leu Asp
20 25 30
Thr Tyr Ile Lys Asp Asn Lys Glu Arg Asp His Leu Phe Arg Ala Ile
35 40 45
Glu Thr Ile Pro Cys Val Ala Lys Lys Ala Gln Trp Ala Met Lys Trp
50 55 60
Ile Asp Gly Ser Gln Thr Phe Ala Glu Arg Ile Ile Ala Phe Ala Cys

65	70	75	80
Val Glu Gly Ile Phe Phe Ser Gly Ser Phe Cys Ser Ile Phe Trp Leu			
	85	90	95
Lys Lys Arg Gly Leu Met Pro Gly Leu Thr Phe Ser Asn Glu Leu Ile			
	100	105	110
Ser Arg Asp Glu Gly Leu His Cys Asp Phe Ala Cys Leu Leu Tyr Thr			
	115	120	125
Leu Leu Lys Thr Lys Leu Ser Glu Glu Arg Val Lys Ser Xaa Arg Leu			
	130	135	140
Arg Arg Gly Arg Asn Arg Glu Arg Val Cys Val Arg Arg Ala Ser Val			
	145	150	155
Arg Val Gly Trp Asp Glu Pro			160
	165		

(2) INFORMATION FOR SEQ ID NO:962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1388
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

```

cgaagattct cgttgatgc tatctcgatt cctctttttt cccagaaaaag      60
tcgctattgg aatcgaacga aagtgttgaa gattttacca gtcagaggta tatatatata      120
gagagagagt tatggtattg gatcaatgga ttccaaggt taaagatggt cagcatctct      180
ccgaagacga gcttcagcct ctctgcgaat acgtgaaaga gattctgatt gaggagtcac      240
acgtacacgc tgtaaaacgt ccagtcaccg tatgtggtga tatccatggc cagtttcatg      300
attctatgga gctttttcag accggagggtC atgttccoga caccattacc atttttatgg      360
gggacttcgt ggatagaggt tacaacagcc ttgaagtctt cactattctt ttacttctta      420
aagctagata tccagccaat attacacttt tgcgcggaaa tcatgaaagt aggcagctaa      480
cgcagggtga tggttttctat gacgaatgcc agaggaagta tggtaacgct aatgcgtggc      540
gatattgcac agatgttttt gactatctta cctctgcagc tattatagat ggcaacagttc      600
tatgtgttca cgttgccctt tccccggatg tccggacaat tgatcagata agactgatcg      660
agcgaatcgt cgaaattcct catgaagggc ccttttgoga tcttatgtgag atgcatcctg      720
aagatattga aacatggggc gtttagtccac gtggagctgg ttggcttttc ggatccaggg      780
ttaccactga gtttaaccat atcaacaagc tggatctagt atgcgcgtcg caccactgtg      840
tacaagaagg tcttaagtag atgttccaag ataaaggcct tgtaactgta tggctctcac      900
ctaataactg ttaccgctgt gggaaatgtc cttctatatt gagtttcaat gcaacactgg      960
aaagggaagt gaagtctctc acagagacag aagagaacaa tcaaatgaga ggcccaagga      1020
ctggagtctc gtatttctta tgaagaatca cacttattat attgctgtg atgatgaagc      1080
ctgtgctgcc attggcaata tgttcagttc aatgtggaaa aggttaatat atgattatat      1140
atatattacta ctgatggggt togttacta tcatattttt tgtccattag gttacattc      1200
ccttttgaaa gttacaagtc aaacactttg gtaatagctc tagtcatttt gattctctgc      1260
tctcttttct ttcccccaat ctttctcttg taatgttatt tttttcattg ttcaactgta      1320
ctgttctctc tgtttttctt gttgtgtgtg tgaagatgac attaatctta aaataatcaa      1380
acatcggt

```

(2) INFORMATION FOR SEQ ID NO:963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..303
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

Met Asp Leu Asp Gln Trp Ile Ser Lys Val Lys Asp Gly Gln His Leu
1 5 10 15
Ser Glu Asp Glu Leu Gln Leu Leu Cys Glu Tyr Val Lys Glu Ile Leu
20 25 30
Ile Glu Glu Ser Asn Val Gln Pro Val Asn Ser Pro Val Thr Val Cys
35 40 45
Gly Asp Ile His Gly Gln Phe His Asp Leu Met Lys Leu Phe Gln Thr
50 55 60
Gly Gly His Val Pro Asp Thr Asn Tyr Ile Phe Met Gly Asp Phe Val
65 70 75 80
Asp Arg Gly Tyr Asn Ser Leu Glu Val Phe Thr Ile Leu Leu Leu Leu
85 90 95
Lys Ala Arg Tyr Pro Ala Asn Ile Thr Leu Leu Arg Gly Asn His Glu
100 105 110
Ser Arg Gln Leu Thr Gln Val Tyr Gly Phe Tyr Asp Glu Cys Gln Arg
115 120 125
Lys Tyr Gly Asn Ala Asn Ala Trp Arg Tyr Cys Thr Asp Val Phe Asp
130 135 140
Tyr Leu Thr Leu Ser Ala Ile Ile Asp Gly Thr Val Leu Cys Val His
145 150 155 160
Gly Gly Leu Ser Pro Asp Val Arg Thr Ile Asp Gln Ile Arg Leu Ile
165 170 175
Glu Arg Asn Arg Glu Ile Pro His Glu Gly Pro Phe Cys Asp Leu Met
180 185 190
Trp Ser Asp Pro Glu Asp Ile Glu Thr Trp Ala Val Ser Pro Arg Gly
195 200 205
Ala Gly Trp Leu Phe Gly Ser Arg Val Thr Thr Glu Phe Asn His Ile
210 215 220
Asn Lys Leu Asp Leu Val Cys Arg Ser His Gln Leu Val Gln Glu Gly
225 230 235 240
Leu Lys Tyr Met Phe Gln Asp Lys Gly Leu Val Thr Val Trp Ser Ala
245 250 255
Pro Asn Asn Cys Tyr Arg Cys Gly Asn Val Ala Ser Ile Leu Ser Phe
260 265 270
Asn Asp Asn Met Glu Arg Glu Val Lys Phe Phe Thr Glu Thr Glu Glu
275 280 285
Asn Asn Gln Met Arg Gly Pro Arg Thr Gly Val Pro Tyr Phe Leu
290 295 300

(2) INFORMATION FOR SEQ ID NO:964:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..245

(D) OTHER INFORMATION: / Ceres Seq. ID 1568514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

Met Lys Leu Phe Gln Thr Gly Gly His Val Pro Asp Thr Asn Tyr Ile
1 5 10 15
Phe Met Gly Asp Phe Val Asp Arg Gly Tyr Asn Ser Leu Glu Val Phe
20 25 30
Thr Ile Leu Leu Leu Lys Ala Arg Tyr Pro Ala Asn Ile Thr Leu
35 40 45
Leu Arg Gly Asn His Glu Ser Arg Gln Leu Thr Gln Val Tyr Gly Phe
50 55 60
Tyr Asp Glu Cys Gln Arg Lys Tyr Gly Asn Ala Asn Ala Trp Arg Tyr
65 70 75 80
Cys Thr Asp Val Phe Asp Tyr Leu Thr Leu Ser Ala Ile Ile Asp Gly

Met	Gly	Asp	Phe	Val	Asp	Arg	Gly	Tyr	Asn	Ser	Leu	Glu	Val	Phe	Thr
1				5					10					15	
Ile	Leu	Leu	Leu	Leu	Lys	Ala	Arg	Tyr	Pro	Ala	Asn	Ile	Thr	Leu	Leu
			20					25					30		
Arg	Gly	Asn	His	Glu	Ser	Arg	Gln	Leu	Thr	Gln	Val	Tyr	Gly	Phe	Tyr
		35					40					45			
Asp	Glu	Cys	Gln	Arg	Lys	Tyr	Gly	Asn	Ala	Asn	Ala	Trp	Arg	Tyr	Cys
	50					55					60				
Thr	Asp	Val	Phe	Asp	Tyr	Leu	Thr	Leu	Ser	Ala	Ile	Ile	Asp	Gly	Thr
65					70				75					80	
Val	Leu	Cys	Val	His	Gly	Gly	Leu	Ser	Pro	Asp	Val	Arg	Thr	Ile	Asp
				85					90					95	
Gln	Ile	Arg	Glu	Ile	Glu	Arg	Asn	Arg	Glu	Ile	Pro	His	Glu	Gly	Pro
		100						105					110		
Phe	Cys	Asp	Leu	Met	Trp	Ser	Asp	Pro	Glu	Asp	Ile	Glu	Thr	Trp	Ala
		115					120					125			
Val	Ser	Pro	Arg	Gly	Ala	Gly	Trp	Leu	Phe	Gly	Ser	Arg	Val	Thr	Thr
		130				135				140					
Glu	Phe	Asn	His	Ile	Asn	Lys	Leu	Asp	Leu	Val	Cys	Arg	Ser	His	Gln
145					150					155				160	
Leu	Val	Gln	Glu	Gly	Leu	Lys	Tyr	Met	Phe	Gln	Asp	Lys	Gly	Leu	Val
			165						170					175	
Thr	Val	Trp	Ser	Ala	Pro	Asn	Asn	Cys	Tyr	Arg	Cys	Gly	Asn	Val	Ala
		180						185					190		
Ser	Ile	Leu	Ser	Phe	Asn	Asp	Asn	Met	Glu	Arg	Glu	Val	Lys	Phe	Phe
		195					200					205			
Thr	Glu	Thr	Glu	Glu	Asn	Asn	Gln	Met	Arg	Gly	Pro	Arg	Thr	Gly	Val
	210					215					220				

Pro Tyr Phe Leu
225

(2) INFORMATION FOR SEQ ID NO:966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..660
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

gaccaagaaa	tgtatacttt	ataagagaaa	tgtacttgat	attcaaaaaa	acaaaaaata	60
aactaggttg	gttaagatta	ttcaaaacttc	aaaggcaaaa	ccaaatgagc	ttcgtgtggt	120
ccgtcgcggt	ttgggtcata	gctgtagcgg	Anttgttgtg	attagcaaat	ggttataccg	180
atggtcgaaac	ccgaagtga	atggtaagtt	accaccggga	tcaatgggtt	taccgatcat	240
cggagagaca	tgcgacttct	ttgagcccca	tggattatac	gagatcccac	cctttgtcaa	300
gaagaggatg	ttaaagtacg	ggccattggt	tcggaacaaac	attttcggat	ccaacaccgt	360
ggttttgaca	gaagctgata	tcattcttga	ggttttcocg	caagagaaca	agtcttttgt	420
gactagctat	ccagaggcca	ttctcaagcc	atttgaaaaa	gaacagtggt	cctcaaacat	480
ggaaacatcc	acaagcacgt	caaacaatc	agtcttcaac	ttcttggtct	tgaggcttta	540
aaaaaacaga	tgataggaga	aatagacaga	gtaacctatg	agcatcttag	atcgaaagct	600
aacgagggta	gcttcgatgc	taaggaggca	gttaaaagtg	tacttacata	gtttcttaat	660

(2) INFORMATION FOR SEQ ID NO:967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

Pro	Arg	Asn	Val	Tyr	Phe	Ile	Arg	Glu	Met	Tyr	Leu	Ile	Phe	Lys	Lys
1		5						10						15	
Thr	Lys	Asn	Lys	Leu	Gly	Trp	Leu	Arg	Leu	Phe	Lys	Leu	Gln	Arg	Gln
		20					25						30		
Asn	Gln	Met	Ser	Phe	Val	Trp	Ser	Ala	Ala	Val	Trp	Val	Ile	Ala	Val
		35					40					45			
Ala	Xaa	Leu	Leu												
		50													

(2) INFORMATION FOR SEQ ID NO:968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

Met	Gly	Leu	Pro	Ile	Ile	Gly	Glu	Thr	Cys	Asp	Phe	Phe	Glu	Pro	His
1		5					10						15		
Gly	Leu	Tyr	Glu	Ile	Pro	Pro	Phe	Val	Lys	Arg	Met	Leu	Lys	Tyr	

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{ix} FEATURE:
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(A) NAME/KEY: peptide
(B) LOCATION: 1..97
(D) OTHER INFORMATION: / Ceres Seq. ID 1568577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

Met	Ala	Thr	Lys	Ser	Val	Leu	Ser	Ile	Phe	Ala	Ile	Phe	Thr	Ile	Val
1			5					10					15		
Val	Leu	Val	Ile	Phe	Glu	Ile	Pro	Glu	Ile	Glu	Ala	His	Asp	Ser	Glu
			20					25					30		
Cys	Leu	Lys	Glu	Tyr	Gly	Gly	Asp	Val	Gly	Phe	Gly	Phe	Cys	Ala	Pro
		35					40					45			
Lys	Ile	Phe	Pro	Thr	Ile	Cys	Tyr	Arg	Asn	Cys	Gln	Lys	Asp	Lys	Gly
		50				55					60				
Ala	Asn	Gly	Gly	Lys	Cys	Leu	Trp	Gly	Glu	Gly	Gly	Asn	Val	Lys	Cys
		65				70				75				80	
Leu	Cys	Asp	Phe	Cys	Ser	Lys	Glu	Ser	Phe	Asn	Gln	Phe	Ile	Ser	Leu
			85					90						95	

Thr

(2) INFORMATION FOR SEQ ID NO:972:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 676 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..676
(D) OTHER INFORMATION: / Ceres Seq. ID 1568583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

agatacaaaag	ctttctttat	aaacgctgcg	tcacatcact	gaatcaaaaa	ccctagcgat	60
acttcacatc	tcgagccgga	gccgcgttgc	gaaagcattt	caatcgtagt	ctaagagaat	120
gtcgacagtg	ggagagctcg	cttgMagvta	cgctgttatg	atcctcgagg	atgagggtat	180
tgctatcacg	gctgacaaaa	tcgccacttt	ggtgaaagct	gctggtgtta	ccattgagtc	240
atactggcca	atgctatttc	ccaagatggc	tgagaaacgt	aatgtcactg	atctcatcat	300
gaacgttggt	gctggtgggt	gaggtgggtg	gcctgttgca	gctgctgctc	ctgctgctgg	360
cggtggtgct	gcgcgtgctg	ctcctgctgc	cgaggagaag	aagaaggacg	aaccagcaga	420
agagagtcat	ggagatttgg	gttttggcct	gttcgattaa	gtgcatttta	cttgttkttt	480
cttcttcgat	ttgagactat	ttttttttcg	tatcgagcta	ttactgtgtt	tggtctggct	540
gaagaactat	aattagttgt	ttctgaacc	atatgttgta	tgacacaaat	tttcaagcaa	600
accctatggc	tccttctttc	cttagaagt	attttgtcac	ctcttttttt	tttaattcat	660
tcgagatatt	agtgctg					

(2) INFORMATION FOR SEQ ID NO:973:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..113
(D) OTHER INFORMATION: / Ceres Seq. ID 1568584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

Met	Ser	Thr	Val	Gly	Glu	Leu	Ala	Xaa	Xaa	Tyr	Ala	Val	Met	Ile	Leu
1				5						10				15	
Glu	Asp	Glu	Gly	Ile	Ala	Ile	Thr	Ala	Asp	Lys	Ile	Ala	Thr	Leu	Val
			20					25					30		
Lys	Ala	Ala	Gly	Val	Thr	Ile	Glu	Ser	Tyr	Trp	Pro	Met	Leu	Phe	Ala
		35					40					45			
Lys	Met	Ala	Glu	Lys	Arg	Asn	Val	Thr	Asp	Leu	Ile	Met	Asn	Val	Gly

50 55 60
Ala Gly Gly Gly Gly Gly Ala Pro Val Ala Ala Ala Pro Ala Ala
65 70 75 80
Gly Gly Gly Ala Ala Ala Ala Ala Pro Ala Ala Glu Glu Lys Lys Lys
85 90 95
Asp Glu Pro Ala Glu Glu Ser Asp Gly Asp Leu Gly Phe Gly Leu Phe
100 105 110
Asp

(2) INFORMATION FOR SEQ ID NO:974:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1568585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

Met Ile Leu Glu Asp Glu Gly Ile Ala Ile Thr Ala Asp Lys Ile Ala
1 5 10 15
Thr Leu Val Lys Ala Ala Gly Val Thr Ile Glu Ser Tyr Trp Pro Met
20 25 30
Leu Phe Ala Lys Met Ala Glu Lys Arg Asn Val Thr Asp Leu Ile Met
35 40 45
Asn Val Gly Ala Gly Gly Gly Gly Ala Pro Val Ala Ala Ala Ala
50 55 60
Pro Ala Ala Gly Gly Gly Ala Ala Ala Ala Pro Ala Ala Glu Glu
65 70 75 80
Lys Lys Lys Asp Glu Pro Ala Glu Glu Ser Asp Gly Asp Leu Gly Phe
85 90 95
Gly Leu Phe Asp
100

(2) INFORMATION FOR SEQ ID NO:975:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1568586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

Met Leu Phe Ala Lys Met Ala Glu Lys Arg Asn Val Thr Asp Leu Ile
1 5 10 15
Met Asn Val Gly Ala Gly Gly Gly Gly Ala Pro Val Ala Ala Ala
20 25 30
Ala Pro Ala Ala Gly Gly Gly Ala Ala Ala Ala Pro Ala Ala Glu
35 40 45
Glu Lys Lys Lys Asp Glu Pro Ala Glu Glu Ser Asp Gly Asp Leu Gly
50 55 60
Phe Gly Leu Phe Asp
65

(2) INFORMATION FOR SEQ ID NO:976:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 930 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..930
(D) OTHER INFORMATION: / Ceres Seq. ID 1568595
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

gcgcaccata	gaaggagaaaa	caaatcttca	ttccagcaat	ggcgattcgt	tgtgtagcga	60
gtagaaaaac	cctagccggc	ttgaaggaga	catactcgag	gctattgagg	atcagaggga	120
ttcagacttt	tacgtctcct	gatcttcctt	acgattatgg	cgcatttgaa	ccggccatta	180
gtggagagat	catgcagatt	catcaccaga	agcatcacca	gccttatggt	actaattaca	240
ataatgctct	tgagcagctt	gatcaagctg	tgaacaaggg	agatgcttcc	actgttgtta	300
agttgcagag	cgccatcaaa	ttcaacggcg	gaggtcatgt	caaccattcg	attttctgga	360
agaaacctgc	tccctccagt	gaagggtggt	gagagccacc	aaaaggatct	cttggtagtg	420
ccattgacgc	tcactttggc	tcccttgaag	gtctggtgaa	aaagatgagt	gctgaggggt	480
ctgcagtgtca	aggctcagga	tgggtgtggc	tcggactaga	caaagaactg	aagaagctag	540
ttgttgacac	aactgccaat	caggatccat	tagtgacaaa	aggaggaagc	ttggtacctc	600
tgggtgggtat	agatgttttg	gagcacgcct	actacttgca	gtacaaaaat	gtgaggcctg	660
agtatctgaa	gaatgtatgg	aaagtgatca	actggaataa	tgaacgcgag	gtttatgaga	720
aggaagaacaa	ctgaatcggt	tacacgatga	cataaggaga	tgaaccagtt	ccagctcagc	780
ttttgtttta	aggtttgctg	aaacaaactt	acagtgtctc	tttggttttt	aagatttgct	840
caactcagct	gtgtgggtacg	ttgttttaca	atgaaagttt	Kcaagaataa	aaatttgcta	900
ttattgtcag	aaagcgctat	tgtttatctt				

(2) INFORMATION FOR SEQ ID NO:977:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..231
(D) OTHER INFORMATION: / Ceres Seq. ID 1568596
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

Met	Ala	Ile	Arg	Cys	Val	Ala	Ser	Arg	Lys	Thr	Leu	Ala	Gly	Leu	Lys	
1				5					10					15		
Glu	Thr	Ser	Ser	Arg	Leu	Leu	Arg	Ile	Arg	Gly	Ile	Gln	Thr	Phe	Thr	
				20				25				30				
Leu	Pro	Asp	Leu	Pro	Tyr	Asp	Tyr	Gly	Ala	Leu	Glu	Pro	Ala	Ile	Ser	
				35				40				45				
Gly	Glu	Ile	Met	Gln	Ile	His	His	Gln	Lys	His	His	Gln	Ala	Tyr	Val	
				50				55				60				
Thr	Asn	Tyr	Asn	Asn	Ala	Leu	Glu	Gln	Leu	Asp	Gln	Ala	Val	Asn	Lys	
				65				70				75			80	
Gly	Asp	Ala	Ser	Thr	Val	Val	Lys	Leu	Gln	Ser	Ala	Ile	Lys	Phe	Asn	
				85				90						95		
Gly	Gly	Gly	His	Val	Asn	His	Ser	Ile	Phe	Trp	Lys	Asn	Leu	Ala	Pro	
				100				105					110			
Ser	Ser	Glu	Gly	Gly	Gly	Glu	Pro	Pro	Lys	Gly	Ser	Leu	Gly	Ser	Ala	
				115				120				125				
Ile	Asp	Ala	His	Phe	Gly	Ser	Leu	Glu	Gly	Leu	Val	Lys	Lys	Met	Ser	
				130				135				140				
Ala	Glu	Gly	Ala	Ala	Val	Gln	Gly	Ser	Gly	Trp	Val	Trp	Leu	Gly	Leu	
				145				150				155			160	
Asp	Lys	Glu	Leu	Lys	Lys	Leu	Val	Val	Asp	Thr	Thr	Ala	Asn	Gln	Asp	
				165				170					175			
Pro	Leu	Val	Thr	Lys	Gly	Gly	Ser	Leu	Val	Pro	Leu	Val	Gly	Ile	Asp	
				180				185					190			
Val	Trp	Glu	His	Ala	Tyr	Tyr	Leu	Gln	Tyr	Lys	Asn	Val	Arg	Pro	Glu	

195 200 205
Tyr Leu Lys Asn Val Trp Lys Val Ile Asn Trp Lys Tyr Ala Ser Glu
210 215 220
Val Tyr Glu Lys Glu Ser Asn
225 230

(2) INFORMATION FOR SEQ ID NO:978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

Met	Gln	Ile	His	His	Gln	Lys	His	His	Gln	Ala	Tyr	Val	Thr	Asn	Tyr
1			5						10					15	
Asn	Asn	Ala	Leu	Glu	Gln	Leu	Asp	Gln	Ala	Val	Asn	Lys	Gly	Asp	Ala
			20					25					30		
Ser	Thr	Val	Val	Lys	Leu	Gln	Ser	Ala	Ile	Lys	Phe	Asn	Gly	Gly	Gly
			35				40					45			
His	Val	Asn	His	Ser	Ile	Phe	Trp	Lys	Asn	Leu	Ala	Pro	Ser	Ser	Glu
			50				55					60			
Gly	Gly	Gly	Glu	Pro	Pro	Lys	Gly	Ser	Leu	Gly	Ser	Ala	Ile	Asp	Ala
			65			70				75			80		
His	Phe	Gly	Ser	Leu	Glu	Gly	Leu	Val	Lys	Lys	Met	Ser	Ala	Glu	Gly
			85					90					95		
Ala	Ala	Val	Gln	Gly	Ser	Gly	Trp	Val	Trp	Leu	Gly	Leu	Asp	Lys	Glu
			100				105					110			
Leu	Lys	Lys	Leu	Val	Val	Asp	Thr	Thr	Ala	Asn	Gln	Asp	Pro	Leu	Val
			115				120					125			
Thr	Lys	Gly	Gly	Ser	Leu	Val	Pro	Leu	Val	Gly	Ile	Asp	Val	Trp	Glu
			130				135					140			
His	Ala	Tyr	Tyr	Leu	Gln	Tyr	Lys	Asn	Val	Arg	Pro	Glu	Tyr	Leu	Lys
			145			150				155				160	
Asn	Val	Trp	Lys	Val	Ile	Asn	Trp	Lys	Tyr	Ala	Ser	Glu	Val	Trp	Glu
			165					170						175	
Lys	Glu	Ser	Asn												

(2) INFORMATION FOR SEQ ID NO:979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1270
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568598

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

cgaaaagcat	tgatttggtc	ctccttctc	ttctattcta	ttcattaaga	acctaattctt	60
catcttctcc	atctcttctt	tcaaggactc	caactcgctc	atccaggaga	gtttattagt	120
agtaaccaat	ccaagtgttc	cttttgtttg	aagcaacaag	ctttgtgata	ttatcctgag	180
agacaatggt	tgggtttaag	aaatcacccg	caaatcttcc	caagcataac	tcagtcgacc	240
tcaagtcttc	caagccaaat	ctcttcgatt	cagatgatga	atctgacaac	aaacataccc	300
ttaaccYtTt	ctaagaggac	tacctctgaa	ccctctttgg	ctgatgatgc	aaacccctttt	360
ggtggtgaga	gagttcagaa	aggagatagt	agttcatcca	aacagtcatt	gttttcgaa	420
tccaaatacc	agtacaagaa	caatttccgt	gattctgggt	gtattgaaaa	ccagtcgggt	480

caggagcttg	aaggttatgc	tgtgtacaag	gctgaagaga	ctacgaaatc	tgtacaaggt	540
tggtttgaag	tagcagaaga	tataaggtct	gatgctacca	gaacttttgt	catgttacac	600
gatcaggcgc	agcaaatcac	taggacgcac	cataaagcgc	ttgaaatcga	ccatgatctc	660
agtcgtgggt	agaagctctt	tggaagcctt	ggaggcatgt	tttcaaagac	ttggaaacaa	720
aagaagactc	gttcctataa	tggtcccgct	gtaaccagag	atgactcacc	aacgagaaga	780
gttaaccact	tagagaaaag	ggaaaaactg	ggactgaact	cagaccaccg	aggacaatca	840
agaacccgag	aaccactccc	cgaatcagct	gatgcttacc	agagagtgga	gatggaaaaa	900
gctaagcaag	acgatgggct	ttcagacttg	agtgatatac	tcggcgagct	aaagaacatg	960
gctgtgtaca	tggaagacga	aatcgagaag	cagaacaaag	gacttgacca	tcttcctgat	1020
gatgtgtacg	aactcaactt	cagagtgcac	caatcaaacg	aacgtggctg	ccgtttgtct	1080
ggaaagtaga	tgaacagagg	gtttatatgt	tcattacact	cattcctcgt	ttgtttttat	1140
ctctatgaag	ttgttcttta	aaactggaaa	gattctttac	atgttaaaata	cattatttgt	1200
atctgtgttt	gtatttgatc	ttgtgacaaa	aaaccaaata	acttattgat	caaacagaga	1260
caactttggc						

(2) INFORMATION FOR SEQ ID NO:980:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1568599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

Met	Met	Asn	Leu	Thr	Thr	Asn	Ile	Pro	Leu	Thr	Xaa	Ser	Lys	Arg	Thr
1		5						10					15		
Thr	Ser	Glu	Pro	Ser	Leu	Ala	Asp	Met	Thr	Asn	Pro	Phe	Gly	Gly	Glu
		20						25					30		
Arg	Val	Gln	Lys	Gly	Asp	Ser	Ser	Ser	Lys	Gln	Ser	Leu	Phe	Ser	
		35				40					45				
Asn	Ser	Lys	Tyr	Gln	Tyr	Lys	Asn	Asn	Phe	Arg	Asp	Ser	Gly	Gly	Ile
		50				55					60				
Glu	Asn	Gln	Ser	Val	Gln	Glu	Leu	Glu	Gly	Tyr	Ala	Val	Tyr	Lys	Ala
		65			70				75				80		
Glu	Glu	Thr	Thr	Lys	Ser	Val	Gln	Gly	Cys	Leu	Lys	Val	Ala	Glu	Asp
		85						90					95		
Ile	Arg	Ser	Asp	Ala	Thr	Arg	Thr	Leu	Val	Met	Leu	His	Asp	Gln	Gly
		100					105						110		
Glu	Gln	Ile	Thr	Arg	Thr	His	His	Lys	Ala	Val	Glu	Ile	Asp	His	Asp
		115			120						125				
Leu	Ser	Arg	Gly	Glu	Lys	Leu	Leu	Gly	Ser	Leu	Gly	Met	Phe	Ser	
		130			135						140				
Lys	Thr	Trp	Lys	Pro	Lys	Lys	Thr	Arg	Pro	Ile	Asn	Gly	Pro	Val	Val
		145			150				155					160	
Thr	Arg	Asp	Asp	Ser	Pro	Thr	Arg	Arg	Val	Asn	His	Leu	Glu	Lys	Arg
		165							170					175	
Glu	Lys	Leu	Gly	Leu	Asn	Ser	Ala	Pro	Arg	Gly	Gln	Ser	Arg	Thr	Arg
		180					185						190		
Glu	Pro	Leu	Pro	Glu	Ser	Ala	Asp	Ala	Tyr	Gln	Arg	Val	Glu	Met	Glu
		195				200						205			
Lys	Ala	Lys	Gln	Asp	Asp	Gly	Leu	Ser	Asp	Leu	Ser	Asp	Ile	Leu	Gly
		210				215					220				
Glu	Leu	Lys	Asn	Met	Ala	Val	Asp	Met	Gly	Ser	Glu	Ile	Glu	Lys	Gln
		225			230				235						
Asn	Lys	Gly	Leu	Asp	His	Leu	His	Asp	Asp	Val	Asp	Glu	Leu	Asn	Phe
		245						250						255	
Arg	Val	Gln	Gln	Ser	Asn	Gln	Arg	Gly	Arg	Arg	Leu	Leu	Gly	Lys	
		260					265						270		

(2) INFORMATION FOR SEQ ID NO:981:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 270 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..270
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568600
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

Met	Asn	Leu	Thr	Thr	Asn	Ile	Pro	Leu	Thr	Xaa	Ser	Lys	Arg	Thr	Thr
1				5					10				-	15	
Ser	Glu	Pro	Ser	Leu	Ala	Asp	Met	Thr	Asn	Pro	Phe	Gly	Gly	Glu	Arg
				20				25					30		
Val	Gln	Lys	Gly	Asp	Ser	Ser	Ser	Lys	Gln	Ser	Leu	Phe	Ser	Asn	
			35				40				45				
Ser	Lys	Tyr	Gln	Tyr	Lys	Asn	Asn	Phe	Arg	Asp	Ser	Gly	Gly	Ile	Glu
	50				55					60					
Asn	Gln	Ser	Val	Gln	Glu	Leu	Glu	Gly	Tyr	Ala	Val	Tyr	Lys	Ala	Glu
65				70				75						80	
Glu	Thr	Thr	Lys	Ser	Val	Gln	Gly	Cys	Leu	Lys	Val	Ala	Glu	Asp	Ile
			85					90					95		
Arg	Ser	Asp	Ala	Thr	Arg	Thr	Leu	Val	Met	Leu	His	Asp	Gln	Gly	Glu
			100				105						110		
Gln	Ile	Thr	Arg	Thr	His	His	Lys	Ala	Val	Glu	Ile	Asp	His	Asp	Leu
	115				120					125					
Ser	Arg	Gly	Glu	Lys	Leu	Leu	Gly	Ser	Leu	Gly	Gly	Met	Phe	Ser	Lys
	130				135					140					
Thr	Trp	Lys	Pro	Lys	Lys	Thr	Arg	Pro	Ile	Asn	Gly	Pro	Val	Val	Thr
145				150				155						160	
Arg	Asp	Asp	Ser	Pro	Thr	Arg	Arg	Val	Asn	His	Leu	Glu	Lys	Arg	Glu
			165					170					175		
Lys	Leu	Gly	Leu	Asn	Ser	Ala	Pro	Arg	Gly	Gln	Ser	Arg	Thr	Arg	Glu
	180						185						190		
Pro	Leu	Pro	Glu	Ser	Ala	Asp	Ala	Tyr	Gln	Arg	Val	Glu	Met	Glu	Lys
	195						200					205			
Ala	Lys	Gln	Asp	Asp	Gly	Leu	Ser	Asp	Leu	Ser	Asp	Ile	Leu	Gly	Glu
	210				215						220				
Leu	Lys	Asn	Met	Ala	Val	Asp	Met	Gly	Ser	Glu	Ile	Glu	Lys	Gln	Asn
225				230				235						240	
Lys	Gly	Leu	Asp	His	Leu	His	Asp	Asp	Val	Asp	Glu	Leu	Asn	Phe	Arg
			245					250					255		
Val	Gln	Gln	Ser	Asn	Gln	Arg	Gly	Arg	Arg	Leu	Leu	Gly	Lys		
	260							265					270		

(2) INFORMATION FOR SEQ ID NO:982:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 247 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..247
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568601
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

Met	Thr	Asn	Pro	Phe	Gly	Gly	Glu	Arg	Val	Gln	Lys	Gly	Asp	Ser	Ser
1			5					10					15		
Ser	Ser	Lys	Gln	Ser	Leu	Phe	Ser	Asn	Ser	Lys	Tyr	Gln	Thr	Lys	Asn
			20					25					30		


```

Asn Phe Arg Asp Ser Gly Gly Ile Glu Asn Gln Ser Val Gln Glu Leu
    35          40          45
Glu Gly Tyr Ala Val Tyr Lys Ala Glu Glu Thr Thr Lys Ser Val Gln
    50          55          60
Gly Cys Leu Lys Val Ala Glu Asp Ile Arg Ser Asp Ala Thr Arg Thr
    65          70          75          80
Leu Val Met Leu His Asp Gln Gly Glu Gln Ile Thr Arg Thr His His
    85          90          95
Lys Ala Val Glu Ile Asp His Asp Leu Ser Arg Gly Glu Lys Leu Leu
    100         105         110
Gly Ser Leu Gly Gly Met Phe Ser Lys Thr Trp Lys Pro Lys Lys Thr
    115         120         125
Arg Pro Ile Asn Gly Pro Val Val Thr Arg Asp Asp Ser Pro Thr Arg
    130         135         140
Arg Val Asn His Leu Glu Lys Arg Glu Lys Leu Gly Leu Asn Ser Ala
    145         150         155         160
Pro Arg Gly Gln Ser Arg Thr Arg Glu Pro Leu Pro Glu Ser Ala Asp
    165         170         175
Ala Tyr Gln Arg Val Glu Met Glu Lys Ala Lys Gln Asp Asp Gly Leu
    180         185         190
Ser Asp Leu Ser Asp Ile Leu Gly Glu Leu Lys Asn Met Ala Val Asp
    195         200         205
Met Gly Ser Glu Ile Glu Lys Gln Asn Lys Gly Leu Asp His Leu His
    210         215         220
Asp Asp Val Asp Glu Leu Asn Phe Arg Val Gln Gln Ser Asn Gln Arg
    225         230         235         240
Gly Arg Arg Leu Leu Gly Lys
    245

```

(2) INFORMATION FOR SEQ ID NO:983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..678
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

```

gatttttttag ggtttcaagt gaaaagagta atagcgcggc ggaGCcatgc ttetcaagac      60
tgagcttttgc cgattcagtg gccagaaaat ttacctctgt agagggatca gatttatccg      120
atcggactct caggtgtttt tgtttctcaa ctccaaatgt aagaggtatt tccacaacaa      180
gttgaagcca tctaagcttt gctggactgc tatgtaccga aagcagcaca agaaggacgc      240
agcacaaagag gctgtgaaga gaaggagacg tgcaactaag aagccttact caaggtcgat      300
tgtcgtgtct actttggagg ttattcagaa gaagcagaca gagaagcctg aagttcgtga      360
tgccgctaga gaagctgccc tacgtgagat caaggagaga atcaagaaga ccaaggacga      420
gaagaaggca aagaaggtcg agtatgcac aaagcaaacag aagtcacaag tgaaggga      480
tatccccaag agtgcgtcac ccaaggctgc taagatgggt ggtgggtgag gcagacgttg      540
aatggagcta tagagtagcc cactcttctc tcttcaacta tctttctttc ttgktttgac      600
attgktttgt tttgtcagcc attttttagt tttgcaccag atctaataata ttcagtttat      660
gaaaactttt tgtttggc

```

(2) INFORMATION FOR SEQ ID NO:984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1568603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

```
Met Val Leu Lys Thr Glu Leu Cys Arg Phe Ser Gly Gln Lys Ile Tyr
1      5      10      15
Pro Gly Arg Gly Ile Arg Phe Ile Arg Ser Asp Ser Gln Val Phe Leu
20      25      30
Phe Leu Asn Ser Lys Cys Lys Arg Tyr Phe His Asn Lys Leu Lys Pro
35      40      45
Ser Lys Leu Cys Trp Thr Ala Met Tyr Arg Lys Gln His Lys Lys Asp
50      55      60
Ala Ala Gln Glu Ala Val Lys Arg Arg Arg Ala Thr Lys Lys Pro
65      70      75      80
Tyr Ser Arg Ser Ile Val Gly Ala Thr Leu Glu Val Ile Gln Lys Lys
85      90      95
Arg Ala Glu Lys Pro Glu Val Arg Asp Ala Ala Arg Glu Ala Ala Leu
100      105      110
Arg Glu Ile Lys Glu Arg Ile Lys Lys Thr Lys Asp Glu Lys Lys Ala
115      120      125
Lys Lys Val Glu Tyr Ala Ser Lys Gln Gln Lys Ser Gln Val Lys Gly
130      135      140
Asn Ile Pro Lys Ser Ala Ala Pro Lys Ala Ala Lys Met Gly Gly Gly
145      150      155      160
Gly Gly Arg Arg
```

(2) INFORMATION FOR SEQ ID NO:985:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1568604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

```
Met Tyr Arg Lys Gln His Lys Lys Asp Ala Ala Gln Glu Ala Val Lys
1      5      10      15
Arg Arg Arg Arg Ala Thr Lys Lys Pro Tyr Ser Arg Ser Ile Val Gly
20      25      30
Ala Thr Leu Glu Val Ile Gln Lys Lys Arg Ala Glu Lys Pro Glu Val
35      40      45
Arg Asp Ala Ala Arg Glu Ala Ala Leu Arg Glu Ile Lys Glu Arg Ile
50      55      60
Lys Lys Thr Lys Asp Glu Lys Lys Ala Lys Lys Val Glu Tyr Ala Ser
65      70      75      80
Lys Gln Gln Lys Ser Gln Val Lys Gly Asn Ile Pro Lys Ser Ala Ala
85      90      95
Pro Lys Ala Ala Lys Met Gly Gly Gly Gly Arg Arg
100      105
```

(2) INFORMATION FOR SEQ ID NO:986:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..344

(D) OTHER INFORMATION: / Ceres Seq. ID 1568605
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:
aaacttaatc acacacaagg agagaagaga gaaagagaga aagagagaca gagataatgg 60
cgtacagtg cgtgttttcta caccagagcg cattggcttc atcagccgca cgaatcatcat 120
cttcctctc atccacagcgt cacgtgtcgc tctccaaacc tgttcagatc atctgtaaaag 180
cacaagctgg agacaagagg tggttcaagg gagccaggaa atttgtcgag aqcgccagcCa 240
cttctttcag tgtgtcttga gtgaaagcaa cacaacgtaa caatgctctg cttgtctttc 300
tcatttgtct cttgtaaaaa atggaaaatg aaactgagct ttg

(2) INFORMATION FOR SEQ ID NO:987:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..58
(D) OTHER INFORMATION: / Ceres Seq. ID 1568606
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:
Asn Leu Ile Thr His Lys Glu Arg Arg Glu Lys Glu Arg Lys Arg Asp
1 5 10 15
Arg Asp Asn Gly Val Gln Cys Val Phe Pro Thr Pro Glu Arg Ile Gly
20 25 30
Phe Ile Ser Arg Thr Ile Ile Phe Leu Leu Ile Pro Ala Ser Arg
35 40 45
Val Ala Leu Gln Thr Cys Ser Asp His Leu
50 55

(2) INFORMATION FOR SEQ ID NO:988:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..67
(D) OTHER INFORMATION: / Ceres Seq. ID 1568607
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:
Met Ala Tyr Ser Ala Cys Phe Leu His Gln Ser Ala Leu Ala Ser Ser
1 5 10 15
Ala Ala Arg Ser Ser Ser Ser Ser Ser Gln Arg His Val Ser Leu
20 25 30
Ser Lys Pro Val Gln Ile Ile Cys Lys Ala Gln Ala Gly Asp Lys Arg
35 40 45
Trp Phe Lys Gly Ala Arg Lys Phe Val Glu Ser Ala Ala Thr Ser Phe
50 55 60
Ser Val Ala
65

(2) INFORMATION FOR SEQ ID NO:989:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1001 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1001
(D) OTHER INFORMATION: / Ceres Seq. ID 1568614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

ctcacacaca	caccaacgca	aacctccaaa	acagggccgg	ggcgattcat	tcacaatctc	60
ggcgattctc	tcttcogtct	cgagtcgctg	agatccatca	gtaaaaggtc	tgcaaaatgg	120
ttgctcaggg	attcactgtg	gatcttaaaa	agcccccgtg	atttcagggt	ggtcactctg	180
gagaagatta	tgaggaatgg	gttcaccaac	ctatcgcgac	caaggaaggg	cctcggtttt	240
ttcagagtga	cttttgggag	ttcttgacac	ttacagtttg	gtgggcaggt	cctgtcattt	300
gggttcaggt	tgtagtctgg	tgcataatca	ggtcagtaag	tatgggagtg	tcactccagc	360
aaatcgctcc	aattgtgtgc	atgggaatat	tcactcggac	attttttgaa	tacgtttctc	420
accggttctg	tttccacata	aaaacgaaga	gttactgggg	aaacactgca	cactactctt	480
ttcacggatg	ccatcataag	caccogatgg	accacottcg	gctcgtcttt	cctcctactg	540
caacagcgat	tttatgcttt	ccgttctgga	acattcggcg	tatctcaact	ccttcaaccc	600
cacctcgatt	gttttgggga	ggcatgctcg	gatattgtag	gtacgagtgc	actctatttt	660
accttcacca	tgcccaacct	actagaccag	tgaccaaaaa	tctcaagaag	taccatttga	720
atcatcactt	caggattcag	gacaaaggat	ttggtatAac	ttcgtcgtta	tgggacatag	780
ctcttggggc	acttccacc	acaaaagccc	ccagaaaaga	gcaatagtag	taaaaggcaa	840
aaactaaaaa	gatgttttga	atacatttta	tttaattctt	agttattaat	catcctctct	900
aaatttgaga	tggtttaatc	gaggtttcat	ttggatcact	gtcttttgta	gtttgtaaat	960
caatacttca	caatccta	ataatattt	tctgcgaaag	t		

(2) INFORMATION FOR SEQ ID NO:990:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1568615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

Met	Val	Ala	Gln	Gly	Phe	Thr	Val	Asp	Leu	Lys	Lys	Pro	Leu	Val	Phe
1			5					10					15		
Gln	Val	Gly	His	Leu	Gly	Glu	Asp	Tyr	Glu	Glu	Trp	Val	His	Gln	Pro
			20					25					30		
Ile	Ala	Thr	Lys	Glu	Gly	Pro	Arg	Phe	Phe	Gln	Ser	Asp	Phe	Trp	Glu
			35					40					45		
Phe	Leu	Thr	Leu	Thr	Val	Trp	Trp	Ala	Val	Pro	Val	Ile	Trp	Leu	Pro
			50					55				60			
Val	Val	Val	Trp	Cys	Ile	Ser	Arg	Ser	Val	Ser	Met	Gly	Cys	Ser	Leu
			65					70				75			80
Pro	Glu	Ile	Val	Pro	Ile	Val	Val	Met	Gly	Ile	Phe	Ile	Trp	Thr	Phe
			85					90					95		
Phe	Glu	Tyr	Val	Leu	His	Arg	Phe	Val	Phe	His	Ile	Lys	Thr	Lys	Ser
			100					105					110		
Tyr	Trp	Gly	Asn	Thr	Ala	His	Tyr	Leu	Ile	His	Gly	Cys	His	His	Lys
			115					120					125		
His	Pro	Met	Asp	His	Leu	Arg	Leu	Val	Phe	Pro	Pro	Thr	Ala	Thr	Ala
			130					135					140		
Ile	Leu	Cys	Phe	Pro	Phe	Trp	Asn	Ile	Ala	Ala	Ile	Ser	Thr	Pro	Ser
			145					150					155		160
Thr	Ala	Pro	Ala	Leu	Phe	Gly	Gly	Gly	Met	Leu	Gly	Tyr	Val	Met	Tyr
			165					170					175		
Asp	Val	Thr	His	Tyr	Tyr	Leu	His	His	Ala	Gln	Pro	Thr	Arg	Pro	Val
			180					185					190		
Thr	Lys	Asn	Leu	Lys	Lys	Tyr	His	Leu	Asn	His	His	Phe	Arg	Ile	Gln
			195					200					205		
Asp	Lys	Gly	Phe	Gly	Ile	Thr	Ser	Ser	Leu	Trp	Asp	Ile	Val	Phe	Gly
			210					215					220		
Thr	Leu	Pro	Thr	Thr	Lys	Ala	Pro	Arg	Lys	Glu	Gln				
			225					230					235		

(2) INFORMATION FOR SEQ ID NO:991:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..161
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568616
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

Met	Gly	Cys	Ser	Leu	Pro	Glu	Ile	Val	Pro	Ile	Val	Val	Met	Gly	Ile
1			5					10					15		
Phe	Ile	Trp	Thr	Phe	Phe	Glu	Tyr	Val	Leu	His	Arg	Phe	Val	Phe	His
		20					25					30			
Ile	Lys	Thr	Lys	Ser	Tyr	Trp	Gly	Asn	Thr	Ala	His	Tyr	Leu	Ile	His
		35				40					45				
Gly	Cys	His	His	Lys	His	Pro	Met	Asp	His	Leu	Arg	Leu	Val	Phe	Pro
	50				55					60					
Pro	Thr	Ala	Thr	Ala	Ile	Leu	Cys	Phe	Pro	His	Trp	Asn	Ile	Ala	Ala
65			70					75						80	
Ile	Ser	Thr	Pro	Ser	Thr	Ala	Pro	Ala	Leu	Phe	Gly	Gly	Gly	Met	Leu
			85					90						95	
Gly	Tyr	Val	Met	Tyr	Asp	Val	Thr	His	Tyr	Tyr	Leu	His	His	Ala	Gln
		100					105						110		
Pro	Thr	Arg	Pro	Val	Thr	Lys	Asn	Leu	Lys	Lys	Tyr	His	Leu	Asn	His
		115				120						125			
His	Phe	Arg	Ile	Gln	Asp	Lys	Gly	Phe	Gly	Ile	Thr	Ser	Ser	Leu	Trp
	130				135					140					
Asp	Ile	Val	Phe	Gly	Thr	Leu	Pro	Thr	Thr	Lys	Ala	Pro	Arg	Lys	Glu
145				150					155						160
Gln															

(2) INFORMATION FOR SEQ ID NO:992:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 148 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..148
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568617
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

Met	Gly	Ile	Phe	Ile	Trp	Thr	Phe	Phe	Glu	Tyr	Val	Leu	His	Arg	Phe
1			5						10				15		
Val	Phe	His	Ile	Lys	Thr	Lys	Ser	Tyr	Trp	Gly	Asn	Thr	Ala	His	Tyr
		20					25					30			
Leu	Ile	His	Gly	Cys	His	His	Lys	His	Pro	Met	Asp	His	Leu	Arg	Leu
		35				40					45				
Val	Phe	Pro	Pro	Thr	Ala	Thr	Ala	Ile	Leu	Cys	Phe	Pro	Phe	Trp	Asn
	50				55					60					
Ile	Ala	Ala	Ile	Ser	Thr	Pro	Ser	Thr	Ala	Pro	Ala	Leu	Phe	Gly	Gly
65			70					75						80	
Gly	Met	Leu	Gly	Tyr	Val	Met	Tyr	Asp	Val	Thr	His	Tyr	Tyr	Leu	His
			85				90						95		
His	Ala	Gln	Pro	Thr	Arg	Pro	Val	Thr	Lys	Asn	Leu	Lys	Lys	Tyr	His
		100				105						110			
Leu	Asn	His	His	Phe	Arg	Ile	Gln	Asp	Lys	Gly	Phe	Gly	Ile	Thr	Ser
		115				120						125			

Ser Leu Trp Asp Ile Val Phe Gly Thr Leu Pro Thr Thr Lys Ala Pro
130 135 140
Arg Lys Glu Gln
145

(2) INFORMATION FOR SEQ ID NO:993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:

```
gagtttcaat ggcggaattt tttctctctt tcttttttctt cttctctctt atcgtctctc 60
ttctcatcat cttatctttc atcgtagcgc caagatccgt cactgctccc atcaagtgtc 120
gccacgtgtt catcaccggt ggatacaagc gaatcggtct cgtctcgtct caccgtgcgc 180
ttctcgaagg cgtcaaaagt tccatctctc ctcgttcaac tgaagaagtc gccgaagcca 240
aacgatccat ccagctagct accggtgtgc aggtcgccac gttctctcgc gacgttcgcg 300
attacgagcg cgtttcgaaa gcgattgatg aatcgggacc gatcgatgtg ttgattgtta 360
atacaggcgt gtttatggg aaagagattg agaaacagag tcttgaggag gttaaagtta 420
tgattgatgt gaactctgact gggagcttca atgtgattaa cctctgatga cctctgatga 480
aagctaggga aagtctgtgt tctgcttcca tttctcttgt gtcctctcaa gctggtcagg 540
caggtatata tggttacact gcataattcg cgagcaagtt tggggttcag gtttatgcgc 600
aagcattgca gccagaagtt atttctgatg acattcatgt gactctcttg tttctctcgt 660
acactgatac acccggtgtt gaacaagaac tgaagaagag gccagaacta acttcaatca 720
tagcgcgcat atcgggttca atgaaaacca aggaagtggc caagatatgt ttgatgtgta 780
tcaagcagc aaaatttaca gtgacatgcc attttattgg cttcttacta tcaattgcta 840
gcaccggcat gtccctcagc ggatcgtttt Gcgttcgctg cattgaagt atattcgtgt 900
gtctaataag attcgtcagc ttggtttttc aatggcaatg gtacaaaacc atagaaaagt 960
ggagcaaaga aaacaagta aatagtaagt tagcttaggt tatttgtac aatggtagta 1020
atactatagt atcagttctt tgtacagtga acagggtcat ggtgttgtag ttccaacttc 1080
ggcttctctg ttttcaattt gaataaattg tg
```

(2) INFORMATION FOR SEQ ID NO:994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..331
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

```
Val Ser Met Ala Ala Ile Phe Ser Leu Phe Leu Phe Phe Ile Leu Phe
1 5 10 15
Ile Val Ser Leu Leu Ile Ile Leu Ser Phe Ile Val Arg Pro Arg Ser
20 25 30
Val Thr Ile Pro Ile Lys Phe Arg His Val Phe Ile Thr Gly Gly Ser
35 40 45
Ser Gly Ile Gly Leu Ala Leu Ala His Arg Ala Val Ser Glu Gly Ala
50 55 60
Lys Val Ser Ile Leu Ala Arg Ser Thr Glu Lys Leu Ala Glu Ala Lys
65 70 75 80
Arg Ser Ile Gln Leu Ala Thr Gly Val Glu Val Ala Thr Phe Ser Ala
85 90 95
Asp Val Arg Asp Tyr Asp Ala Val Ser Lys Ala Ile Asp Glu Ser Gly
100 105 110
```

Pro Ile Asp Val Leu Ile Val Asn Gln Gly Val Phe Ile Gly Lys Glu
115 120 125
Ile Glu Lys Gln Ser Pro Glu Glu Val Lys Phe Met Ile Asp Val Asn
130 135 140
Leu Thr Gly Ser Phe Asn Val Ile Lys Ala Ala Leu Pro Ala Met Lys
145 150 155 160
Ala Arg Glu Ser Arg Gly Ser Ala Ser Ile Ser Leu Val Ser Ser Gln
165 170 175
Ala Gly Gln Ala Gly Ile Tyr Gly Tyr Thr Ala Tyr Ser Ala Ser Lys
180 185 190
Phe Gly Leu Gln Gly Leu Ala Gln Ala Leu Gln Gln Glu Val Ile Ser
195 200 205
Asp Asp Ile His Val Thr Leu Leu Phe Pro Pro Asp Thr Asp Thr Pro
210 215 220
Gly Phe Glu Gln Glu Leu Lys Lys Arg Pro Glu Leu Thr Ser Ile Ile
225 230 235 240
Ala Ala Ser Ser Gly Ser Met Lys Thr Lys Glu Val Ala Lys Ile Cys
245 250 255
Phe Asp Gly Ile Lys Ala Gly Lys Phe Thr Val Thr Cys His Phe Ile
260 265 270
Gly Phe Leu Leu Ser Ile Ala Ser Thr Gly Met Ser Pro Gln Gly Ser
275 280 285
Phe Trp Leu Ala Leu Ile Glu Val Ile Phe Gly Gly Leu Ile Arg Phe
290 295 300
Val Ser Leu Val Phe Gln Trp Gln Trp Tyr Lys Thr Ile Glu Lys Trp
305 310 315 320
Ser Lys Glu Lys Gln Val Asn Ser Lys Leu Ala
325 330

(2) INFORMATION FOR SEQ ID NO:995:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..329

(D) OTHER INFORMATION: / Ceres Seq. ID 1568637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

Met Ala Ala Ile Phe Ser Leu Phe Leu Phe Phe Ile Leu Phe Ile Val
1 5 10 15
Ser Leu Leu Ile Ile Leu Ser Phe Ile Val Arg Pro Arg Ser Val Thr
20 25 30
Ile Pro Ile Lys Phe Arg His Val Phe Ile Thr Gly Gly Ser Ser Gly
35 40 45
Ile Gly Leu Ala Leu Ala His Arg Ala Val Ser Glu Gly Ala Lys Val
50 55 60
Ser Ile Leu Ala Arg Ser Thr Glu Lys Leu Ala Glu Ala Lys Arg Ser
65 70 75 80
Ile Gln Leu Ala Thr Gly Val Glu Val Ala Thr Phe Ser Ala Asp Val
85 90 95
Arg Asp Tyr Asp Ala Val Ser Lys Ala Ile Asp Glu Ser Gly Pro Ile
100 105 110
Asp Val Leu Ile Val Asn Gln Gly Val Phe Ile Gly Lys Glu Ile Glu
115 120 125
Lys Gln Ser Pro Glu Glu Val Lys Phe Met Ile Asp Val Asn Leu Thr
130 135 140
Gly Ser Phe Asn Val Ile Lys Ala Ala Leu Pro Ala Met Lys Ala Arg
145 150 155 160
Glu Ser Arg Gly Ser Ala Ser Ile Ser Leu Val Ser Ser Gln Ala Gly

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1267
(D) OTHER INFORMATION: / Ceres Seq. ID 1568645
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

```

aaacaaaWWY WNaWccaaag acgagccaga gccacctcta acaccatcgg cgacttctcc 60
tctactect cegtgcgga cgtgttgat ttacaacgat tcggtggcta atcgttggta 120
gatttagaat taaagggtta aggagacgac gacgagagat gccgtcaaac ggagatctcg 180
accgtcagat cgaacagcta atggagtgtta agccgttagg tgaagcagac gtgaagatgcc 240
tttgcgatca agctaaaagg attctcgttg aggaatataa tgttcaaccg gttaaagtgtc 300
cggttacagg atgcgcgcat atccatggac agttttatga cctaattgag ctatttcgta 360
ttgggtggtta tgctctcgat actaattacc tcttcattgg agattatgta gtcgtggct 420
actattctgt agaacagct tctctattgg tggcattgaa ggtgcgttac agggacagac 480
ttacgatctc gcgagggaat catgagagcc gtcagattac acaagctcat ggtttttatg 540
acgaatgctt gaggaaatac ggaaatgcaa atgtgtggaa gtattttacg gaccttttcg 600
attatctccc tctaacagca ctcatagaga gtcaggtttt ctgtttgcat ggaggccottt 660
caccttctct gaatactctt gacaatatcc gaagcttgga tcaatacaaa gaggttccac 720
acgaaggacc aatgtgcgat ctactctggt ctgatccga cgatcgttgt ggatggggaa 780
tatctctcct tgggtcgttg tacacgtttg gacaggacat tgcctacgag ttcaatcata 840
acaatggact gagtctgata tcaagagcgc atcaacttgt aatggaaggg tataattggt 900
gtcaggaaaa gaacgtagtg acagtgttta gtgcacaaaa ctactgttac agatgtggaa 960
acatggcgcc aattcttgag attggagaaa agatggaaca gaacttctct caattcgatc 1020
cagcacttag acaagtcgaa cccgatacca caccgaaagc cctgattat ttttctgtat 1080
ttcatttttt ttcttcaaaa gtttctgttg tctgtatca ttgtagatgt gtcctctgtt 1140
tatttgtttt ttctcagctc ctagatggaa tgtgatacca aagacgaaaa accatcatt 1200
ttttgttgga tgttgatact gaaacaggtt tgtagaagcc tcttcttatt atagaaaaatg 1260
tcttttg

```

(2) INFORMATION FOR SEQ ID NO:998:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..306
(D) OTHER INFORMATION: / Ceres Seq. ID 1568646
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:

```

Met Pro Ser Asn Gly Asp Leu Asp Arg Glu Ile Glu Gln Leu Met Glu
1      5      10      15
Cys Lys Pro Leu Gly Glu Ala Asp Val Lys Ile Leu Cys Asp Gln Ala
20     25     30
Lys Ala Ile Leu Val Glu Glu Tyr Asn Val Gln Pro Val Lys Cys Pro
35     40     45
Val Thr Val Cys Gly Asp Ile His Gly Gln Phe Tyr Asp Leu Ile Glu
50     55     60
Leu Phe Arg Ile Gly Gly Asn Ala Pro Asp Thr Asn Tyr Leu Phe Met
65     70     75
Gly Asp Tyr Val Asp Arg Gly Tyr Tyr Ser Val Glu Thr Val Ser Leu
85     90     95
Leu Val Ala Leu Lys Val Arg Tyr Arg Asp Arg Leu Thr Ile Leu Arg
100    105    110
Gly Asn His Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly Phe Tyr Asp
115    120    125
Glu Cys Leu Arg Lys Tyr Gly Asn Ala Asn Val Trp Lys Tyr Phe Thr

```

130 135 140
Asp Leu Phe Asp Tyr Leu Pro Leu Thr Ala Leu Ile Glu Ser Gln Val
145 150 155 160
Phe Cys Leu His Gly Gly Leu Ser Pro Ser Leu Asp Thr Leu Asp Asn
165 170 175
Ile Arg Ser Leu Asp Arg Ile Gln Glu Val Pro His Glu Gly Pro Met
180 185 190
Cys Asp Leu Leu Trp Ser Asp Pro Asp Asp Arg Cys Gly Trp Gly Ile
195 200 205
Ser Pro Arg Gly Ala Gly Tyr Thr Phe Gly Gln Asp Ile Ala Thr Gln
210 215 220
Phe Asn His Asn Asn Gly Leu Ser Leu Ile Ser Arg Ala His Gln Leu
225 230 235 240
Val Met Glu Gly Tyr Asn Trp Cys Gln Glu Lys Asn Val Val Thr Val
245 250 255
Phe Ser Ala Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Met Ala Ala Ile
260 265 270
Leu Glu Ile Gly Glu Lys Met Glu Gln Asn Phe Leu Gln Phe Asp Pro
275 280 285
Ala Pro Arg Gln Val Glu Pro Asp Thr Thr Arg Lys Thr Pro Asp Tyr
290 295 300
Phe Leu
305

(2) INFORMATION FOR SEQ ID NO:999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..292
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:

Met Glu Cys Lys Pro Leu Gly Glu Ala Asp Val Lys Ile Leu Cys Asp
1 5 10 15
Gln Ala Lys Ala Ile Leu Val Glu Glu Tyr Asn Val Gln Pro Val Lys
20 25 30
Cys Pro Val Thr Val Cys Gly Asp Ile His Gly Gln Phe Tyr Asp Leu
35 40 45
Ile Glu Leu Phe Arg Ile Gly Gly Asn Ala Pro Asp Thr Asn Tyr Leu
50 55 60
Phe Met Gly Asp Tyr Val Asp Arg Gly Tyr Tyr Ser Val Glu Thr Val
65 70 75 80
Ser Leu Leu Val Ala Leu Lys Val Arg Tyr Arg Asp Arg Leu Thr Ile
85 90 95
Leu Arg Gly Asn His Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly Phe
100 105 110
Tyr Asp Glu Cys Leu Arg Lys Tyr Gly Asn Ala Asn Val Trp Lys Tyr
115 120 125
Phe Thr Asp Leu Phe Asp Tyr Leu Pro Leu Thr Ala Leu Ile Glu Ser
130 135 140
Gln Val Phe Cys Leu His Gly Gly Leu Ser Pro Ser Leu Asp Thr Leu
145 150 155 160
Asp Asn Ile Arg Ser Leu Asp Arg Ile Gln Glu Val Pro His Glu Gly
165 170 175
Pro Met Cys Asp Leu Leu Trp Ser Asp Pro Asp Asp Arg Cys Gly Trp
180 185 190
Gly Ile Ser Pro Arg Gly Ala Gly Tyr Thr Phe Gly Gln Asp Ile Ala
195 200 205

(2) INFORMATION FOR SEQ ID NO:1000:

(A) LENGTH: 227 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..227
(D) OTHER INFORMATION: / Ceres Seq. ID 1568648

[illegible]

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1354

(D) OTHER INFORMATION: / Ceres Seq. ID 1568657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

acacacaaac	aacacatcca	ctcgaatttt	ctatttcgga	ataacaaaaa	cgatcgggcg	60
agacatgacg	ggggcacaag	ggaactctaa	cgagactctg	ttttcttctt	acaagatggg	120
aagattctgat	ctctctcatt	gagtggttct	ggcgccgatg	acgcggtgca	ggcggttgaa	180
cgagatacca	aacgcggcgt	tggcagagta	ttatgctcaa	cggaaccttc	ccggcggttt	240
ctctactccc	gaaggcacca	gtgtctctcc	cggaatcgca	Gggttccacc	atgtccctgg	300
aattctattca	gatgaacaag	tagaagcatg	gaagcaagtt	gtggaagcag	ttcacgctaa	360
gggaggtttc	atcttttgtc	aattatggca	tggttgaactg	gcttctcatg	caagtgtatca	420
acctaatgga	ggatcaccaa	tatcgtcaac	gaacaaacca	atctcgggaaa	acaggtggcg	480
agtttttgtt	cccgatgggt	cccacgtgaa	gtaccggaaa	cctcggggtt	tagaagcttc	540
cgagataacct	cggttggttg	aggattattg	cctttctgct	ttgaatcgca	ttcgagctgg	600
tttcgatggg	attgagatcc	acggggcgca	tggttacctc	attgatcagt	ttttgaaaga	660
cgggatcaat	gaccgtactg	accaatacgg	aggatccatt	gaaaaccgtt	gtagattctt	720
gaacaagaata	gtggaaaggtg	tagtttcagc	cataggagct	agtaaaagtt	gtgtgagggt	780
atctccagct	atagatcaat	tggacgcaac	tgattctaac	ccattatcac	tcgggctagt	840
ctgtgttgat	atgctcaata	agttacaaga	tgttaatggc	ttgaagctcg	cttaccttca	900
cgtttaccaa	cgtcgtctacc	acgcctacgg	gcaaacagag	tcgggaaggc	aagggaagtga	960
tgaggagaata	gctaagctaa	tgaagagctt	gagaatggct	tataaaggaa	cctttatgtc	1020
cagtgaggaga	ttcaataaag	aactaggcat	gcaagctgtt	tcgggaaggc	atgctgattt	1080
ggtttccat	ggcaggcttt	ttatcgcaaa	cccgattttg	gtttcgggtg	tcaagattga	1140
tggaaagttg	aataaataata	atcgggaagc	gtttttacct	caagatccag	ttgttggtca	1200
cacggattat	cctttcttgg	ctcctttttc	cgccctctga	gtttgataat	cgaggagaaa	1260
aattgtattga	tggtgtataa	agacaataata	ttaatatgta	aaatgacaa	gttattgtta	1320
tcacattaat	gaatagtcac	gtatcttatt	gttt			

(2) INFORMATION FOR SEQ ID NO:1002:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 412 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..412

(D) OTHER INFORMATION: / Ceres Seq. ID 1568658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

His	Asn	Asn	Asn	Thr	Ser	Thr	Arg	Ile	Phe	Tyr	Phe	Arg	Ile	Thr	Lys
1				5				10					15		
Pro	Ile	Gly	Gly	Asp	Met	Thr	Ala	Ala	Gln	Gly	Asn	Ser	Asn	Glu	Thr
				20				25					30		
Leu	Phe	Ser	Ser	Tyr	Lys	Met	Gly	Arg	Phe	Asp	Leu	Ser	His	Arg	Val
				35				40					45		
Val	Leu	Ala	Pro	Met	Thr	Arg	Cys	Arg	Ala	Leu	Asn	Gly	Val	Pro	Asn
				50				55					60		
Ala	Ala	Leu	Ala	Glu	Tyr	Tyr	Ala	Gln	Arg	Thr	Thr	Pro	Gly	Gly	Phe
65				70				75					80		
Leu	Ile	Ser	Glu	Gly	Thr	Met	Val	Ser	Pro	Gly	Ser	Ala	Gly	Phe	Pro
				85				90					95		
His	Val	Pro	Gly	Ile	Tyr	Ser	Asp	Glu	Gln	Val	Glu	Ala	Trp	Lys	Gln
				100				105					110		
Val	Val	Glu	Ala	Val	His	Ala	Lys	Gly	Gly	Phe	Ile	Phe	Cys	Gln	Leu
				115				120					125		
Trp	His	Val	Gly	Arg	Ala	Ser	His	Ala	Val	Tyr	Gln	Pro	Asn	Gly	Gly
				130				135					140		
Ser	Pro	Ile	Ser	Ser	Thr	Asn	Lys	Pro	Ile	Ser	Glu	Asn	Arg	Trp	Arg
145				150				155					160		
Val	Leu	Leu	Pro	Asp	Gly	Ser	His	Val	Lys	Tyr	Pro	Lys	Pro	Arg	Ala

Met	Thr	Ala	Ala	Gln	Gly	Asn	Ser	Asn	Glu	Thr	Leu	Phe	Ser	Ser	Tyr
1				5					10					15	
Lys	Met	Gly	Arg	Phe	Asp	Leu	Ser	His	Arg	Val	Val	Leu	Ala	Pro	Met
			20					25					30		
Thr	Arg	Cys	Arg	Ala	Leu	Asn	Gly	Val	Pro	Asn	Ala	Ala	Leu	Ala	Glu
		35					40					45			
Tyr	Tyr	Ala	Gln	Arg	Thr	Thr	Pro	Gly	Gly	Phe	Leu	Ile	Ser	Glu	Gly
	50					55					60				
Thr	Met	Val	Ser	Pro	Gly	Ser	Ala	Gly	Phe	Pro	His	Val	Pro	Gly	Ile
65					70					75					80
Tyr	Ser	Asp	Glu	Gln	Val	Glu	Ala	Trp	Lys	Gln	Val	Val	Glu	Ala	Val
			85						90					95	
His	Ala	Lys	Gly	Gly	Phe	Ile	Phe	Cys	Gln	Leu	Trp	His	Val	Gly	Arg
			100					105					110		
Ala	Ser	His	Ala	Val	Tyr	Gln	Pro	Asn	Gly	Gly	Ser	Pro	Ile	Ser	Ser
		115					120					125			
Thr	Asn	Lys	Pro	Ile	Ser	Glu	Asn	Arg	Trp	Arg	Val	Leu	Leu	Pro	Asp
	130					135					140				

Gly Ser His Val Lys Tyr Pro Lys Pro Arg Ala Leu Glu Ala Ser Glu
145 150 155 160
Ile Pro Arg Val Val Glu Asp Tyr Cys Leu Ser Ala Leu Asn Ala Ile
165 170 175
Arg Ala Gly Phe Asp Gly Ile Glu Ile His Gly Ala His Gly Tyr Leu
180 185 190
Ile Asp Gln Phe Leu Lys Asp Gly Ile Asn Asp Arg Thr Asp Gln Tyr
195 200 205
Gly Gly Ser Ile Glu Asn Arg Cys Arg Phe Leu Lys Gln Val Val Glu
210 215 220
Gly Val Val Ser Ala Ile Gly Ala Ser Lys Val Gly Val Arg Val Ser
225 230 235 240
Pro Ala Ile Asp His Leu Asp Ala Thr Asp Ser Asn Pro Leu Ser Leu
245 250 255
Gly Leu Ala Val Val Asp Met Leu Asn Lys Leu Gln Asp Val Asn Gly
260 265 270
Leu Lys Leu Ala Tyr Leu His Val Thr Gln Pro Arg Tyr His Ala Tyr
275 280 285
Gly Gln Thr Glu Ser Gly Arg Gln Gly Ser Asp Glu Glu Ala Lys
290 295 300
Leu Met Lys Ser Leu Arg Met Ala Tyr Lys Gly Thr Phe Met Ser Ser
305 310 315 320
Gly Gly Phe Asn Lys Glu Leu Gly Met Gln Ala Val Gln Gln Gly Asp
325 330 335
Ala Asp Leu Val Ser Tyr Gly Arg Leu Phe Ile Ala Asn Pro Asp Leu
340 345 350
Val Ser Arg Phe Lys Ile Asp Gly Lys Leu Asn Lys Tyr Asn Arg Lys
355 360 365
Thr Phe Tyr Thr Gln Asp Pro Val Val Gly Tyr Thr Asp Tyr Pro Phe
370 375 380
Leu Ala Pro Phe Ser Arg Leu
385 390

(2) INFORMATION FOR SEQ ID NO:1004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..374
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

Met Gly Arg Phe Asp Leu Ser His Arg Val Val Leu Ala Pro Met Thr
1 5 10
Arg Cys Arg Ala Leu Asn Gly Val Pro Asn Ala Ala Leu Ala Glu Tyr
20 25 30
Tyr Ala Gln Arg Thr Thr Pro Gly Gly Phe Leu Ile Ser Glu Gly Thr
35 40 45
Met Val Ser Pro Gly Ser Ala Gly Phe Pro His Val Pro Gly Ile Tyr
50 55 60
Ser Asp Glu Gln Val Glu Ala Trp Lys Gln Val Val Glu Ala Val His
65 70 75 80
Ala Lys Gly Gly Phe Ile Phe Cys Gln Leu Trp His Val Gly Arg Ala
85 90 95
Ser His Ala Val Tyr Gln Pro Asn Gly Gly Ser Pro Ile Ser Ser Thr
100 105 110
Asn Lys Pro Ile Ser Glu Asn Arg Trp Arg Val Leu Leu Pro Asp Gly
115 120 125
Ser His Val Lys Tyr Pro Lys Pro Arg Ala Leu Glu Ala Ser Glu Ile

130	135	140
Pro Arg Val Val Glu Asp Tyr Cys Leu Ser Ala Leu Asn Ala Ile Arg		
145	150	155
Ala Gly Phe Asp Gly Ile Glu Ile His Gly Ala His Gly Tyr Leu Ile		
	165	170
Asp Gln Phe Leu Lys Asp Gly Ile Asn Asp Arg Thr Asp Gln Tyr Gly		
	180	185
Gly Ser Ile Glu Asn Arg Cys Arg Phe Leu Lys Gln Val Val Glu Gly		
	195	200
Val Val Ser Ala Ile Gly Ala Ser Lys Val Gly Val Arg Val Ser Pro		
	210	215
Ala Ile Asp His Leu Asp Ala Thr Asp Ser Asn Pro Leu Ser Leu Gly		
	225	230
Leu Ala Val Val Asp Met Leu Asn Lys Leu Gln Asp Val Asn Gly Leu		
	245	250
Lys Leu Ala Tyr Leu His Val Thr Gln Pro Arg Tyr His Ala Tyr Gly		
	260	265
Gln Thr Glu Ser Gly Arg Gln Gly Ser Asp Glu Glu Glu Ala Lys Leu		
	275	280
Met Lys Ser Leu Arg Met Ala Tyr Lys Gly Thr Phe Met Ser Ser Gly		
	290	295
Gly Phe Asn Lys Glu Leu Gly Met Gln Ala Val Gln Gln Gly Asp Ala		
	305	310
Asp Leu Val Ser Tyr Gly Arg Leu Phe Ile Ala Asn Pro Asp Leu Val		
	325	330
Ser Arg Phe Lys Ile Asp Gly Lys Leu Asn Lys Tyr Asn Arg Lys Thr		
	340	345
Phe Tyr Thr Gln Asp Pro Val Val Gly Tyr Thr Asp Tyr Pro Phe Leu		
	355	360
Ala Pro Phe Ser Arg Leu		
370		

(2) INFORMATION FOR SEQ ID NO:1005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1223
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

acaaaccccttt	ccacaagaag	ttataaaacca	atacatagaa	gaaaaacttc	aaactcaaaa	60
aatgatgaag	ggtgcgaagt	tttcatctct	tcttgtgctt	ttctttattt	ttccgatcgc	120
atttgcctcaa	ctgagagtcg	ggtttttatag	tcaatcatgc	ccccaagccg	agactatcgt	180
acgcaatctg	gtgcgccaac	ggttttggtgt	taccccaacc	gttacccgcg	ctttgctcgc	240
tatgcatttc	cacgactggt	tcgttaaggg	ctgtgacgct	ttctctctca	ttgattcaac	300
caattccgag	aaaactgcgt	gaccaaaacgg	aagcgtcagg	gaatttgacc	tgatagaccg	360
gatcaaggct	cagctagaag	ctgcatgccc	ttccacagtc	tcattgtgctg	acatcgctac	420
attggccaca	ctgactcggg	tggccttagc	cggaggccca	agctacagca	tcaccaacggg	480
aaggcgtgac	ggtagggtct	caaaacaatct	tgatgtaacc	ttaccggcgt	caacgactct	540
cgctctctgga	gccgctagtt	tattcacgaa	caaaagggatg	aaacagcttcg	atgcagtatg	600
tcttttgggt	gcaacactct	ttggtcaagg	aaattgtggt	ctcttttagt	acagaaatcac	660
tagcttccaa	ggaactggac	gaccgcagcc	gtccatggac	cccgcctttg	ttaccagcgt	720
aagggaacaca	tgcagaaaata	gcgcgacggc	ggcactagac	cagtcgagtc	cattgagatt	780
cgacaaccag	ttcttcaaac	aaatccgttaa	aaggagagga	gtgttgcaag	ttgaccaaacg	840
ctctgcctac	gaccacacaaa	ctcgtgggat	tgtggctcgc	tatgctaata	acaacgcctt	900
cttcaagcgt	cagttcgttta	gagcaatggt	gaagatggga	gcgcttagtg	tgttactcgt	960
tcgtaacggt	gagatcagaa	ggaactcgag	aagattcaac	taatgaacta	cagaagcgtg	1020
gatataaat	tacatttgat	acaatatatt	tcaaatcttc	tttatatttt	tactaattca	1080

tttttgggtt tgggtggggt tttcttgcac aaataaggct tttcttaaat tggatggttt 1140
cgatttttoga gaagatttac tatgtactat attgttggct tgcatttggg ggatgtatct 1200
taagttttaca aataattgt ggc

(2) INFORMATION FOR SEQ ID NO:1006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..333

(D) OTHER INFORMATION: / Ceres Seq. ID 1568670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

Gln	Pro	Phe	Pro	Gln	Glu	Val	Ile	Asn	Gln	Tyr	Ile	Glu	Glu	Asn	Phe
1			5						10					15	
Gln	Pro	Gln	Lys	Met	Met	Lys	Gly	Ala	Lys	Phe	Ser	Ser	Leu	Leu	Val
			20					25					30		
Leu	Phe	Phe	Ile	Phe	Pro	Ile	Ala	Phe	Ala	Gln	Leu	Arg	Val	Gly	Phe
		35					40					45			
Tyr	Ser	Gln	Ser	Cys	Pro	Gln	Ala	Glu	Thr	Ile	Val	Arg	Asn	Leu	Val
	50					55					60				
Arg	Gln	Arg	Phe	Gly	Val	Thr	Pro	Thr	Val	Thr	Ala	Ala	Leu	Leu	Arg
	65				70					75				80	
Met	His	Phe	His	Asp	Cys	Phe	Val	Lys	Gly	Cys	Asp	Ala	Ser	Leu	Leu
			85						90					95	
Ile	Asp	Ser	Thr	Asn	Ser	Glu	Lys	Thr	Ala	Gly	Pro	Asn	Gly	Ser	Val
			100					105					110		
Arg	Glu	Phe	Asp	Leu	Ile	Asp	Arg	Ile	Lys	Ala	Gln	Leu	Glu	Ala	Ala
		115					120						125		
Cys	Pro	Ser	Thr	Val	Ser	Cys	Ala	Asp	Ile	Val	Thr	Leu	Ala	Thr	Arg
	130					135					140				
Asp	Ser	Val	Ala	Leu	Ala	Gly	Gly	Pro	Ser	Tyr	Ser	Ile	Pro	Thr	Gly
	145				150					155				160	
Arg	Arg	Asp	Gly	Arg	Val	Ser	Asn	Asn	Leu	Asp	Val	Thr	Leu	Pro	Gly
			165						170					175	
Pro	Thr	Ile	Ser	Val	Ser	Gly	Ala	Val	Ser	Leu	Phe	Thr	Asn	Lys	Gly
			180					185						190	
Met	Asn	Thr	Phe	Asp	Ala	Val	Ala	Leu	Leu	Gly	Ala	His	Thr	Val	Gly
		195						200					205		
Gln	Gly	Asn	Cys	Gly	Leu	Phe	Ser	Asp	Arg	Ile	Thr	Ser	Phe	Gln	Gly
	210						215						220		
Thr	Gly	Arg	Pro	Asp	Pro	Ser	Met	Asp	Pro	Ala	Leu	Val	Thr	Ser	Leu
			230							235					240
Arg	Asn	Thr	Cys	Arg	Asn	Ser	Ala	Thr	Ala	Ala	Leu	Asp	Gln	Ser	Ser
			245						250					255	
Pro	Leu	Arg	Phe	Asp	Asn	Gln	Phe	Phe	Lys	Gln	Ile	Arg	Lys	Arg	Arg
			260					265					270		
Gly	Val	Leu	Gln	Val	Asp	Gln	Arg	Leu	Ala	Ser	Asp	Pro	Gln	Thr	Arg
		275					280					285			
Gly	Ile	Val	Ala	Arg	Tyr	Ala	Asn	Asn	Ala	Phe	Phe	Lys	Arg	Gln	
	290						295				300				
Phe	Val	Arg	Ala	Met	Val	Lys	Met	Gly	Ala	Val	Asp	Val	Leu	Thr	Gly
			310						315						320
Arg	Asn	Gly	Glu	Ile	Arg	Arg	Asn	Cys	Arg	Arg	Phe	Asn			
			325						330						

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..313
(D) OTHER INFORMATION: / Ceres Seq. ID 1568671
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

Met Met Lys Gly Ala Lys Phe Ser Ser Leu Leu Val Leu Phe Phe Ile
1 5 10 15
Phe Pro Ile Ala Phe Ala Gln Leu Arg Val Gly Phe Tyr Ser Gln Ser
20 25 30
Cys Pro Gln Ala Glu Thr Ile Val Arg Asn Leu Val Arg Gln Arg Phe
35 40 45
Gly Val Thr Pro Thr Val Thr Ala Ala Leu Leu Arg Met His Phe His
50 55 60
Asp Cys Phe Val Lys Gly Cys Asp Ala Ser Leu Leu Ile Asp Ser Thr
65 70 75 80
Asn Ser Glu Lys Thr Ala Gly Pro Asn Gly Ser Val Arg Glu Phe Asp
85 90 95
Leu Ile Asp Arg Ile Lys Ala Gln Leu Glu Ala Ala Cys Pro Ser Thr
100 105 110
Val Ser Cys Ala Asp Ile Val Thr Leu Ala Thr Arg Asp Ser Val Ala
115 120 125
Leu Ala Gly Gly Pro Ser Tyr Ser Ile Pro Thr Gly Arg Arg Asp Gly
130 135 140
Arg Val Ser Asn Asn Leu Asp Val Thr Leu Pro Gly Pro Thr Ile Ser
145 150 155 160
Val Ser Gly Ala Val Ser Leu Phe Thr Asn Lys Gly Met Asn Thr Phe
165 170 175
Asp Ala Val Ala Leu Leu Gly Ala His Thr Val Gly Gln Gly Asn Cys
180 185 190
Gly Leu Phe Ser Asp Arg Ile Thr Ser Phe Gln Gly Thr Gly Arg Pro
195 200 205
Asp Pro Ser Met Asp Pro Ala Leu Val Thr Ser Leu Arg Asn Thr Cys
210 215 220
Arg Asn Ser Ala Thr Ala Ala Leu Asp Gln Ser Ser Pro Leu Arg Phe
225 230 235 240
Asp Asn Gln Phe Phe Lys Gln Ile Arg Lys Arg Arg Gly Val Leu Gln
245 250 255
Val Asp Gln Arg Leu Ala Ser Asp Pro Gln Thr Arg Gly Ile Val Ala
260 265 270
Arg Tyr Ala Asn Asn Asn Ala Phe Phe Lys Arg Gln Phe Val Arg Ala
275 280 285
Met Val Lys Met Gly Ala Val Asp Val Leu Thr Gly Arg Asn Gly Glu
290 295 300
Ile Arg Arg Asn Cys Arg Arg Phe Asn
305 310

(2) INFORMATION FOR SEQ ID NO:1008:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..312
(D) OTHER INFORMATION: / Ceres Seq. ID 1568672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

Met Lys Gly Ala Lys Phe Ser Ser Leu Leu Val Leu Phe Phe Ile Phe

1	5	10	15
Pro Ile Ala Phe	Ala Gln Leu Arg Val Gly Phe Tyr Ser Gln Ser Cys		
20	25	30	
Pro Gln Ala Glu Thr Ile Val Arg Asn Leu Val Arg Gln Arg Phe Gly			
35	40	45	
Val Thr Pro Thr Val Thr Ala Ala Leu Leu Arg Met His Phe His Asp			
50	55	60	
Cys Phe Val Lys Gly Cys Asp Ala Ser Leu Leu Ile Asp Ser Thr Asn			
65	70	75	80
Ser Glu Lys Thr Ala Gly Pro Asn Gly Ser Val Arg Glu Phe Asp Leu			
85	90	95	
Ile Asp Arg Ile Lys Ala Gln Leu Glu Ala Ala Cys Pro Ser Thr Val			
100	105	110	
Ser Cys Ala Asp Ile Val Thr Leu Ala Thr Arg Asp Ser Val Ala Leu			
115	120	125	
Ala Gly Gly Pro Ser Tyr Ser Ile Pro Thr Gly Arg Asp Gly Arg			
130	135	140	
Val Ser Asn Asn Leu Asp Val Thr Leu Pro Gly Pro Thr Ile Ser Val			
145	150	155	160
Ser Gly Ala Val Ser Leu Phe Thr Asn Lys Gly Met Asn Thr Phe Asp			
165	170	175	
Ala Val Ala Leu Leu Gly Ala His Thr Val Gly Gln Gly Asn Cys Gly			
180	185	190	
Leu Phe Ser Asp Arg Ile Thr Ser Phe Gln Gly Thr Gly Arg Pro Asp			
195	200	205	
Pro Ser Met Asp Pro Ala Leu Val Thr Ser Leu Arg Asn Thr Cys Arg			
210	215	220	
Asn Ser Ala Thr Ala Ala Leu Asp Gln Ser Ser Pro Leu Arg Phe Asp			
225	230	235	240
Asn Gln Phe Phe Lys Gln Ile Arg Lys Arg Arg Gly Val Leu Gln Val			
245	250	255	
Asp Gln Arg Leu Ala Ser Asp Pro Gln Thr Arg Gly Ile Val Ala Arg			
260	265	270	
Tyr Ala Asn Asn Asn Ala Phe Phe Lys Arg Gln Phe Val Arg Ala Met			
275	280	285	
Val Lys Met Gly Ala Val Asp Val Leu Thr Gly Arg Asn Gly Glu Ile			
290	295	300	
Arg Arg Asn Cys Arg Arg Phe Asn			
305	310		

(2) INFORMATION FOR SEQ ID NO:1009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..604
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

aattcactat tAtgggagaa	agaactaaaa	acaccaagaa	aataaaaaaa	gagaaagagg	60
atgggagaaag agttacatga	atccaagggtg	gctactttaca	ccgaaagagg	cattggatca	120
cacgactcat cgctgaaaaa	ggagaaggaa	aaatctcata	agcatagagg	attattccac	180
ctccatcact caaaagatga	gaaagatgga	gacaaaaaga	aagaagatc	aaagagagag	240
aagatagctg cagcaatggt	tggtcttga	gccactttta	tgaagaagaa	gcacaaaggt	300
ggtggaaaaa aggaaaaaaag	aggaggagga	ggaggaaaaag	aggaagaagg	aggaggagaa	360
gaggaggagg aagaagaaga	ggagtcgtct	tcatcgagg	aggaagaaga	agaagaagaa	420
ggaggaggtg gtggttgaga	tgaagaagag	ggaggaggca	agttttagtc	tttcattaca	480
atgatcgccg aagcctttga	agaatgaaaa	tttaatttgt	gatcactttc	ttgtcatttt	540
tttttttttc aaatttgcta	tcaaatata	gcatttgtaa	tgttttatat	gggatgttga	600

attg

(2) INFORMATION FOR SEQ ID NO:1010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

Met	Glu	Lys	Glu	Leu	His	Glu	Ser	Lys	Val	Ala	Thr	Tyr	Thr	Glu	Arg
1			5						10					15	
Gly	Ile	Gly	Ser	His	Asp	Ser	Ser	Pro	Glu	Lys	Glu	Lys	Glu	Lys	Ser
			20					25						30	
His	Lys	His	Arg	Gly	Leu	Phe	His	Leu	His	His	Ser	Lys	Asp	Glu	Lys
			35				40					45			
Asp	Gly	Asp	Lys	Lys	Lys	Glu	Gly	Ser	Lys	Arg	Glu	Lys	Ile	Ala	Ala
			50				55				60				
Ala	Met	Val	Gly	Leu	Gly	Ala	Thr	Phe	Met	Lys	Lys	Lys	His	Lys	Gly
			65				70			75				80	
Gly	Gly	Lys	Lys	Glu	Lys	Arg	Gly	Gly	Gly	Gly	Gly	Lys	Glu	Glu	Glu
				85					90					95	
Gly	Gly	Gly	Glu	Glu	Glu	Gly	Glu	Glu	Glu	Glu	Glu	Ser	Ser	Ser	Ser
				100					105					110	
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Gly	Gly	Gly	Gly	Gly	Asp	Glu
				115				120					125		
Glu	Glu	Gly	Gly	Gly	Lys	Phe	Ser	Ala	Phe	Ile	Thr	Met	Ile	Ala	Glu
				130			135					140			
Ala	Phe	Glu	Glu												
145															

(2) INFORMATION FOR SEQ ID NO:1011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

Met	Val	Gly	Leu	Gly	Ala	Thr	Phe	Met	Lys	Lys	Lys	His	Lys	Gly	Gly
1				5					10					15	
Gly	Lys	Lys	Glu	Lys	Arg	Gly	Gly	Gly	Gly	Lys	Glu	Glu	Glu	Gly	Gly
				20					25					30	
Gly	Gly	Glu	Glu	Glu	Gly	Glu	Glu	Glu	Glu	Ser	Ser	Ser	Ser	Glu	
				35					40				45		
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Gly	Gly	Gly	Gly	Asp	Glu	Glu	
				50			55				60				
Glu	Gly	Gly	Gly	Lys	Phe	Ser	Ala	Phe	Ile	Thr	Met	Ile	Ala	Glu	Ala
				65			70			75				80	
Phe	Glu	Glu													

(2) INFORMATION FOR SEQ ID NO:1012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..75
(D) OTHER INFORMATION: / Ceres Seq. ID 1568676
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:
Met Lys Lys Lys His Lys Gly Gly Gly Lys Lys Glu Lys Arg Gly Gly
1 5 10 15
Gly Gly Gly Lys Glu Glu Glu Gly Gly Glu Glu Glu Glu Glu Glu
20 25 30
Glu Glu Glu Ser Ser Ser Ser Glu Glu Glu Glu Glu Glu Glu Gly
35 40 45
Gly Gly Gly Gly Gly Asp Glu Glu Glu Gly Gly Gly Lys Phe Ser Ala
50 55 60
Phe Ile Thr Met Ile Ala Glu Ala Phe Glu Glu
65 70 75

(2) INFORMATION FOR SEQ ID NO:1013:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1437 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1437
(D) OTHER INFORMATION: / Ceres Seq. ID 1568683
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

tataaacggtc aggtgtgtcgt tgacacttca ttgtctctaa aaagtctgta ttatagtcac 60
atcattagcgt ttaaacccgt tgctatagct gcaacggaga aggtctcaatt tacagtttaa 120
ggcatgaatc tccgtcggcg tggcacaagg ttactttggt ctgttgaaag aaaaactctg 180
attcaggaaa caacacacga ttcgacgacc agggaggatg acgatttcaa ggacaacaag 240
agattgttga gtgtgtaaac ttctcttggt atatgcctat atagtgtggt caggagattca 300
tggagattga agaccaagga ctccagttaga gcttctctcc ttctcttagt gttgaagatg 360
acgatgtttg ttctgaaatc cgtatacttg aaaccacatt agagtctcaat ggaactgatt 420
ctgctaagca agctatggat ttcatatcat aaatcgggtg gcttctctac agaagtaaac 480
ttgggggaatc agaccacaaat ccaggcggtt tccattaat acgcttccag tggctaattcg 540
agttctcaat ggatcgagag ttggtgcgctg tgatcagaaa gctattaaac atgttctttg 600
atggagctgt tgggtgaatt ttctctccct ctaatgccac actgtcagaa ctgtgccttc 660
ttcacagagc cgtgaggaaa aactcctaag ctatggttga aatgctcttg agatatattc 720
ccaagcaaca aagaacaacg ttgttttagc ccgatgctgc tggctccagc gcccttaaac 780
ctcttcatat tgcagctggt aaagacggtt cagaagatgt gttggatgac ctaacagaa 840
atcctgcaat ggtggggagt gaagcgttga agacatgtgc agacagcaca ggttTcaca 900
ccagaagact acgcacttac ggggtcactt ctcalacatc cacttgattc aacgcaagat 960
caataaaaaa tcaacaactg aagatcatgt tgtgggtcaa atccccagtt cttctctcaga 1020
cagagagcag aaagaaccaa aatcaggtcc gatgggttca gccctgggaa tcacacagat 1080
tccatgcaag ctctgtgacc ataaactggg gtatgggaca acacgcaggt ctgtagcgtta 1140
cagacacgct atgttgttcaa ttgtggcgat tgcgtcggtt tgcgtctgtg ttgcacttct 1200
gtttaagagt tgcctgggaag tgctctatgt gtttcaaccg ttcaagtggt agttatgtga 1260
ctatggaaca agctgagtggt aagttcaact tgaaagatct tctaagatat atatatgaat 1320
gttacttata taaaacccat agagggttga tttctatatg taactatatg agtataagat 1380
atagagacat gttggagaa agattgtttg ttattattgt tgttgttgtt gttgtg

(2) INFORMATION FOR SEQ ID NO:1014:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..224

(D) OTHER INFORMATION: / Ceres Seq. ID 1568684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

Met	Pro	Ile	Leu	Ser	Gly	Arg	Gly	Phe	Met	Glu	Ile	Glu	Asp	Gln	Gly	
1				5					10					15		
Leu	Ser	Ser	Ser	Phe	Phe	Pro	Phe	Leu	Val	Val	Glu	Asp	Asp	Asp	Val	
			20					25					30			
Cys	Ser	Glu	Ile	Arg	Ile	Leu	Glu	Thr	Thr	Leu	Glu	Phe	Thr	Gly	Thr	
		35					40					45				
Asp	Ser	Ala	Lys	Gln	Ala	Met	Asp	Phe	Ile	His	Glu	Ile	Gly	Trp	Leu	
		50				55					60					
Leu	His	Arg	Ser	Lys	Leu	Gly	Glu	Ser	Asp	Pro	Asn	Pro	Gly	Val	Phe	
		65			70				75					80		
Pro	Leu	Ile	Arg	Phe	Gln	Trp	Leu	Ile	Glu	Phe	Ser	Met	Asp	Arg	Glu	
			85						90				95			
Trp	Cys	Ala	Val	Ile	Arg	Lys	Leu	Leu	Asn	Met	Phe	Phe	Asp	Gly	Ala	
			100					105					110			
Val	Gly	Glu	Phe	Ser	Ser	Ser	Ser	Asn	Ala	Thr	Leu	Ser	Glu	Leu	Cys	
		115						120				125				
Leu	Leu	His	Arg	Ala	Val	Arg	Lys	Asn	Ser	Lys	Pro	Met	Val	Glu	Met	
		130				135					140					
Leu	Leu	Arg	Tyr	Ile	Pro	Lys	Gln	Gln	Arg	Asn	Ser	Leu	Phe	Arg	Pro	
		145			150				155					160		
Asp	Ala	Ala	Gly	Pro	Ala	Gly	Leu	Thr	Pro	Leu	His	Ile	Ala	Ala	Gly	
			165					170					175			
Lys	Asp	Gly	Ser	Glu	Asp	Val	Leu	Asp	Ala	Leu	Thr	Glu	Asp	Pro	Ala	
			180				185					190				
Met	Val	Gly	Ile	Glu	Ala	Trp	Lys	Thr	Cys	Arg	Asp	Ser	Thr	Gly	Phe	
		195				200					205					
His	Thr	Arg	Arg	Leu	Arg	Thr	Tyr	Ala	Val	Thr	Ser	His	Thr	Ser	Thr	
		210				215					220					

(2) INFORMATION FOR SEQ ID NO:1015:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..215

(D) OTHER INFORMATION: / Ceres Seq. ID 1568685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

Met	Glu	Ile	Glu	Asp	Gln	Gly	Leu	Ser	Ser	Ser	Phe	Phe	Pro	Phe	Leu	
1				5				10					15			
Val	Val	Glu	Asp	Asp	Val	Cys	Ser	Glu	Ile	Arg	Ile	Leu	Glu	Thr		
			20				25					30				
Thr	Leu	Glu	Phe	Thr	Gly	Thr	Asp	Ser	Ala	Lys	Gln	Ala	Met	Asp	Phe	
		35				40					45					
Ile	His	Glu	Ile	Gly	Trp	Leu	His	Arg	Ser	Lys	Leu	Gly	Glu	Ser		
		50				55				60						
Asp	Pro	Asn	Pro	Gly	Val	Phe	Pro	Leu	Ile	Arg	Phe	Gln	Trp	Leu	Ile	
		65			70			75					80			
Glu	Phe	Ser	Met	Asp	Arg	Glu	Trp	Cys	Ala	Val	Ile	Arg	Lys	Leu	Leu	
			85					90				95				
Asn	Met	Phe	Phe	Asp	Gly	Ala	Val	Gly	Glu	Phe	Ser	Ser	Ser	Ser	Asn	
			100					105					110			

Ala Thr Leu Ser Glu Leu Cys Leu Leu His Arg Ala Val Arg Lys Asn
115 120 125
Ser Lys Pro Met Val Glu Met Leu Leu Arg Tyr Ile Pro Lys Gln Gln
130 135 140
Arg Asn Ser Leu Phe Arg Pro Asp Ala Ala Gly Pro Ala Gly Leu Thr
145 150 155 160
Pro Leu His Ile Ala Ala Gly Lys Asp Gly Ser Glu Asp Val Leu Asp
165 170 175
Ala Leu Thr Glu Asp Pro Ala Met Val Gly Ile Glu Ala Trp Lys Thr
180 185 190
Cys Arg Asp Ser Thr Gly Phe His Thr Arg Arg Leu Arg Thr Tyr Ala
195 200 205
Val Thr Ser His Thr Ser Thr
210 215

(2) INFORMATION FOR SEQ ID NO:1016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

Met Asp Phe Ile His Glu Ile Gly Trp Leu Leu His Arg Ser Lys Leu
1 5 10 15
Gly Glu Ser Asp Pro Asn Pro Gly Val Phe Pro Leu Ile Arg Phe Gln
20 25 30
Trp Leu Ile Glu Phe Ser Met Asp Arg Glu Trp Cys Ala Val Ile Arg
35 40 45
Lys Leu Leu Asn Met Phe Phe Asp Gly Ala Val Gly Glu Phe Ser Ser
50 55 60
Ser Ser Asn Ala Thr Leu Ser Glu Leu Cys Leu Leu His Arg Ala Val
65 70 75 80
Arg Lys Asn Ser Lys Pro Met Val Glu Met Leu Leu Arg Tyr Ile Pro
85 90 95
Lys Gln Gln Arg Asn Ser Leu Phe Arg Pro Asp Ala Ala Gly Pro Ala
100 105 110
Gly Leu Thr Pro Leu His Ile Ala Ala Gly Lys Asp Gly Ser Glu Asp
115 120 125
Val Leu Asp Ala Leu Thr Glu Asp Pro Ala Met Val Gly Ile Glu Ala
130 135 140
Trp Lys Thr Cys Arg Asp Ser Thr Gly Phe His Thr Arg Arg Leu Arg
145 150 155 160
Thr Tyr Ala Val Thr Ser His Thr Ser Thr
165 170

(2) INFORMATION FOR SEQ ID NO:1017:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1748
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

aaatgtcatc tccttcacatc ctcaggtaaa aaaactgagt cGgagatttg gcgacgtgat

gaatcatttg	gtgataatct	ctgtgttctt	gagctcagtg	ttgttatata	gaggagaatc	120
tggaatcaca	agtagtttta	ttcgaatcga	atggcctcgc	gttgatatac	cacttgatca	180
tcattgtttc	aattgtccaa	aaggatataa	tgaccacaaa	caagtacata	taactcaagg	240
tgattatgat	ggtaaaagctg	ttatcatctc	ttgggttaca	cctgatgaac	ctggttctag	300
ccaagtacat	tacgggtcgg	ttcaggggaa	atatgagttt	gttgctcaag	ggacttacca	360
taactacacg	ttttacaagt	ataagtcctg	ctttattcat	cactgccttg	tctctgacct	420
tgagcatgat	acaaaatact	attacaagat	tgaaagcggg	gaatcttctc	gagagttttg	480
gtttgtttta	ccaccacatg	tacatccaga	tgcttccctac	aagtttggtg	ttataggcca	540
tatgggtcag	acattcaact	cgttatccac	gttggaacat	tacatggaga	gtggagctca	600
ggctgtttta	ttctctggag	atctttctta	tgctgataga	tatcagtata	atcacgttgg	660
tgtagagatg	gatagctggg	gtcgttttgt	ggagcgtagt	accgcttctc	aaccgtggct	720
ttgtctgcga	ggaaatcact	aagtagatta	catgccatcc	atgggcgagg	tgacaccttt	780
cagggaattac	cttcagcggt	acactacgcc	ttacttagcc	tcaaaaagta	gcagtcctct	840
ttggtacgct	gttaggcgctg	catctgtcca	tatcattgtc	ctctccagct	attgcctttt	900
tgtagaagat	accccgcaat	ggcactggct	tagtgaagag	cttacaagag	ttgataggga	960
gaaacacact	tggtcaattg	ttttgatgca	cgtcccaata	tacaacagta	atgaagcaca	1020
tttctgggag	ggtgaaaagca	tgcgagcagc	ttttgaagag	gtgtttgtct	aacacaaagt	1080
tgtgttaact	tttgcctggc	atgttctatc	ctacgagaga	tcgtaccgaa	tatcaaatgt	1140
ggcgtataac	gtgtcaagcg	gagatcggtt	cccagttcca	gataagtcag	cgctgtttta	1200
tatcacagtt	ggagacggag	gaaatcaaga	aggtctggct	ggaaggttta	cggaaccaca	1260
gccagagttt	tctgcatttc	gggaagctag	ctatggccac	tctactctgg	atataaagaa	1320
ccgaacacac	gctatatacc	actggaacgc	caatgatgat	gggaagaaag	tggcaacgga	1380
tgaattttgt	ttacacaacc	agtaactggg	aaagaacatt	gcagcgagaa	agcttaagaa	1440
gcattatatt	agaggtgtgt	ttgggtggctg	gatcgccact	taattcacta	agtcctgctc	1500
atgtttttgt	tcaaaagtgtg	tgaggatatt	cttttaactc	ggaacttatt	acttaatttg	1560
atgtttaact	tctttccgcg	ttaagttttc	agcaactctg	aatatgaagg	gaattatgta	1620
ttcttatcag	tcttttgatg	aagttaggtc	tattctctgg	attatggatt	tggtgaataa	1680
tgtattctct	agaacgggtg	taagggaattg	tttcacatgg	gtgtgaattg	agaagtcatt	1740
ttgtgttt						

(2) INFORMATION FOR SEQ ID NO:1018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..493
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

Asn	Val	Ile	Ser	Phe	Ile	Ser	Gln	Val	Lys	Lys	Leu	Ser	Arg	Arg	Phe
1			5						10				15		
Gly	Asp	Val	Met	Asn	His	Leu	Val	Ile	Ile	Ser	Val	Phe	Leu	Ser	Ser
			20						25				30		
Val	Leu	Leu	Tyr	Arg	Gly	Glu	Ser	Gly	Ile	Thr	Ser	Ser	Phe	Ile	Arg
			35						40				45		
Ser	Glu	Trp	Pro	Ala	Val	Asp	Ile	Pro	Leu	Asp	His	His	Val	Phe	Asn
			50						55				60		
Val	Pro	Lys	Gly	Tyr	Asn	Ala	Pro	Gln	Gln	Val	His	Ile	Thr	Gln	Gly
			65						70				75		
Asp	Tyr	Asp	Gly	Lys	Ala	Val	Ile	Ile	Ser	Trp	Val	Thr	Pro	Asp	Glu
			85						90				95		
Pro	Gly	Ser	Ser	Gln	Val	His	Tyr	Gly	Ala	Val	Gln	Gly	Lys	Tyr	Glu
			100						105				110		
Phe	Val	Ala	Gln	Gly	Thr	Tyr	His	Asn	Tyr	Thr	Phe	Tyr	Lys	Tyr	Lys
			115						120				125		
Ser	Gly	Phe	Ile	His	His	Cys	Leu	Val	Ser	Asp	Leu	Glu	His	Asp	Thr
			130						135				140		
Lys	Tyr	Tyr	Tyr	Lys	Ile	Glu	Ser	Gly	Glu	Ser	Ser	Arg	Glu	Phe	Trp
			145						150				155		

Phe Val Thr Pro Pro His Val His Pro Asp Ala Ser Tyr Lys Phe Gly
165 170 175
Ile Ile Gly Asp Met Gly Gln Thr Phe Asn Ser Leu Ser Thr Leu Glu
180 185 190
His Tyr Met Glu Ser Gly Ala Gln Ala Val Leu Phe Leu Gly Asp Leu
195 200 205
Ser Tyr Ala Asp Arg Tyr Gln Tyr Asn Asp Val Gly Val Arg Trp Asp
210 215 220
Ser Trp Gly Arg Phe Val Glu Arg Ser Thr Ala Tyr Gln Pro Trp Leu
225 230 235 240
Trp Ser Ala Gly Asn His Glu Val Asp Tyr Met Pro Tyr Met Gly Glu
245 250 255
Val Thr Pro Phe Arg Asn Tyr Leu Gln Arg Tyr Thr Thr Pro Tyr Leu
260 265 270
Ala Ser Lys Ser Ser Ser Pro Leu Trp Tyr Ala Val Arg Arg Ala Ser
275 280 285
Ala His Ile Ile Val Leu Ser Ser Tyr Ser Pro Phe Val Lys Tyr Thr
290 295 300
Pro Gln Trp His Trp Leu Ser Glu Glu Leu Thr Arg Val Asp Arg Glu
305 310 315 320
Lys Thr Pro Trp Leu Ile Val Leu Met His Val Pro Ile Tyr Asn Ser
325 330 335
Asn Glu Ala His Phe Met Glu Gly Glu Ser Met Arg Ala Ala Phe Glu
340 345 350
Glu Trp Phe Val Gln His Lys Val Asp Val Ile Phe Ala Gly His Val
355 360 365
His Ala Tyr Glu Arg Ser Tyr Arg Ile Ser Asn Val Arg Tyr Asn Val
370 375 380
Ser Ser Gly Asp Arg Tyr Pro Val Pro Asp Lys Ser Ala Pro Val Tyr
385 390 395 400
Ile Thr Val Gly Asp Gly Gly Asn Gln Glu Gly Leu Ala Gly Arg Phe
405 410 415
Thr Glu Pro Gln Pro Asp Tyr Ser Ala Phe Arg Glu Ala Ser Tyr Gly
420 425 430
His Ser Thr Leu Asp Ile Lys Asn Arg Thr His Ala Ile Tyr His Trp
435 440 445
Asn Arg Asn Asp Asp Gly Lys Lys Val Ala Thr Asp Glu Phe Val Leu
450 455 460
His Asn Gln Tyr Trp Gly Lys Asn Ile Arg Arg Arg Lys Leu Lys Lys
465 470 475 480
His Tyr Ile Arg Ser Val Val Gly Gly Trp Ile Ala Thr
485 490

(2) INFORMATION FOR SEQ ID NO:1019:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 474 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..474

(D) OTHER INFORMATION: / Ceres Seq. ID 1568717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

Met Asn His Leu Val Ile Ile Ser Val Phe Leu Ser Ser Val Leu Leu
1 5 10
Tyr Arg Gly Glu Ser Gly Ile Thr Ser Ser Phe Ile Arg Ser Glu Trp
20 25 30
Pro Ala Val Asp Ile Pro Leu Asp His His Val Phe Asn Val Pro Lys
35 40 45
Gly Tyr Asn Ala Pro Gln Gln Val His Ile Thr Gln Gly Asp Tyr Asp

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1.1313
(D) OTHER INFORMATION: / Ceres Seq. ID 1568718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

Met	Gly	Gln	Thr	Phe	Asn	Ser	Leu	Ser	Thr	Leu	Glu	His	Tyr	Met	Glu
1				5						10				15	
Ser	Gly	Ala	Gln	Ala	Val	Leu	Phe	Leu	Gly	Asp	Leu	Ser	Tyr	Ala	Asp
			20					25					30		
Arg	Tyr	Gln	Tyr	Asn	Asp	Val	Gly	Val	Arg	Trp	Asp	Ser	Trp	Gly	Arg
		35				40					45				
Phe	Val	Glu	Arg	Ser	Thr	Ala	Tyr	Gln	Pro	Trp	Leu	Trp	Ser	Ala	Gly
	50				55					60					
Asn	His	Glu	Val	Asp	Tyr	Met	Pro	Tyr	Met	Gly	Glu	Val	Thr	Pro	Phe
65				70					75					80	
Arg	Asn	Tyr	Leu	Gln	Arg	Tyr	Thr	Thr	Pro	Tyr	Leu	Ala	Ser	Lys	Ser
			85					90					95		
Ser	Ser	Pro	Leu	Trp	Tyr	Ala	Val	Arg	Arg	Ala	Ser	Ala	His	Ile	Ile
			100					105					110		
Val	Leu	Ser	Ser	Tyr	Ser	Pro	Phe	Val	Lys	Tyr	Thr	Pro	Gln	Trp	His
			115				120					125			
Trp	Leu	Ser	Glu	Glu	Leu	Thr	Arg	Val	Asp	Arg	Glu	Lys	Thr	Pro	Trp
	130					135					140				
Leu	Ile	Val	Leu	Met	His	Val	Pro	Ile	Tyr	Asn	Ser	Asn	Glu	Ala	His
145				150					155					160	
Phe	Met	Glu	Gly	Glu	Ser	Met	Arg	Ala	Ala	Phe	Glu	Glu	Trp	Phe	Val
			165					170					175		
Gln	His	Lys	Val	Asp	Val	Ile	Phe	Ala	Gly	His	Val	His	Ala	Tyr	Glu
			180				185						190		
Arg	Ser	Tyr	Arg	Ile	Ser	Asn	Val	Arg	Tyr	Asn	Val	Ser	Ser	Gly	Asp
		195				200						205			
Arg	Tyr	Pro	Val	Pro	Asp	Lys	Ser	Ala	Pro	Val	Tyr	Ile	Thr	Val	Gly
	210					215									
Asp	Gly	Gly	Asn	Gln	Glu	Gly	Leu	Ala	Gly	Arg	Phe	Thr	Glu	Pro	Gln
225				230						235				240	
Pro	Asp	Tyr	Ser	Ala	Phe	Arg	Glu	Ala	Ser	Tyr	Gly	His	Ser	Thr	Leu
			245					250					255		
Asp	Ile	Lys	Asn	Arg	Thr	His	Ala	Ile	Tyr	His	Trp	Asn	Arg	Asn	Asp
			260				265						270		
Asp	Gly	Lys	Lys	Val	Ala	Thr	Asp	Glu	Phe	Val	Leu	His	Asn	Gln	Tyr
		275				280						285			
Trp	Gly	Lys	Asn	Ile	Arg	Arg	Arg	Lys	Leu	Lys	Lys	His	Tyr	Ile	Arg
	290					295					300				
Ser	Val	Val	Gly	Gly	Trp	Ile	Ala	Thr							
305				310											

(2) INFORMATION FOR SEQ ID NO:1021:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 596 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..596
(D) OTHER INFORMATION: / Ceres Seq. ID 1568741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

gaataatttc	attctcttat	ggcatatggt	gctataaaaca	aacacactta	ccacgcttga	60
tcttacaaca	catgaaccat	gggtttctta	accactcttt	acttcaccac	tttagcacta	120
accctaactc	tgatcttttcg	tctcatacca	gaacaccacg	catcacgcca	tctgaatgga	180
aagaatccgg	cggtaaattg	agttaccact	actagcgaga	aatacattgt	tctacgccc	240
ttaccacgt	ttttacgacc	ctttttccca	cogttacagt	ttgccgctgc	accgttcgga	300

gggaatatcc cacaaccacc gttacccttca ccacctccaa cattttctacc gtgtctccca 360
ggttttcaagt ttctccctcctt tcagtcctcga aagcctacgc cgcogtaatc gtatatacgt 420
tgacggcatc aagttctaataa ctgtaatgaa atattaaact atctacttta atgtattatc 480
tatctctata tatcacoggtt gatcatctat aaataattga tggtaatatc atgggtatgaa 540
actgtaataa agatactcgg tgtagtaatt aataaaYtga ataaatacta tgttag

(2) INFORMATION FOR SEQ ID NO:1022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

Ile Ile Ser Phe Ser Tyr Gly Ile Trp Cys Tyr Lys Gln Thr His Leu
1 5 10 15
Pro Arg Leu Ile Leu Gln His Met Asn His Gly Phe Phe Asn Pro Leu
20 25 30
Leu Leu His His Phe Ser Thr Asn Pro Asn Leu Asp Leu Ser Ser His
35 40 45
Thr Arg Asn His Arg Ile Thr Pro Ser Glu Trp Lys Glu Ser Gly Gly
50 55 60
Asn Trp Ser Tyr His Tyr
65 70

(2) INFORMATION FOR SEQ ID NO:1023:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568743

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

Met Ala Ser Ser Thr His Ser Tyr Phe Thr Thr Leu Ala Leu Thr Leu
1 5 10 15
Ile Leu Ile Phe Arg Leu Ile Pro Glu Thr Thr Ala Ser Arg His Leu
20 25 30
Asn Gly Lys Asn Pro Ala Val Ile Gly Val Thr Thr Thr Ser Glu Lys
35 40 45
Tyr Ile Val Pro Thr Pro Leu Pro Pro Phe Leu Arg Pro Phe Phe Pro
50 55 60
Pro Leu Gln Phe Ala Ala Ala Pro Phe Gly Gly Asn Ile Pro Gln Pro
65 70 75 80
Pro Leu Pro Ser Pro Pro Pro Thr Phe Leu Pro Cys Leu Pro Gly Phe
85 90 95
Lys Phe Pro Pro Phe Gln Ser Arg Lys Pro Thr Pro Pro
100 105

(2) INFORMATION FOR SEQ ID NO:1024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..447

(D) OTHER INFORMATION: / Ceres Seq. ID 1568751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

aaWactgata gtagaaaaaa aaagagagaa gaaaaatggt gttgacaatc tatgctccat	60
tattcgcttc ttcaaaagaga gctgttgtga cattgtgtgga gaagggagta tcattcgaaa	120
ctgtcaatgt cgaatctcatg aaaggagaac agagacagcc tgagtatctc gcgattcagg	180
ttccgatttt ccctcttttt tactaaaatgt ttcttttttt ccggtgacta ttccgatca	240
tgatcccttt ttccgatcga tgcagccttt cggtaaaatc ccagtcctcg tcgacggaga	300
ctacaaaatc ttccgtacac ttctctcttt ttaagctact actacacgag tcgatgctcg	360
ataatggatc tgatcattg cgaatcatgat caatgaatca catgatcttt aagatttttt	420
tgattgtttg gaagagattg tttaggt	

(2) INFORMATION FOR SEQ ID NO:1025:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1568752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

Xaa	Leu	Ile	Val	Glu	Lys	Lys	Arg	Glu	Lys	Lys	Asn	Gly	Val	Asp	Asn
1				5					10					15	
Leu	Cys	Ser	Ile	Ile	Arg	Phe	Phe	Lys	Glu	Ser	Cys	Cys	Asp	Ile	Gly
			20					25					30		
Gly	Glu	Gly	Ser	Ile	Ile	Arg	Asn	Cys	Gln	Cys	Arg	Ser	His	Glu	Arg
			35				40						45		
Arg	Thr	Glu	Thr	Ala											
			50												

(2) INFORMATION FOR SEQ ID NO:1026:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1568753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

Met	Val	Leu	Thr	Ile	Tyr	Ala	Pro	Leu	Phe	Ala	Ser	Ser	Lys	Arg	Ala
1				5					10				15		
Val	Val	Thr	Leu	Val	Glu	Lys	Gly	Val	Ser	Phe	Glu	Thr	Val	Asn	Val
			20				25					30			
Asp	Leu	Met	Lys	Gly	Glu	Gln	Arg	Gln	Pro	Glu	Tyr	Leu	Ala	Ile	Gln
			35				40					45			
Val	Pro	Ile	Phe	Pro	Leu	Phe	Thr								
			50				55								

(2) INFORMATION FOR SEQ ID NO:1027:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..38

(D) OTHER INFORMATION: / Ceres Seq. ID 1568754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

Met Ile Pro Phe Ser Asp Arg Cys Ser Leu Ser Val Lys Ser Gln Ser
1 5 10 15
Ser Ser Thr Glu Thr Thr Lys Ser Ser Val His Phe Phe Ser Phe Lys
20 25 30
Leu Leu Leu His Glu Ser
35

(2) INFORMATION FOR SEQ ID NO:1028:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1592 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1592

(D) OTHER INFORMATION: / Ceres Seq. ID 1568758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

aaagactctct ctgcttttcga ccmAaaaacc ttctctctct ctctgggaga tctccatctt 60
cttcgcttct tgccttcccc gcttgaacaa attactcgat ctgcgcggcg gaacaagctc 120
tcgcttttct ttctccggcag atcgattctt ccaattccct attcctttct aggtcttctt 180
taagaaaccc ttaactttct caaaatctgc atttatggcg attagggtta ccttcaccta 240
ctccagctat gttgctagga cgaattgctt atccgcggcg actcgtgtcg gtaccggcga 300
cgttagatca tgccttcgaaa catgggttctg tcccagggtc tgcggccaca atcagatacc 360
agatattgtt gataaatctc ccggatccaa cacatggggt ccaagctcag gccctcgtgc 420
tcgaccagct tcatcaatgt atagcaccat tgcgagggaa atcctcgaag aaggctgcga 480
gagtcacatt gtcttgggta tgatctctct catgaatttg actggagctc cacagtcttc 540
gggtgtgacc ggtctcggga tctctccctt taagacttct tctgtcatcc cgttccattg 600
gggttccaaq tggatgcctt gtgattcttc ggcgacgtta tcaacggata ttgctgaggt 660
tgatagagga gaaagaggtc gtgatcctaa agtgaagttg gagttgagtg ataaagtctc 720
gaatggtgga aacggatggg ttaataagct gttgaatctc tgcctcggag atgctaagtc 780
tgctttcaag cgggttaact ttctctctct ttcccgatcg gctttggcgc agccaaagtc 840
tataccttca acatctatgc ttctactctc cgaatgtggg gatcgtgtta tagccagaga 900
ggtctcctac tttttcagga agccagaggt ttccagacata gttatcttca aggtcctctc 960
tatttttggt gaacatgggt acagttgtgc tgatgttttc ataaaaagga tagttgtcag 1020
cgaaggtgac tgggttgaag ttgtgtatgg aaagctctta tgaattgaca ctgttcaagc 1080
agaggatttt gtcttagagc caattgacta tgaatggaa ccaatgtttg tccctgaagg 1140
ttatgtcttc gtcttagagg acaaccgcga caaaagcttt gattctcata actggggctcc 1200
acttccaata aagaacatca tagggagatc tgtgtttcgc tattggccac caaagcaagt 1260
gtcagacata atacaccatg aacaagttag ccaaaagaga gctgtgtgat ttcttgcacc 1320
aacgcagatg gtatcttagg attaagcaga aaatttgatt agatgagctg tgcctatgca 1380
accattttgg cgtcgaagcg aacagagcaa ttctttcttc ctgtctaggc ttgatggcgg 1440
acatggaatg cactgggaaa tccatataaa aagaacaaag aaattgatat ttgtcttgg 1500
attttttttg atgtgttgaa acctaaatgc atccagtgtg attggcagta gctgtcaaac 1560

(2) INFORMATION FOR SEQ ID NO:1029:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..367

(D) OTHER INFORMATION: / Ceres Seq. ID 1568759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

Met Ala Ile Arg Val Thr Phe Thr Tyr Ser Ser Tyr Val Ala Arg Ser

1	5	10	15
Ile Ala Ser Ser Ala Gly Thr Arg Val Gly Thr Gly Asp Val Arg Ser			
20		25	30
Cys Phe Glu Thr Trp Val Arg Pro Arg Phe Cys Gly His Asn Gln Ile			
35		40	45
Pro Asp Ile Val Asp Lys Ser Pro Gly Ser Asn Thr Trp Gly Pro Ser			
50	55	60	
Ser Gly Pro Arg Ala Arg Pro Ala Ser Ser Met Tyr Ser Thr Ile Ala			
65	70	75	80
Arg Glu Ile Leu Glu Glu Gly Cys Lys Ser Pro Leu Val Leu Gly Met			
85		90	95
Ile Ser Leu Met Asn Leu Thr Gly Ala Pro Gln Phe Ser Gly Val Thr			
100		105	110
Gly Leu Gly Ile Ser Pro Phe Lys Thr Ser Ser Val Ile Pro Phe Leu			
115		120	125
Arg Gly Ser Lys Trp Met Pro Cys Ser Ile Pro Ala Thr Leu Ser Thr			
130	135	140	
Asp Ile Ala Glu Val Asp Arg Gly Gly Lys Val Cys Asp Pro Lys Val			
145	150	155	160
Lys Leu Glu Leu Ser Asp Lys Val Ser Asn Gly Gly Asn Gly Trp Val			
165		170	175
Asn Lys Leu Leu Asn Ile Cys Ser Glu Asp Ala Lys Ala Ala Phe Thr			
180		185	190
Ala Val Thr Phe Ser Leu Leu Phe Arg Ser Ala Leu Ala Glu Pro Lys			
195		200	205
Ser Ile Pro Ser Thr Ser Met Leu Pro Thr Leu Asp Val Gly Asp Arg			
210	215	220	
Val Ile Ala Glu Lys Val Ser Tyr Phe Phe Arg Lys Pro Glu Val Ser			
225	230	235	240
Asp Ile Val Ile Phe Lys Ala Pro Pro Ile Leu Val Glu His Gly Tyr			
245		250	255
Ser Cys Ala Asp Val Phe Ile Lys Arg Ile Val Ala Ser Glu Gly Asp			
260		265	270
Trp Val Glu Val Cys Asp Gly Lys Leu Leu Val Asn Asp Thr Val Gln			
275		280	285
Ala Glu Asp Phe Val Leu Glu Pro Ile Asp Tyr Glu Met Glu Pro Met			
290	295	300	
Phe Val Pro Glu Gly Tyr Val Phe Val Leu Gly Asp Asn Arg Asn Lys			
305	310	315	320
Ser Phe Asp Ser His Asn Trp Gly Pro Leu Pro Ile Lys Asn Ile Ile			
325		330	335
Gly Arg Ser Val Phe Arg Tyr Trp Pro Pro Ser Lys Val Ser Asp Ile			
340		345	350
Ile His His Glu Gln Val Ser Gln Lys Arg Ala Val Asp Val Ser			
355	360	365	

(2) INFORMATION FOR SEQ ID NO:1030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..293

(D) OTHER INFORMATION: / Ceres Seq. ID 1568760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

Met Tyr Ser Thr Ile Ala Arg Glu Ile Leu Glu Glu Gly Cys Lys Ser
1 5 10 15
Pro Leu Val Leu Gly Met Ile Ser Leu Met Asn Leu Thr Gly Ala Pro
20 25 30

Gln Phe Ser Gly Val Thr Gly Leu Gly Ile Ser Pro Phe Lys Thr Ser
35 40 45
Ser Val Ile Pro Phe Leu Arg Gly Ser Lys Trp Met Pro Cys Ser Ile
50 55 60
Pro Ala Thr Leu Ser Thr Asp Ile Ala Glu Val Asp Arg Gly Gly Lys
65 70 75 80
Val Cys Asp Pro Lys Val Lys Leu Glu Leu Ser Asp Lys Val Ser Asn
85 90 95
Gly Gly Asn Gly Trp Val Asn Lys Leu Leu Asn Ile Cys Ser Glu Asp
100 105 110
Ala Lys Ala Ala Phe Thr Ala Val Thr Phe Ser Leu Leu Phe Arg Ser
115 120 125
Ala Leu Ala Glu Pro Lys Ser Ile Pro Ser Thr Ser Met Leu Pro Thr
130 135 140
Leu Asp Val Gly Asp Arg Val Ile Ala Glu Lys Val Ser Tyr Phe Phe
145 150 155 160
Arg Lys Pro Glu Val Ser Asp Ile Val Ile Phe Lys Ala Pro Pro Ile
165 170 175
Leu Val Glu His Gly Tyr Ser Cys Ala Asp Val Phe Ile Lys Arg Ile
180 185 190
Val Ala Ser Glu Gly Asp Trp Val Glu Val Cys Asp Gly Lys Leu Leu
195 200 205
Val Asn Asp Thr Val Gln Ala Glu Asp Phe Val Leu Glu Pro Ile Asp
210 215 220
Tyr Glu Met Glu Pro Met Phe Val Pro Glu Gly Tyr Val Phe Val Leu
225 230 235 240
Gly Asp Asn Arg Asn Lys Ser Phe Asp Ser His Asn Trp Gly Pro Leu
245 250 255
Pro Ile Lys Asn Ile Ile Gly Arg Ser Val Phe Arg Tyr Trp Pro Pro
260 265 270
Ser Lys Val Ser Asp Ile Ile His His Glu Gln Val Ser Gln Lys Arg
275 280 285
Ala Val Asp Val Ser
290

(2) INFORMATION FOR SEQ ID NO:1031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..272

(D) OTHER INFORMATION: / Ceres Seq. ID 1568761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

Met Ile Ser Leu Met Asn Leu Thr Gly Ala Pro Gln Phe Ser Gly Val
1 5 10 15
Thr Gly Leu Gly Ile Ser Pro Phe Lys Thr Ser Ser Val Ile Pro Phe
20 25 30
Leu Arg Gly Ser Lys Trp Met Pro Cys Ser Ile Pro Ala Thr Leu Ser
35 40 45
Thr Asp Ile Ala Glu Val Asp Arg Gly Gly Lys Val Cys Asp Pro Lys
50 55 60
Val Lys Leu Glu Leu Ser Asp Lys Val Ser Asn Gly Gly Asn Gly Trp
65 70 75 80
Val Asn Lys Leu Leu Asn Ile Cys Ser Glu Asp Ala Lys Ala Ala Phe
85 90 95
Thr Ala Val Thr Phe Ser Leu Leu Phe Arg Ser Ala Leu Ala Glu Pro
100 105 110
Lys Ser Ile Pro Ser Thr Ser Met Leu Pro Thr Leu Asp Val Gly Asp

(2) INFORMATION FOR SEQ ID NO:1032:

(A) LENGTH: 1188 base pairs

(C) STRANDEDNESS: single

MOLECULE TYPE: DNA (q

(A) NAM

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:1032:

tcaacagtatg	gtccagatcgt	tftcttaaac	tctctctctt	taccaccaca	ctctgggtgct	120
cctgtatgga	acaaacaactc	ctccatgacc	tgttgagacca	gaggtctcat	cctctcttgag	180
gattaccatc	tcgttgagaa	gctgtccaa	ttcgaaagg	aacgatctc	agagcgtgtg	240
gttcacgga	gaggagccag	tgtcaaaagt	tcttttgagg	tatctctaac		300
ctcaacttgg	ctgacattct	cogagctccc	gggtgtcaga	ctctctgtat	tgctccggttc	360
tcacacgtta	tcctatgagg	tgggaagtcc	gagaccttga	gagacccctg	tcggttttgca	420
cgtaagttt	acaccagaga	gggaacattt	gactctgttg	gaacaacatt	ctctgttttc	480
ttcatccggc	atgtgatgaa	gttccctgac	atgtgtcaacg	ctcttaaggc	gaacccaaaa	540
ttctcacatc	aagagaactg	gagaactcct	gaactctctt	ccccacacc	tgaagttttg	600
aacatctctc	cttctcctct	cgatgatata	gggatccccc	aagattacag	gcacatggat	660
ggtttcaggt	tcacaacata	catgttgtatc	aacaaagctg	ccaaagctga	ctacgtgaag	720
ttccattgga	aaccaaacat	tggagtcaag	tctctttttg	aagaagatga	aattcgtgtt	780
ggagacagga	accacagctg	tgctactcaa	gacttgtatg	acttatgtgc	tgctgaaac	840
tacctcgaa	ggaagtcttc	ttaccaaatt	atgtgatcct	ctgtagaaga	caagctgcag	900
tttgaccgcc	tcgatgtta	caacagcctc	ctctcaagata	tcttgctctt	ccaaactgtc	960
ggagctcttg	tgttgtaacaa	gaacatttgc	aactctcttg	cagagaatga	gcaacttggc	1020
ttctgtctctg	caattattgt	tcocaggata	cactactcag	acgacagaat	gcttcaaac	1080
ctgtctctct	ctctatgcga	tactcagaga	acccgtcttg	gacaaacta	ccttcagcta	1140
ccagGtcaat	ctctcgaatt	gtcttcacca	caacaaccac	catagaag		

(2) INFORMATION FOR SEQ ID NO:

(A) LENGTH: 394 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1033:

1	Val	Leu	Ile	5	Ile	Ser	Glu	Ser	Leu	Gln	Ala	Leu	Phe	Ser	Ser
1	Thr	Met	Asp	20	Tyr	Lys	Tyr	Arg	Pro	Ala	Ser	Ser	Tyr	Asn	Ser
	Phe	Phe	Thr	20	Asn	Ser	Gly	Ala	Pro	Val	Trp	Asn	Asn	Asn	Ser
	Met	Thr	Val	35	Gly	Pro	Arg	Gly	Pro	Ile	Leu	Leu	Glu	Asp	His
	Val	Glu	Lys	50	Leu	Ala	Asn	Phe	Asp	Arg	Glu	Arg	Ile	Pro	Glu
65	Val	His	Ala	70	Gly	Ala	Ser	Ala	Lys	Gly	75	Phe	Phe	Glu	Val
	Asp	Ile	Ser	85	Leu	Thr	Cys	Ala	Asp	Phe	Leu	Arg	Ala	Pro	Gly
	Gln	Thr	Pro	100	Val	Ile	Val	Arg	Phe	Ser	Thr	Val	Ile	His	Arg
	Ser	Pro	Glu	115	Thr	Leu	Arg	Asp	Pro	Arg	Gly	Phe	Ala	Val	Lys
	Thr	Arg	Glu	130	Gly	Asn	Phe	Asp	Leu	Val	Gly	Asn	Asn	Phe	Pro
145	Phe	Ile	Arg	150	Gly	Met	Lys	Phe	Pro	Asp	Met	Val	His	Ala	Leu
	Pro	Asn	Pro	165	Ser	His	Ile	Gln	Glu	Asn	Trp	Arg	Ile	Leu	Asp
	Phe	Ser	His	180	Pro	Glu	Ser	Leu	Asn	Met	Phe	Thr	Phe	Leu	Phe
	Asp	Ile	Gly	195	Ile	Pro	Gln	Asp	Tyr	Arg	His	Met	Asp	Gly	Ser
	Asn	Thr	Tyr	210	Met	Leu	Ile	Asn	Lys	Ala	Gly	Lys	Ala	His	Tyr
225	Phe	His	Trp	230	Lys	Pro	Thr	Cys	Gly	Val	Lys	Ser	Leu	Leu	Glu
	Ala	Ile	Arg	245	Val	Gly	Gly	Thr	Asn	His	Ser	His	Ala	Thr	Gln
	Tyr	Asp	Ser	260	Ile	Ala	Ala	Gly	Asn	Tyr	Pro	Glu	Trp	Lys	Leu
	Gln	Ile	Ile	275	Asp	Pro	Ala	Asp	Glu	Asp	Lys	Phe	Asp	Phe	Asp
	Asp	Val	Thr	290	Lys	Thr	Trp	Pro	Glu	Asp	Ile	Leu	Pro	Leu	Gln
305	Gly	Arg	Met	310	Val	Leu	Asn	Lys	Asn	Ile	Asp	Asn	Phe	Phe	Ala
	Glu	Gln	Leu	325	Ala	Phe	Cys	Pro	Ala	Ile	Val	Pro	Gly	Ile	His
	Ser	Asp	Asp	340	Lys	Leu	Leu	Gln	Thr	Arg	Val	Phe	Ser	Tyr	Ala
	Gln	Arg	His	355	Arg	Gly	Pro	Asn	Tyr	Leu	Gln	Leu	Pro	Gly	Gln
370	Ser	Lys	Met	385	Cys	Ser	Pro	Gln	Gln	Pro	Pro				

(2) INFORMATION FOR SEQ ID NO:1034:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..377

(D) OTHER INFORMATION: / Ceres Seq. ID 1568779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:

Met	Asp	Pro	Tyr	Lys	Tyr	Arg	Pro	Ala	Pro	Ala	Pro	Val	Trp	Asn	Asn	Asn	Asn	Ser	Pro	Phe
1				5								10							15	
Phe	Thr	Thr	Asn	Ser	Gly	Ala	Pro	Val	Trp	Asn	Asn	Asn	Asn	Ser	Ser	Ser	Met			
			20					25						30						
Thr	Val	Gly	Pro	Arg	Gly	Pro	Ile	Leu	Leu	Glu	Asp	Tyr	His	Leu	Val					
		35					40				45									
Glu	Lys	Leu	Ala	Asn	Phe	Asp	Arg	Glu	Arg	Ile	Pro	Glu	Arg	Val	Val					
		50				55					60									
His	Ala	Arg	Gly	Ala	Ser	Ala	Lys	Gly	Phe	Phe	Glu	Val	Thr	His	Asp					
65					70				75						80					
Ile	Ser	Asn	Leu	Thr	Cys	Ala	Asp	Phe	Leu	Arg	Ala	Pro	Gly	Val	Gln					
			85						90					95						
Thr	Pro	Val	Ile	Val	Arg	Phe	Ser	Thr	Val	Ile	His	Glu	Arg	Gly	Ser					
			100					105						110						
Pro	Glu	Thr	Leu	Arg	Asp	Pro	Arg	Gly	Phe	Ala	Val	Lys	Phe	Tyr	Thr					
		115					120					125								
Arg	Glu	Gly	Asn	Phe	Asp	Leu	Val	Gly	Asn	Asn	Phe	Pro	Val	Phe	Phe					
		130				135					140									
Ile	Arg	Asp	Gly	Met	Lys	Phe	Pro	Asp	Met	Val	His	Ala	Leu	Lys	Pro					
145				150					155					160						
Asn	Pro	Lys	Ser	His	Ile	Gln	Glu	Asn	Trp	Arg	Ile	Leu	Asp	Phe	Phe					
			165						170					175						
Ser	His	His	Pro	Glu	Ser	Leu	Asn	Met	Phe	Thr	Phe	Leu	Phe	Asp	Asp					
			180					185					190							
Ile	Gly	Ile	Pro	Gln	Asp	Tyr	Arg	His	Met	Asp	Gly	Ser	Gly	Val	Asn					
		195				200					205									
Thr	Tyr	Met	Leu	Ile	Asn	Lys	Ala	Gly	Lys	Ala	His	Tyr	Val	Lys	Phe					
		210				215					220									
His	Trp	Lys	Pro	Thr	Cys	Gly	Val	Lys	Ser	Leu	Glu	Glu	Asp	Ala						
225					230				235					240						
Ile	Arg	Val	Gly	Gly	Thr	Asn	His	Ser	His	Ala	Thr	Gln	Asp	Leu	Tyr					
			245						250					255						
Asp	Ser	Ile	Ala	Ala	Gly	Asn	Tyr	Pro	Glu	Trp	Lys	Leu	Phe	Ile	Gln					
		260						265					270							
Ile	Ile	Asp	Pro	Ala	Asp	Glu	Asp	Lys	Phe	Asp	Phe	Asp	Pro	Leu	Asp					
		275					280					285								
Val	Thr	Lys	Thr	Trp	Pro	Glu	Asp	Ile	Leu	Pro	Leu	Gln	Pro	Val	Gly					
		290				295					300									
Arg	Met	Val	Leu	Asn	Lys	Asn	Ile	Asp	Asn	Phe	Phe	Ala	Glu	Asn	Glu					
				310					315					320						
Gln	Leu	Ala	Phe	Cys	Pro	Ala	Ile	Ile	Val	Pro	Gly	Ile	His	Tyr	Ser					
			325						330					335						
Asp	Asp	Lys	Leu	Leu	Gln	Thr	Arg	Val	Phe	Ser	Tyr	Ala	Asp	Thr	Gln					
			340				345						350							
Arg	His	Arg	Leu	Gly	Pro	Asn	Tyr	Leu	Gln	Leu	Pro	Gly	Gln	Cys	Ser					
		355				360						365								
Lys	Met	Cys	Ser	Pro	Gln	Gln	Pro	Pro												
		370				375														

(2) INFORMATION FOR SEQ ID NO:1035:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..346
(D) OTHER INFORMATION: / Ceres Seq. ID 1568780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:

Met Thr Val Gly Pro Arg Gly Pro Ile Leu Leu Glu Asp Tyr His Leu
1 5 10 15
Val Glu Lys Leu Ala Asn Phe Asp Arg Gly Arg Ile Pro Glu Arg Val
20 25 30
Val His Ala Arg Gly Ala Ser Ala Lys Gly Phe Phe Glu Val Thr His
35 40 45
Asp Ile Ser Asn Leu Thr Cys Ala Asp Phe Leu Arg Ala Pro Gly Val
50 55 60
Gln Thr Pro Val Ile Val Arg Phe Ser Thr Val Ile His Glu Arg Gly
65 70 75 80
Ser Pro Glu Thr Leu Arg Asp Pro Arg Gly Phe Ala Val Lys Phe Tyr
85 90 95
Thr Arg Glu Gly Asn Phe Asp Leu Val Gly Asn Asn Phe Pro Val Phe
100 105 110
Phe Ile Arg Asp Gly Met Lys Phe Pro Asp Met Val His Ala Leu Lys
115 120 125
Pro Asn Pro Lys Ser His Ile Gln Glu Asn Trp Arg Ile Leu Asp Phe
130 135 140
Phe Ser His His Pro Glu Ser Leu Asn Met Phe Thr Phe Leu Phe Asp
145 150 155 160
Asp Ile Gly Ile Pro Gln Asp Tyr Arg His Met Asp Gly Ser Gly Val
165 170 175
Asn Thr Tyr Met Leu Ile Asn Lys Ala Gly Lys Ala His Tyr Val Lys
180 185 190
Phe His Thr Lys Pro Thr Cys Gly Val Lys Ser Leu Leu Glu Glu Asp
195 200 205
Ala Ile Arg Val Gly Gly Thr Asn His Ser His Ala Thr Gln Asp Leu
210 215 220
Tyr Asp Ser Ile Ala Ala Gly Asn Tyr Pro Glu Trp Lys Leu Phe Ile
225 230 235
Gln Ile Ile Asp Pro Ala Asp Glu Asp Lys Phe Asp Phe Asp Pro Leu
245 250 255
Asp Val Thr Lys Thr Trp Pro Glu Asp Ile Leu Pro Leu Gln Pro Val
260 265 270
Gly Arg Met Val Leu Asn Lys Asn Ile Asp Asn Phe Phe Ala Glu Asn
275 280 285
Glu Gln Leu Ala Phe Cys Pro Ala Ile Ile Val Pro Gly Ile His Tyr
290 295 300
Ser Asp Asp Lys Leu Leu Gln Thr Arg Val Phe Ser Tyr Ala Asp Thr
305 310 315 320
Gln Arg His Arg Leu Gly Pro Asn Tyr Leu Gln Leu Pro Gly Gln Cys
325 330 335
Ser Lys Met Cys Ser Pro Gln Gln Pro Pro
340 345

(2) INFORMATION FOR SEQ ID NO:1036:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1466 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1466
(D) OTHER INFORMATION: / Ceres Seq. ID 1568781

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:

tgtagttagg tcaatggaac agacaaagga tgattctgat ttgaggatg attttgaaac

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gaagaagatg gagactgata catcagctca agaggcaagg aatggtaaag acatacaagg 120
gattcagttg gaagggttta agtatactac agacgagttt cgtgacacta ggttgaaca 180
ttatgataac ttgtgttaata tcttaaggcc tagctctcga gaaaagcttg ataaggaaca 240
tgggcaagta gttgagaagg gaaagaactt ttatgacttc caattcaata caaggcttgt 300
cacttccact attgtgcatt ttcagttggg agtactgtct gagcagccag cagcataaag 360
atatggcttc ggaatttgtt atggggcgaca tctaaagcatg atgtatatct cagcaaaa 420
tattcaactca tgcacttgct atctctactc cagagagggg aagaagtagt taatgtcgc 480
agatcagtta cccccaactca gaaactacct ggattgtttt ctgagccact ctctagggtg 540
caagttagca gcatggcagt caaagaaaat ctgatccttt taggagggtt cgacggggag 600
cttctctgca agtgtgttaa tcaagcctggg gttgcttttt gcacaagatt atcaacggaa 660
gataatgcca tcacacacag ttgatataa ccgagaccca agtggctccc ttaggcttat 720
aaccgcaaat aacgactgta aaatccgggt attcgatgct cagagottta cacgtgtcag 780
tgaatttact ttgtatttgt ctgtcaataa tacctcagtt agcccggatg ggaagctact 840
cgctgtactc ggggacagta cagaatgctt gatctctgat tccattctg aaaaagttat 900
ttcaagcctc agaggccaca aagactactc atttgcatc gcttggcacc cgaattggtc 960
aatcttagca acgggaaacc aagacacgac atgccgtctc tgggacattc gtaaccgcgtc 1020
agaatcattc gctgtcctga aaggaacatc gggagccatc agaggactga agttcacacc 1080
agaagggcgg ttctctgcaa tggctgagcc tcgacacttt gttcacatct tcgacacgca 1140
gtccgggttt ctacagtcoc aagagattga tctgtttgga gaaatagccg ggatctcctt 1200
cagcccccac ccagagcgac tatatgttgg gtcgcagac cgacttatg gaagtgttat 1260
ggagtataag aggagtaagg ataataccta tatggactcc tttaactgag aaaaggtaaa 1320
tggaagtaaa aaagcatcta atatgttgtc acaagttggg ttttacccta ttagtgtgta 1380
tatgtagaca gaattggtag ttcttttgtt tatgtatggt gtatgtaacc cataatatat 1440
cttgccaac tttaagtatg ttttgt

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(2) INFORMATION FOR SEQ ID NO:1037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..118
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1568782

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

```

Val Val Arg Ser Met Glu Gln Thr Lys Asp Asp Ser Asp Phe Glu Asp
1          5          10          15
Asp Phe Glu Thr Lys Lys Met Glu Thr Asp Thr Ser Ala Gln Glu Ala
20          25          30
Arg Asn Gly Lys Asp Ile Gln Gly Ile Gln Trp Glu Gly Phe Lys Tyr
35          40          45
Thr Thr Asp Glu Phe Arg Asp Thr Arg Leu Lys His Tyr Asp Asn Phe
50          55          60
Val Asn Ile Leu Arg Pro Ser Ser Arg Glu Lys Leu Asp Lys Glu His
65          70          75          80
Gly Gln Val Val Glu Lys Gly Lys Asn Phe Tyr Asp Phe Gln Phe Asn
85          90          95
Thr Arg Leu Val Thr Ser Thr Ile Val His Phe Gln Leu Glu Val Leu
100          105          110
Ser Glu Gln Pro Ala Ala
115

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(2) INFORMATION FOR SEQ ID NO:1038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1568783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

Met Glu Gln Thr Lys Asp Asp Ser Asp Phe Glu Asp Asp Phe Glu Thr
1 5 10 15
Lys Lys Met Glu Thr Asp Thr Ser Ala Gln Glu Ala Arg Asn Gly Lys
20 25 30
Asp Ile Gln Gly Ile Gln Trp Glu Gly Phe Lys Tyr Thr Thr Asp Glu
35 40 45
Phe Arg Asp Thr Arg Leu Lys His Tyr Asp Asn Phe Val Asn Ile Leu
50 55 60
Arg Pro Ser Ser Arg Glu Lys Leu Asp Lys Glu His Gly Gln Val Val
65 70 75 80
Glu Lys Gly Lys Asn Phe Tyr Asp Phe Gln Phe Asn Thr Arg Leu Val
85 90 95
Thr Ser Thr Ile Val His Phe Gln Leu Gly Val Leu Ser Glu Gln Pro
100 105 110
Ala Ala

(2) INFORMATION FOR SEQ ID NO:1039:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1568784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

Met Pro Ser His Thr Val Asp Ile Tyr Arg Asp Pro Ser Gly Ser Leu
1 5 10 15
Arg Leu Ile Thr Ala Asn Asn Asp Cys Lys Ile Arg Val Phe Asp Ala
20 25 30
Gln Ser Phe Thr Arg Val Ser Glu Phe Thr Phe Asp Trp Ser Val Asn
35 40 45
Asn Thr Ser Val Ser Pro Asp Gly Lys Leu Leu Ala Val Leu Gly Asp
50 55 60
Ser Thr Glu Cys Leu Ile Ser Asp Ser His Ser Glu Lys Val Ile Ser
65 70 75 80
Ser Leu Arg Gly His Lys Asp Tyr Ser Phe Ala Ser Ala Trp His Pro
85 90 95
Asn Gly Leu Ile Leu Ala Thr Gly Asn Gln Asp Thr Thr Cys Arg Leu
100 105 110
Trp Asp Ile Arg Asn Pro Ser Glu Ser Phe Ala Val Leu Lys Gly Asn
115 120 125
Met Gly Ala Ile Arg Gly Leu Lys Phe Thr Pro Glu Gly Arg Phe Leu
130 135 140
Ala Met Ala Glu Pro Ala Asp Phe Val His Ile Phe Asp Thr Gln Ser
145 150 155 160
Gly Phe Leu Gln Ser Gln Glu Ile Asp Leu Phe Gly Glu Ile Ala Gly
165 170 175
Ile Ser Phe Ser Pro Asp Ser Glu Ala Leu Tyr Val Gly Val Ala Asp
180 185 190
Arg Thr Tyr Gly Ser Leu Met Glu Tyr Lys Arg Ser Lys Asp Asn His
195 200 205
Tyr Met Asp Ser Phe Tyr
210

(2) INFORMATION FOR SEQ ID NO:1040:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1129 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1129

(D) OTHER INFORMATION: / Ceres Seq. ID 1568803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

atcatcgatt	cgttctctcc	acgcctccac	gtttctccac	ctcatctcca	aactaacocac	60
aagatccttc	tttttagata	acagatcacg	gagagataga	gagagatgac	agagtcacgt	120
tcgaatggct	ctatagcttc	ttctctttcc	accaccctac	ttctctcttc	taggggtttt	180
ctctcttcaa	agttcttctt	ttatcttctt	accgtctctg	ttcccagaac	ctcactacac	240
ttctctggat	catctctctt	ttcttgttct	gggtttctca	ttctcggttc	ctccaccacc	300
agccctgcgc	gtccacgcgc	gaactctgcc	gtccaggctc	aggtgcataa	tttaccactg	360
ctgcgtaata	agggcgcgtc	tttttgagaa	gaggcaggtt	ttgtatcaag	tttccataag	420
gtgaagactc	ctfgatcacat	tgcgtaaaag	tatgtttaic	tattcttcta	ccctttggac	480
ttcaactttg	ttctgccccc	tggagttact	gccttcaagt	accgttgata	agaaatttag	540
aagctaaacg	ccgaagattt	aggggtcttc	gtccagacgt	tgttctcgca	ttccgcgtgg	600
gtccaaacag	acagaaagtc	gggagggtct	gggtgatctg	tattctctct	tggttcggat	660
atactcaaat	ccatttcaaa	atcgttttga	gtgctcatic	ctgtacaggc	cattgcacgt	720
agagggtctt	ttcatcatga	caagggaaga	gtcattcagc	attccaccat	caacacacct	780
ggattttggc	gaagtgtgtg	tgcagacagt	aggaacctcc	aggcataata	gtatgttcaa	840
gaaaacccgc	atagaagtgt	ctcgctggga	tggaaagccg	gggagaatac	aatgaaacct	900
gaccocaaag	tcagacaaga	atacttttga	gtcatctaga	ggcataagtt	gaacacagtt	960
ttgtgtgaaa	ttagcaatca	gaggttgttt	attcatcttt	taagaatttg	agcagagtgt	1020
ttatttttag	ccaaagaacc	tttgttatct	ttctatcttt	ctctctgttt	tgctatgtga	1080
ttctctctaa	attgaatcaa	aaataaagaa	atctctcttt	ttctttggc		

(2) INFORMATION FOR SEO ID NO:1041:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..273

(D) OTHER INFORMATION: / Ceres Seq. ID 1568804

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:
```

Met	Ser	Met	Ala	Ser	Ile	Ala	Ser	Ser	Ser	Ser	Thr	Thr	Leu	Leu	Ser	Leu	Ser
1				5					10						15		
Ser	Ser	Arg	Val	Leu	Leu	Pro	Ser	Lys	Ser	Ser	Leu	Leu	Ser	Pro	Thr		
			20					25					30				
Val	Ser	Val	Pro	Arg	Thr	Leu	His	Ser	Ser	Ser	Ala	Ser	Ser	Ser	Ser		
		35					40					45					
Leu	Cys	Ser	Gly	Phe	Ser	Ser	Leu	Gly	Ser	Leu	Thr	Thr	Ser	Arg	Ser		
	50					55						60					
Ala	Ser	Arg	Arg	Asn	Phe	Ala	Val	Lys	Ala	Gln	Ala	Asp	Asp	Leu	Pro		
65					70					75					80		
Leu	Val	Gly	Asn	Lys	Ala	Pro	Asp	Phe	Glu	Ala	Glu	Ala	Val	Phe	Asp		
			85						90					95			
Gln	Glu	Phe	Ile	Lys	Val	Lys	Leu	Ser	Glu	Tyr	Ile	Gly	Lys	Lys	Tyr		
			100					105					110				
Val	Ile	Leu	Phe	Phe	Thr	Pro	Leu	Asp	Phe	Thr	Phe	Val	Cys	Pro	Thr		
		115					120					125					
Glu	Ile	Thr	Ala	Phe	Ser	Asp	Arg	Tyr	Glu	Glu	Ala	Lys	Leu	Asn			
		130				135					140						
Thr	Glu	Val	Leu	Gly	Val	Ser	Val	Asp	Ser	Val	Phe	Ser	His	Leu	Ala		
145					150					155					160		

Trp	Val	Gln	Thr	Asp	Arg	Lys	Ser	Gly	Gly	Leu	Gly	Asp	Leu	Asn	Tyr	
				165					170					175		
Pro	Leu	Val	Ser	Asp	Ile	Thr	Lys	Ser	Ile	Ser	Lys	Ser	Phe	Gly	Val	
				180					185					190		
Leu	Ile	Pro	Asp	Gln	Gly	Ile	Ala	Leu	Arg	Gly	Leu	Phe	Ile	Ile	Asp	
				195				200				205				
Lys	Glu	Gly	Val	Ile	Gln	His	Ser	Thr	Ile	Asn	Asn	Leu	Gly	Ile	Gly	
				210				215				220				
Arg	Ser	Val	Asp	Glu	Thr	Met	Arg	Thr	Leu	Gln	Ala	Leu	Gln	Tyr	Val	
				225				230				235				240
Gln	Glu	Asn	Pro	Asp	Glu	Val	Cys	Pro	Ala	Gly	Trp	Lys	Pro	Gly	Glu	
				245				250						255		
Lys	Ser	Met	Lys	Pro	Asp	Pro	Lys	Leu	Ser	Lys	Glu	Tyr	Phe	Ser	Ala	
				260				265					270			
Ile																

(2) INFORMATION FOR SEQ ID NO:1042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..271
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

Met	Ala	Ser	Ile	Ala	Ser	Ser	Ser	Ser	Thr	Thr	Leu	Leu	Ser	Ser	Ser	
1				5					10				15			
Arg	Val	Leu	Leu	Pro	Ser	Lys	Ser	Ser	Leu	Leu	Ser	Pro	Thr	Val	Ser	
				20				25				30				
Val	Pro	Arg	Thr	Leu	His	Ser	Ser	Ser	Ala	Ser	Ser	Ser	Ser	Leu	Cys	
				35				40				45				
Ser	Gly	Phe	Ser	Ser	Leu	Gly	Ser	Leu	Thr	Thr	Ser	Arg	Ser	Ala	Ser	
				50				55			60					
Arg	Arg	Asn	Phe	Ala	Val	Lys	Ala	Gln	Ala	Asp	Asp	Leu	Pro	Leu	Val	
				65				70			75			80		
Gly	Asn	Lys	Ala	Pro	Asp	Phe	Glu	Ala	Glu	Ala	Val	Phe	Asp	Gln	Glu	
				85				90				95				
Phe	Ile	Lys	Val	Lys	Leu	Ser	Glu	Tyr	Ile	Gly	Lys	Lys	Tyr	Val	Ile	
				100				105				110				
Leu	Phe	Phe	Tyr	Pro	Leu	Asp	Phe	Thr	Phe	Val	Cys	Pro	Thr	Glu	Ile	
				115				120				125				
Thr	Ala	Phe	Ser	Asp	Arg	Tyr	Glu	Glu	Phe	Glu	Lys	Leu	Asn	Thr	Glu	
				130				135				140				
Val	Leu	Gly	Val	Ser	Val	Asp	Ser	Val	Phe	Ser	His	Leu	Ala	Trp	Val	
				145				150			155			160		
Gln	Thr	Asp	Arg	Lys	Ser	Gly	Gly	Leu	Gly	Asp	Leu	Asn	Tyr	Pro	Leu	
				165				170				175				
Val	Ser	Asp	Ile	Thr	Lys	Ser	Ile	Ser	Lys	Ser	Phe	Gly	Val	Leu	Ile	
				180				185				190				
Pro	Asp	Gln	Gly	Ile	Ala	Leu	Arg	Gly	Leu	Phe	Ile	Ile	Asp	Lys	Glu	
				195				200				205				
Gly	Val	Ile	Gln	His	Ser	Thr	Ile	Asn	Asn	Leu	Gly	Ile	Gly	Arg	Ser	
				210				215				220				
Val	Asp	Glu	Thr	Met	Arg	Thr	Leu	Gln	Ala	Leu	Gln	Tyr	Val	Gln	Glu	
				225				230			235			240		
Asn	Pro	Asp	Glu	Val	Cys	Pro	Ala	Gly	Trp	Lys	Pro	Gly	Glu	Lys	Ser	
				245				250				255				
Met	Lys	Pro	Asp	Pro	Lys	Leu	Ser	Lys	Glu	Tyr	Phe	Ser	Ala	Ile		

260 265 270
(2) INFORMATION FOR SEQ ID NO:1043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1510 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1510

(D) OTHER INFORMATION: / Ceres Seq. ID 1568826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

aattattttt	ccattctct	tcactatctc	tctccctaga	aaattgccag	aagaagaagg	60
ttctccaatt	caaaaaaata	gaacctcgct	accattcatt	tcaaaaaaatt	tcttggttaa	120
ttacgttttt	ttcttttttt	ttgcttcttt	cggttcttatt	gtcttagaag	acaaaagaga	180
ctagagagga	tagaaaaatg	gaagcttcaa	gcacaagaag	cgagaagaag	aagaagaaga	240
agacgataca	gagagaaaaa	accgatactc	aaaagaaaaa	aaagctaccc	agtgtttggt	300
tttcaattaa	gaaatctctc	ccctgcaaat	ctgatgtctc	cgatgtccac	attccgagat	360
ccaaaaaaga	gtctagctccc	atatccaacta	agagaacaac	aacctctctc	ggcgccgggg	420
tcggcgccag	gtccggttgt	tcaagatcca	tagccaatct	taaagacgta	atccatggaa	480
accaacggca	tttagagaa	cgctttgtcg	ctagccctcg	ttctatagga	agcagcgagt	540
ttctcaatcc	cattactcac	gatgtaatct	ttagcaactc	cacctgcgag	ctcaagatca	600
ccgcgcgcgg	agcaacagaa	ttcgtcgga	atcttagacc	agggacgcgc	gtcaattact	660
ctcttctcag	ccgtagccaa	acttcgagaa	aggcttcttc	tttagataga	gaaggattag	720
ggtttccaca	gagcagaaga	gagaatgata	gagaagccgc	cattaacgca	gacaattctc	780
ctgtttcttg	ccatacaatg	ggcgagaaat	ttagcaaatc	cgaagctgca	gaagctcatt	840
atctaaccaa	acacgcgcgtg	actgagctaa	tggaaaggaga	ctcgtcgagag	agaaatagtGg	900
agataatctg	cagaacaacg	tggttaaaga	cagagaatca	aggagggaga	atcgatcgga	960
tttgaagaat	acacaacatg	caaaaaacct	tagcgagatt	cgaagaatac	agagatacac	1020
tgaagatcac	agcaagcaag	ttacaaaaa	aacatccgag	atgtatcgcc	gacggaaaacg	1080
agcttctcag	gttttcacggc	accactgtgg	cttgccgttt	gggataaac	gggtcgacga	1140
gtctgtgttc	gtcgaaaaag	tggtgcgttt	gtcgattatt	acgaaatggg	ttctcggcga	1200
aacgggagat	gaataacgga	attgggggtt	ttactgcgtc	gacgagtga	agggcggttg	1260
agtcatttgt	gattggagat	gggtgtgtgt	gtgatcggaa	ggcgttgatt	gtgtgtcgag	1320
tgattgcggg	gagggttcat	cgcccggttg	agaaatgaga	ggagatgggt	gggttgtttg	1380
gtgggttttg	ttcattgttg	ggtaaaagtg	gggtgtacac	aaatgtttag	gagctctatt	1440
tgctcaattc	tcgagctttg	cttctctgtt	tgtgtcaatc	tgcaaaacct	aaatcaaat	1500
tttaggtgtg						

(2) INFORMATION FOR SEQ ID NO:1044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1568827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

Met	Glu	Ala	Ser	Ser	Thr	Arg	Ser	Glu	Lys	Lys	Lys	Lys	Lys	Thr
1			5					10					15	
Ile	Gln	Arg	Glu	Asn	Thr	Asp	Thr	Gln	Lys	Lys	Lys	Lys	Leu	Ser
			20					25					30	
Val	Trp	Phe	Ser	Leu	Lys	Lys	Ser	Leu	Pro	Cys	Lys	Ser	Asp	Ser
			35					40				45		
Asp	Val	His	Ile	Pro	Arg	Ser	Ser	Lys	Lys	Glu	Leu	Ala	Pro	Ile
			50					55				60		
Lys	Arg	Thr	Thr	Thr	Ser	Ser	Gly	Gly	Gly	Val	Gly	Gly	Arg	Gly
65			70					75				80		

Cys Ser Arg Ser Ile Ala Asn Leu Lys Asp Val Ile His Gly Asn Gln
85 90 95
Arg His Leu Glu Lys Pro Leu Cys Ser Ser Pro Arg Ser Ile Gly Ser
100 105 110
Ser Glu Phe Leu Asn Pro Ile Thr His Asp Val Ile Phe Ser Asn Ser
115 120 125
Thr Cys Glu Leu Lys Ile Thr Ala Ala Gly Ala Thr Glu Phe Val Gly
130 135 140
Asn Leu Arg Pro Gly Thr Pro Val Asn Tyr Ser Ser Ser Arg Arg Ser
145 150 155 160
Gln Thr Ser Arg Lys Ala Ser Ser Leu Asp Arg Glu Gly Leu Gly Phe
165 170 175
His Gln Ser Arg Arg Glu Asn Asp Arg Glu Ala Ala Ile Asn Gly Asp
180 185 190
Asn Ser Ser Val Ser Cys His Lys Cys Gly Glu Lys Phe Ser Lys Leu
195 200 205
Glu Ala Ala Glu Ala His His Leu Thr Lys His Ala Val Thr Glu Leu
210 215 220
Met Glu Gly Asp Ser Ser Arg Arg Ile Val Glu Ile Ile Cys Arg Thr
225 230 235 240
Ser Trp Leu Lys Thr Glu Asn Gln Gly Gly Arg Ile Asp Arg Ile Leu
245 250 255
Lys Val His Asn Met Gln Lys Thr Leu Ala Arg Phe Glu Glu Tyr Arg
260 265 270
Asp Thr Val Lys Ile Arg Ala Ser Lys Leu Gln Lys Lys His Pro Arg
275 280 285
Cys Ile Ala Asp Gly Asn Glu Leu Leu Arg Phe His Gly Thr Thr Val
290 295 300
Ala Cys Ala Leu Gly Ile Asn Gly Ser Thr Ser Leu Cys Ser Ser Glu
305 310 315 320
Lys Cys Cys Val Cys Arg Ile Ile Arg Asn Gly Phe Ser Ala Lys Arg
325 330 335
Glu Met Asn Asn Gly Ile Gly Val Phe Thr Ala Ser Thr Ser Glu Arg
340 345 350
Ala Phe Glu Ser Ile Val Ile Gly Asp Gly Gly Gly Gly Asp Arg Lys
355 360 365
Ala Leu Ile Val Cys Arg Val Ile Ala Gly Arg Val His Arg Pro Val
370 375 380
Glu Asn Val Glu Glu Met Gly Gly Leu Leu Ser Gly Phe Asp Ser Leu
385 390 395 400
Ala Gly Lys Val Gly Leu Tyr Thr Asn Val Glu Leu Tyr Leu Leu
405 410 415
Asn Ser Arg Ala Leu Leu Pro Val Leu Cys
420 425

(2) INFORMATION FOR SEQ ID NO:1045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1088 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1088
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

aaaagathct ataatagtag agatcaaaga cctgagcaaa aactgaaaaa aaaaaaaaaa	60
aaaaaagact tctctctcaa aatggcggtt acactagggt gaagagctgc tgcgtctagtc	120
ctctgcaacat caattcatca aaatggtttg ttacacaaac tgcaacaaat tggatcggat	180
cgggtttcagc ttggtgaagc aaaagcaata agattactac ccaggagaaac aaacatggtt	240
caagaattag gaatcaggga agaatttatg gatccaacaa gagaacacaga gacaagtatt	300

(2) INFORMATION FOR SEQ ID NO:1046:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..317

(D) OTHER INFORMATION: / Ceres Seq. ID 1568860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

1	lys	Arg	Xaa	Tyr	5	Ser	Arg	Asp	Gln	Arg	Pro	Glu	Gln	Lys	Leu	Lys
1	Lys	Lys	Lys	Lys	5	Lys	Lys	Asp	Phe	Ser	Ser	Lys	Met	Ala	Phe	Thr
				20						25				30		
Gly	Gly	Arg	Ala	Arg	Arg		Leu	Val	Ser	Ser	Ala	Thr	Ser	Ile	His	Gln
		35						40						45		Asn
Gly	Cys	Leu	His	Lys	Leu		Gln	Gln	Ile	Gly	Ser	Asp	Arg	Phe	Gln	Leu
		50					55					60				
Gly	Glu	Ala	Lys	Ala	Ile		Arg	Leu	Leu	Pro	Arg	Arg	Thr	Asn	Met	Val
65					70						75				80	
Gln	Glu	Leu	Gly	Ile	Arg		Glu	Glu	Phe	Met	Asp	Pro	Asn	Arg	Glu	Thr
				85						90					95	
Glu	Thr	Ser	Tyr	Asp	Phe		Leu	Asp	Glu	Met	Arg	His	Arg	Phe	Leu	Lys
			100						105					110		
Phe	Lys	Arg	Gln	Lys	Tyr		Leu	Pro	Glu	Ile	Glu	Lys	Phe	Lys	Ala	Leu
			115						120				125			
Ala	Ile	Ala	Gln	Ser	Pro		Lys	Val	Met	Val	Ile	Gly	Cys	Ala	Asp	Phe
			130				135					140				
Arg	Val	Cys	Pro	Ser	Tyr		Val	Leu	Gly	Phe	Gln	Pro	Gly	Glu	Ala	Ser
145					150						155					160
Thr	Ile	Arg	Asn	Val	Ala		Asn	Leu	Val	Thr	Pro	Val	Gln	Asn	Gly	Pro
				165						170					175	
Thr	Glu	Thr	Asn	Ser	Ala		Leu	Glu	Phe	Ala	Val	Thr	Thr	Leu	Gln	Val
			180						185					190		
Glu	Asn	Ile	Ile	Val	Met		Gly	His	Ser	Asn	Cys	Gly	Gly	Ile	Ala	Ala
		195						200					205			
Leu	Met	Ser	His	Gln	Asn		His	Gln	Gly	Gln	His	Ser	Ser	Leu	Val	Glu
		210					215					220				
Arg	Trp	Val	Met	Asn	Gly		Lys	Ala	Ala	Lys	Leu	Arg	Thr	Gln	Leu	Ala
225				230							235					240
Ser	Ser	His	Leu	Ser	Phe		Asp	Glu	Gln	Cys	Arg	Asn	Cys	Glu	Lys	Glu
				245						250					255	
Ser	Ile	Lys	Asp	Ser	Val		Met	Asn	Leu	Ile	Thr	Tyr	Ser	Trp	Ile	Arg
			260						265					270		
Asp	Arg	Val	Lys	Arg	Gly		Glu	Val	Lys	Ile	His	Gly	Cys	Tyr	Tyr	Asn

275 280 285
Leu Ser Asp Cys Ser Leu Glu Lys Trp Arg Leu Ser Ser Asp Lys Thr
290 295 300
Asn Tyr Gly Phe Tyr Ile Ser Asp Arg Glu Ile Trp Ser
305 310 315

(2) INFORMATION FOR SEQ ID NO:1047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..290

(D) OTHER INFORMATION: / Ceres Seq. ID 1568861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

Met Ala Phe Thr Leu Gly Gly Arg Ala Arg Arg Leu Val Ser Ala Thr
1 5 10 15
Ser Ile His Gln Asn Gly Cys Leu His Lys Leu Gln Gln Ile Gly Ser
20 25 30
Asp Arg Phe Gln Leu Gly Glu Ala Lys Ala Ile Arg Leu Leu Pro Arg
35 40 45
Arg Thr Asn Met Val Gln Gly Leu Gly Ile Arg Glu Glu Phe Met Asp
50 55 60
Pro Asn Arg Glu Thr Glu Thr Ser Tyr Asp Phe Leu Asp Glu Met Arg
65 70 75 80
His Arg Phe Leu Lys Phe Lys Arg Gln Lys Tyr Leu Pro Glu Ile Glu
85 90 95
Lys Phe Lys Ala Leu Ala Ile Ala Gln Ser Pro Lys Val Met Val Ile
100 105 110
Gly Cys Ala Asp Ser Arg Val Cys Pro Ser Tyr Val Leu Gly Phe Gln
115 120 125
Pro Gly Glu Ala Phe Thr Ile Arg Asn Val Ala Asn Leu Val Thr Pro
130 135 140
Val Gln Asn Gly Pro Thr Glu Thr Asn Ser Ala Leu Glu Phe Ala Val
145 150 155 160
Thr Thr Leu Gln Val Glu Asn Ile Ile Val Met Gly His Ser Asn Cys
165 170 175
Gly Gly Ile Ala Ala Leu Met Ser His Gln Asn His Gln Gly Gln His
180 185 190
Ser Ser Leu Val Glu Arg Trp Val Met Asn Gly Lys Ala Ala Lys Leu
195 200 205
Arg Thr Gln Leu Ala Ser Ser His Leu Ser Phe Asp Glu Gln Cys Arg
210 215 220
Asn Cys Glu Lys Glu Ser Ile Lys Asp Ser Val Met Asn Leu Ile Thr
225 230 235 240
Tyr Ser Trp Ile Arg Asp Arg Val Lys Arg Gly Glu Val Lys Ile His
245 250 255
Gly Cys Tyr Tyr Asn Leu Ser Asp Cys Ser Leu Glu Lys Trp Arg Leu
260 265 270
Ser Ser Asp Lys Thr Asn Tyr Gly Phe Tyr Ile Ser Asp Arg Glu Ile
275 280 285
Trp Ser
290

(2) INFORMATION FOR SEQ ID NO:1048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1568862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

Met	Val	Gln	Glu	Leu	Gly	Ile	Arg	Glu	Glu	Phe	Met	Asp	Pro	Asn	Arg
1			5					10					15		
Glu	Thr	Glu	Thr	Ser	Tyr	Asp	Phe	Leu	Asp	Glu	Met	Arg	His	Arg	Phe
			20					25					30		
Leu	Lys	Phe	Lys	Arg	Gln	Lys	Tyr	Leu	Pro	Glu	Ile	Glu	Lys	Phe	Lys
		35					40					45			
Ala	Leu	Ala	Ile	Ala	Gln	Ser	Pro	Lys	Val	Met	Val	Ile	Gly	Cys	Ala
		50				55				60					
Asp	Ser	Arg	Val	Cys	Pro	Ser	Tyr	Val	Leu	Gly	Phe	Gln	Pro	Gly	Glu
		65			70					75				80	
Ala	Phe	Thr	Ile	Arg	Asn	Val	Ala	Asn	Leu	Val	Thr	Pro	Val	Gln	Asn
			85						90					95	
Gly	Pro	Thr	Glu	Thr	Asn	Ser	Ala	Leu	Glu	Phe	Ala	Val	Thr	Thr	Leu
			100					105					110		
Gln	Val	Glu	Asn	Ile	Ile	Val	Met	Gly	His	Ser	Asn	Cys	Gly	Gly	Ile
		115				120						125			
Ala	Ala	Leu	Met	Ser	His	Gln	Asn	His	Gln	Gly	Gln	His	Ser	Ser	Leu
		130				135						140			
Val	Glu	Arg	Trp	Val	Met	Asn	Gly	Lys	Ala	Ala	Lys	Leu	Arg	Thr	Gln
		145			150					155				160	
Leu	Ala	Ser	Ser	His	Leu	Ser	Phe	Asp	Glu	Gln	Cys	Arg	Asn	Cys	Glu
			165					170						175	
Lys	Glu	Ser	Ile	Lys	Asp	Ser	Val	Met	Asn	Leu	Ile	Thr	Tyr	Ser	Trp
		180					185						190		
Ile	Arg	Asp	Arg	Val	Lys	Arg	Gly	Glu	Val	Lys	Ile	His	Gly	Cys	Tyr
		195				200						205			
Tyr	Asn	Leu	Ser	Asp	Cys	Ser	Leu	Glu	Lys	Trp	Arg	Leu	Ser	Ser	Asp
		210				215						220			
Lys	Thr	Asn	Tyr	Gly	Phe	Tyr	Ile	Ser	Asp	Arg	Glu	Ile	Trp	Ser	
		225			230					235					

(2) INFORMATION FOR SEQ ID NO:1049:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1540 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1540

(D) OTHER INFORMATION: / Ceres Seq. ID 1568863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

acaatctgac	caattcaatg	aaggcaattg	gtgttgacat	attgactgga	tttggcagtg	60
tctctgggtcc	acaaaagggt	aaatatggga	aggacaatat	tattactgca	aaagatataa	120
tcatctggcac	tgatctctgtg	ccgtttgtcc	ctaaaggaaat	tgaagttgat	ggaaagactg	180
tgatcaccag	tgaccatgct	ttgaaattag	agtctgtccc	tgagttggatt	gcaattgtag	240
gaagtgggta	tattggtctt	gagttcagtg	atgtttacac	agctcttgga	agtgaagtga	300
cttttataga	agcactggat	cagctaatgc	ctggatttga	tcctgagatc	agtaagctag	360
ctcagagggt	tttgataaat	ccaagaaaga	ttgactatca	tactggagtc	tttgcaagca	420
aaattactcc	ggcaagggat	gggaaaccag	ttctgattga	gcttattgat	gccaaaacca	480
aggaacctaa	ggatactttg	gaggtagatg	ctgctcttat	tgctactggg	agagctccat	540
tcaccaatgg	acttggcttg	gaaaatgtca	atgttgtgac	gcagagaggt	ttcataccag	600
ttgatgagcg	aatgcgtgtg	atcgatggaa	aggggactct	gggtccgaac	ttgtactgca	660
ttggtgatgc	caatggtaaa	ttgatgcttg	cacatgcagc	cagtgcccaa	ggaatttctg	720
tggtcgagca	agtcagcgcc	agagatcatg	tgcttaatac	tcttagcatc	ccagctgctt	780

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gctttactca tctctAaaat cagcatgggtg ggattaacag agcctcaagc aaaagaaaaa 840
ggcgagaagg aaggatttaa agttagtgtt gtcaagacaa gtttcaaggc taacacaaag 900
ggcctagctg aaatgaagg agaaggaata gctaagatga tataccgacc tgacaacggg 960
gaaattcttag gagttcatat atttggactg catgcagctg accttatcca tgaagcttct 1020
aatgcgattg ctctaggaac gcgtattcag gacataaaat tggcgagtta tgacacatcca 1080
acactctctg aggtctctga cgaactgttc aaagcagcca aggttgaag tcattgctacg 1140
acaaggacag taagtgaaaa agtggttgta taataagaaa ccaaaaaact attggggtgg 1200
ggagaacat ctggaagaaa gaaaatttgt gattgtactt tagggagatg caaagataaa 1260
gctaaacacg aaccaggaag atcgaaaagg aagaagaaga ggagagagatg atgagaacaa 1320
accttcogta agtaaaagact tgaagatat atctacaagg ccttcttctt tctttgagaa 1380
tatttctgtt ggagctctgt ctctgctttc acgtatatctt gtttaattgt tccatggttt 1440
caattagtg agattgtgg tttgtttatt gtatgtttgt ttgatgtgaa cgattttgga 1500
tgattctctt cttttacta gtaaaatcac ttgtctgtcc

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(2) INFORMATION FOR SEQ ID NO:1050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..285
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

```

Asn Leu Thr Asn Ser Met Lys Ala Ile Gly Val Asp Ile Leu Thr Gly
1      5      10
Phe Gly Ser Val Leu Gly Pro Gln Lys Val Lys Tyr Gly Lys Asp Asn
20     25     30
Ile Ile Thr Ala Lys Asp Ile Ile Ala Thr Gly Ser Val Pro Phe
35     40     45
Val Pro Lys Gly Ile Glu Val Asp Gly Lys Thr Val Ile Thr Ser Asp
50     55     60
His Ala Leu Lys Leu Glu Ser Val Pro Glu Trp Ile Ala Ile Val Gly
65     70     75     80
Ser Gly Tyr Ile Gly Leu Glu Phe Ser Asp Val Tyr Thr Ala Leu Gly
85     90     95
Ser Glu Val Thr Phe Ile Glu Ala Leu Asp Gln Leu Met Pro Gly Phe
100    105    110
Asp Pro Glu Ile Ser Lys Leu Ala Gln Arg Val Leu Ile Asn Pro Arg
115    120    125
Lys Ile Asp Tyr His Thr Gly Val Phe Ala Ser Lys Ile Thr Pro Ala
130    135    140
Arg Asp Gly Lys Pro Val Leu Ile Glu Leu Ile Asp Ala Lys Thr Lys
145    150    155    160
Glu Pro Lys Asp Thr Leu Glu Val Asp Ala Ala Leu Ile Ala Thr Gly
165    170    175
Arg Ala Pro Phe Thr Asn Gly Leu Gly Leu Glu Asn Val Asn Val Val
180    185    190
Thr Gln Arg Gly Phe Ile Pro Val Asp Glu Arg Met Arg Val Ile Asp
195    200    205
Gly Lys Gly Thr Leu Val Pro Asn Leu Tyr Cys Ile Gly Asp Ala Asn
210    215    220
Gly Lys Leu Met Leu Ala His Ala Ala Ser Ala Gln Gly Ile Ser Val
225    230    235    240
Val Glu Gln Val Ser Gly Arg Asp His Val Leu Asn His Leu Ser Ile
245    250    255
Pro Ala Ala Cys Phe Thr His Pro Glu Asn Gln His Gly Gly Ile Asn
260    265    270
Arg Ala Ser Ser Lys Arg Lys Arg Arg Glu Gly Arg Ile
275    280    285

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(2) INFORMATION FOR SEQ ID NO:1051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..280
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

Met Lys Ala Ile Gly Val Asp Ile Leu Thr Gly Phe Gly Ser Val Leu
1 5 10 15
Gly Pro Gln Lys Val Lys Tyr Gly Lys Asp Asn Ile Ile Thr Ala Lys
20 25 30
Asp Ile Ile Ile Ala Thr Gly Ser Val Pro Phe Val Pro Lys Gly Ile
35 40 45
Glu Val Asp Gly Lys Lys Thr Val Ile Thr Ser Asp His Ala Leu Lys Leu
50 55 60
Glu Ser Val Pro Glu Trp Ile Ala Ile Val Gly Ser Gly Tyr Ile Gly
65 70 75 80
Leu Glu Phe Ser Asp Val Tyr Thr Ala Leu Gly Ser Glu Val Thr Phe
85 90 95
Ile Glu Ala Leu Asp Gln Leu Met Pro Gly Phe Asp Pro Glu Ile Ser
100 105 110
Lys Leu Ala Gln Arg Val Leu Ile Asn Pro Arg Lys Ile Asp Tyr His
115 120 125
Thr Gly Val Phe Ala Ser Lys Ile Thr Pro Ala Arg Asp Gly Lys Pro
130 135 140
Val Leu Ile Glu Leu Ile Asp Ala Lys Thr Lys Glu Pro Lys Asp Thr
145 150 155 160
Leu Glu Val Asp Ala Ala Leu Ile Ala Thr Gly Arg Ala Pro Phe Thr
165 170 175
Asn Gly Leu Gly Leu Glu Asn Val Asn Val Val Thr Gln Arg Gly Phe
180 185 190
Ile Pro Val Asp Glu Arg Met Arg Val Ile Asp Gly Lys Gly Thr Leu
195 200 205
Val Pro Asn Leu Tyr Cys Ile Gly Asp Ala Asn Gly Lys Leu Met Leu
210 215 220
Ala His Ala Ala Ser Ala Gln Gly Ile Ser Val Val Glu Gln Val Ser
225 230 235 240
Gly Arg Asp His Val Val Leu Asn His Leu Ser Ile Pro Ala Ala Cys Phe
245 250 255
Thr His Pro Glu Asn Gln His Gly Gly Ile Asn Arg Ala Ser Ser Lys
260 265 270
Arg Lys Arg Arg Glu Gly Arg Ile
275 280

(2) INFORMATION FOR SEQ ID NO:1052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..177
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

Met Pro Gly Phe Asp Pro Glu Ile Ser Lys Leu Ala Gln Arg Val Leu

1	5	10	15
Ile Asn Pro Arg Lys Ile Asp Tyr His Thr Gly Val Phe Ala Ser Lys			
	20	25	30
Ile Thr Pro Ala Arg Asp Gly Lys Pro Val Leu Ile Glu Leu Ile Asp			
	35	40	45
Ala Lys Thr Lys Glu Pro Lys Asp Thr Leu Glu Val Asp Ala Ala Leu			
	50	55	60
Ile Ala Thr Gly Arg Ala Pro Phe Thr Asn Gly Leu Gly Leu Glu Asn			
65	70	75	80
Val Asn Val Val Thr Gln Arg Gly Phe Ile Pro Val Asp Glu Arg Met			
	85	90	95
Arg Val Ile Asp Gly Lys Gly Thr Leu Val Pro Asn Leu Tyr Cys Ile			
	100	105	110
Gly Asp Ala Asn Gly Lys Leu Met Leu Ala His Ala Ser Ala Gln			
	115	120	125
Gly Ile Ser Val Val Glu Gln Val Ser Gly Arg Asp His Val Leu Asn			
	130	135	140
His Leu Ser Ile Pro Ala Ala Cys Phe Thr His Pro Glu Asn Gln His			
145	150	155	160
Gly Gly Ile Asn Arg Ala Ser Ser Lys Arg Lys Arg Arg Glu Gly Arg			
	165	170	175
Ile			

(2) INFORMATION FOR SEQ ID NO:1053:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

actcccatca aagcaaaact atctttctcc ttctcattcc tttttctctc actctctctcc	60
attaaagctc tgcactttct caaagagaat gttcatgggt aagatggggt ttttgggaat	120
tgctctgttg tgtttttgct caatgtgttg ctctgttcat ggatatgacg ctggatgggt	180
caatgctcat gctaccttct atggtggaag tgatgcttca ggaacaatgg ttggagcttg	240
tggtcacggg aacctctaca gtcaagggtta cgggaccaac acggcggcgt tgagcactgc	300
ctcgttcaac aacgggtctta gctgcggggc gtgttttgag atcaaatgtc agagcgacgc	360
cgcgtgtgtg ttacctgtgt ctatcatgtg cacagccacc aatttctgtc ctccatacaa	420
cgtctctccc aataacgctg gtggttggtg taaccctcgc ctccatcatt tcatctctcc	480
tcagccctgt ttccaacgca ttgctcagta caaagctggg gtgtgccctg ttctctacag	540
aagggttcgc tgtatgagaa gaggaggtat aagattcaca atcaacggct actcttactt	600
caacctgtgc ttggtgacca atgttggtgg tgcgtgagat gtccattcgg ttgcggttaa	660
aggttctagg acaaggtggc aacaaatgtc aagaaaatgg ggcagagaact ggcaagcaaa	720
caatctctta aacggtcaag cattgtcatt taaggtgact gctagtgatg gtcgtaccgt	780
cgtctctaac aacattgctc cagctagtgt gtcccttgga caaaccttca ccggccgcta	840
attccgttaa aatttgagta agttcggttt tatatagttt taggggtttg tagtagttg	900
gttgaggaaa gagttagaaa agagagaggg tttaaaggctt tttaggtgtt ttaagtggag	960
agccttgaaa ctctctcttt gactcttgag ggttaaaatg gagaaaagag cttgttttat	1020
aagggtcctt tttagcatgt taaggattag ggttttagta agtgggtgtt gagtagtaga	1080
gtggtgtgtc ttaagggaac tctatgttcc accaatgggt tcctttgttt tatcaacttt	1140
ttattttgtt ttatctcttt ttccaagctc tctgtcttgt ggtttaaaaa gcagaagtgg	1200
gtaggggcag agggagaatt tcaccacccg cctatgtgtt ttctcttttg ggtcggtttg	1260
gtttatgtta tgaagtgtta attgtaattg agatcaacca atgggtttga taagtgtttt	1320
gttacc	

(2) INFORMATION FOR SEQ ID NO:1054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..282
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568868
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:
Leu Pro Ser Lys Gln Asn Tyr Leu Ser Pro Ser His Ser Phe Phe Ser
1 5 10 15
His Ser Pro Pro Leu Lys Leu Cys Thr Phe Ser Lys Arg Met Phe Met
 20 25 30
Gly Lys Met Gly Leu Leu Gly Ile Ala Leu Leu Cys Phe Ala Ala Met
 35 40 45
Val Cys Ser Val His Gly Tyr Asp Ala Gly Trp Val Asn Ala His Ala
 50 55 60
Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly Gly Ala Cys
65 70 75 80
Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn Thr Ala Ala
 85 90 95
Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly Ala Cys Phe
 100 105 110
Glu Ile Lys Cys Gln Ser Asp Gly Ala Trp Cys Leu Pro Gly Ala Ile
 115 120 125
Ile Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Asn Ala Leu Pro Asn
 130 135 140
Asn Ala Gly Gly Trp Cys Asn Pro Pro Leu His His Phe Asp Leu Ser
145 150 155 160
Gln Pro Val Phe Gln Arg Ile Ala Gln Tyr Lys Ala Gly Val Val Pro
 165 170 175
Val Ser Tyr Arg Arg Val Pro Cys Met Arg Arg Gly Gly Ile Arg Phe
 180 185 190
Thr Ile Asn Gly His Ser Tyr Phe Asn Leu Val Val Thr Asn Val
 195 200 205
Gly Gly Ala Gly Asp Val His Ser Val Ala Val Lys Gly Ser Arg Thr
 210 215 220
Arg Trp Gln Gln Met Ser Arg Asn Trp Gly Gln Asn Trp Gln Ser Asn
225 230 235 240
Asn Leu Leu Asn Gly Gln Ala Leu Ser Phe Lys Val Thr Ala Ser Asp
 245 250 255
Gly Arg Thr Val Val Ser Asn Asn Ile Ala Pro Ala Ser Trp Ser Phe
 260 265 270
Gly Gln Thr Phe Thr Gly Arg Gln Phe Arg
 275 280
(2) INFORMATION FOR SEQ ID NO:1055:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..253
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568869
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:
Met Phe Met Gly Lys Met Gly Leu Leu Gly Ile Ala Leu Leu Cys Phe
1 5 10 15
Ala Ala Met Val Cys Ser Val His Gly Tyr Asp Ala Gly Trp Val Asn
 20 25 30

Ala His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly
35 40 45
Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn
50 55 60
Thr Ala Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly
65 70 75 80
Ala Cys Phe Glu Ile Lys Cys Gln Ser Asp Gly Ala Trp Cys Leu Pro
85 90 95
Gly Ala Ile Ile Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Asn Ala
100 105 110
Leu Pro Asn Asn Ala Gly Gly Trp Cys Asn Pro Pro Leu His His Phe
115 120 125
Asp Leu Ser Gln Pro Val Phe Gln Arg Ile Ala Gln Tyr Lys Ala Gly
130 135 140
Val Val Pro Val Ser Tyr Arg Arg Val Pro Cys Met Arg Arg Gly Gly
145 150 155 160
Ile Arg Phe Thr Ile Asn Gly His Ser Tyr Phe Asn Leu Val Leu Val
165 170 175
Thr Asn Val Gly Gly Ala Gly Asp Val His Ser Val Ala Val Lys Gly
180 185 190
Ser Arg Thr Arg Trp Gln Gln Met Ser Arg Asn Trp Gly Gln Asn Trp
195 200 205
Gln Ser Asn Asn Leu Leu Asn Gly Gln Ala Leu Ser Phe Lys Val Thr
210 215 220
Ala Ser Asp Gly Arg Thr Val Val Ser Asn Asn Ile Ala Pro Ala Ser
225 230 235 240
Trp Ser Phe Gly Gln Thr Phe Thr Gly Arg Gln Phe Arg
245 250

(2) INFORMATION FOR SEQ ID NO:1056:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..251

(D) OTHER INFORMATION: / Ceres Seq. ID 1568870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:

Met Gly Lys Met Gly Leu Leu Gly Ile Ala Leu Leu Cys Phe Ala Ala
1 5 10 15
Met Val Cys Ser Val His Gly Tyr Asp Ala Gly Trp Val Asn Ala His
20 25 30
Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly Gly Ala
35 40 45
Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn Thr Ala
50 55 60
Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly Ala Cys
65 70 75 80
Phe Glu Ile Lys Cys Gln Ser Asp Gly Ala Trp Cys Leu Pro Gly Ala
85 90 95
Ile Ile Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Asn Ala Leu Pro
100 105 110
Asn Asn Ala Gly Gly Trp Cys Asn Pro Pro Leu His His Phe Asp Leu
115 120 125
Ser Gln Pro Val Phe Gln Arg Ile Ala Gln Tyr Lys Ala Gly Val Val
130 135 140
Pro Val Ser Tyr Arg Arg Val Pro Cys Met Arg Arg Gly Gly Ile Arg
145 150 155 160
Phe Thr Ile Asn Gly His Ser Tyr Phe Asn Leu Val Leu Val Thr Asn

[illegible]

(2) INFORMATION FOR SEO ID NO:1057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1270
(D) OTHER INFORMATION: / Ceres Seq. ID 1568871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:

caaaaaggg	tacaaaaggga	gatgtcacag	cactaaaagc	cactatataag	acagctgttcc	60
gaagctatct	tgatcgtgtc	atggatggtg	tcgcgaaaaa	ggttgatga	aagggcggaat	120
tgctcaaaaga	attgtttgac	tgttcgatat	ctcggcgatt	atctgcgaat	aatggaagtt	180
gggtttggagc	ctggggatgt	gaaaagcctt	tgtgggatgt	gcttgtgttc	aggaataatt	240
ctgcagtggt	ggggaggtcaa	atttcgctat	tgtctctctg	tgtgtccctc	ttctcttggt	300
acactcagag	attcattaae	atttcggttg	gggtgcocat	ggctcgaaga	tatgggctca	360
cagagactgt	tctgtgttga	acctctctct	aggtttgagg	cacatccgtt	ggcgagatgt	420
gtgtcccaat	tctctgtctc	tttgtaaagc	tagtaagact	ggcggaagct	gggtatctaa	480
ccagtgtaac	gccaaatccc	cgtgtgttga	ttaataattg	tggctcaaat	atacagctgt	540
ggtatttcaa	aaataggagag	aaaactcaag	aagtgctcaa	tggtgatgaa	agaggaatga	600
gtgtgttcca	ccacaggagac	ataggacgat	tctaccctga	tggtcgcttc	gagataatag	660
accgaaaaaa	ggatatacgt	aaacttcagc	accgagaata	tgtctctctg	ggcagaagtt	720
acagctgctc	agataataagt	ccctatggtt	aaaactcaat	ggttactcgt	gttgctttct	780
acagttactg	tgtggtctct	gtgttcgcgt	cccaaccatac	agttgaaagt	tgggcttcaa	840
aggaAggaat	agasitttgc	aacttcgaag	aaactgtgac	gaaagagcaa	gcctgtgaa	900
aagttgtatgc	ttatcttctg	agggcgctga	aacatatcac	attggagaag	tttgagatac	960
cmgcaaaagct	caaatgtgtt	gcacttcgat	ggagccgaga	tgaaggatta	gtccacagag	1020
ctctaaagct	taaaagagac	gtaataggat	gggaattctc	tgaagatctc	accagtttat	1080
atgctctaaac	ttttctctct	ttcttacttt	gttttatctt	tatcgtctct	atcattctga	1140
aagacgcaca	agctgcacaa	aaacttaatt	ctaaagaaag	tgtatctttt	ctctctgtga	1200
tgtctgtctt	ttctgtcaaa	tgtatggggg	taactgtgac	gagactgaaa	gaaagaaagt	1260
ttatggctctt						

(2) INFORMATION FOR SEQ ID NO:1058:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..361
(D) OTHER INFORMATION: / Ceres Seq. ID 1568872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

Lys	Lys	Gly	Thr	Lys	Gly	Asp	Val	Thr	Ala	Leu	Lys	Pro	Thr	Ile	Met
1				5					10					15	
Thr	Ala	Val	Pro	Ala	Ile	Leu	Asp	Arg	Val	Arg	Asp	Gly	Val	Arg	Lys
			20					25					30		

Lys Val Asp Ala Lys Gly Gly Leu Ser Lys Lys Leu Phe Asp Phe Ala
35 40 45
Tyr Ala Arg Arg Leu Ser Ala Ile Asn Gly Ser Trp Phe Gly Ala Trp
50 55 60
Gly Leu Glu Lys Leu Leu Trp Asp Val Leu Val Phe Arg Lys Ile Arg
65 70 75 80
Ala Val Leu Gly Gly Gln Ile Arg Tyr Leu Leu Ser Gly Gly Ala Pro
85 90 95
Leu Ser Gly Asp Thr Gln Arg Phe Ile Asn Ile Cys Val Gly Ala Pro
100 105 110
Ile Gly Gln Gly Tyr Gly Leu Thr Glu Thr Cys Ala Gly Gly Thr Phe
115 120 125
Ser Glu Phe Glu Asp Thr Ser Val Gly Arg Val Gly Ala Pro Leu Pro
130 135 140
Cys Ser Phe Val Lys Leu Val Asp Trp Ala Glu Gly Gly Tyr Leu Thr
145 150 155 160
Ser Asp Lys Pro Met Pro Arg Gly Glu Ile Val Ile Gly Gly Ser Asn
165 170 175
Ile Thr Leu Gly Tyr Phe Lys Asn Glu Glu Lys Thr Lys Glu Val Tyr
180 185 190
Lys Val Asp Glu Lys Gly Met Arg Trp Phe Tyr Thr Gly Asp Ile Gly
195 200 205
Arg Phe His Pro Asp Gly Cys Leu Glu Ile Ile Asp Arg Lys Lys Asp
210 215 220
Ile Val Lys Leu Gln His Gly Glu Tyr Val Ser Leu Gly Lys Val Glu
225 230 235 240
Ala Ala Leu Ser Ile Ser Pro Tyr Val Glu Asn Ile Met Val His Ala
245 250 255
Asp Ser Phe Tyr Ser Tyr Cys Val Ala Leu Val Val Ala Ser Gln His
260 265 270
Thr Val Glu Gly Trp Ala Ser Lys Xaa Gly Ile Xaa Phe Ala Asn Phe
275 280 285
Glu Glu Leu Cys Thr Lys Glu Gln Ala Val Lys Glu Val Tyr Ala Tyr
290 295 300
Leu Val Lys Ala Ala Lys Gln Ser Arg Leu Glu Lys Phe Glu Ile Xaa
305 310 315 320
Ala Lys Ile Lys Leu Leu Ala Ser Pro Trp Thr Pro Glu Ser Gly Leu
325 330 335
Val Thr Ala Ala Leu Lys Leu Lys Arg Asp Val Ile Arg Arg Glu Phe
340 345 350
Ser Glu Asp Leu Thr Lys Leu Tyr Ala
355 360

(2) INFORMATION FOR SEQ ID NO:1059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..346
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

Met Thr Ala Val Pro Ala Ile Leu Asp Arg Val Arg Asp Gly Val Arg
1 5 10 15
Lys Lys Val Asp Ala Lys Gly Gly Leu Ser Lys Lys Leu Phe Asp Phe
20 25 30
Ala Tyr Ala Arg Arg Leu Ser Ala Ile Asn Gly Ser Trp Phe Gly Ala
35 40 45
Trp Gly Leu Glu Lys Leu Leu Trp Asp Val Leu Val Phe Arg Lys Ile

50	55	60
Arg Ala Val Leu Gly Gly Gln Ile Arg Tyr	Leu Leu Ser Gly Gly Ala	
65	70	75
Pro Leu Ser Gly Asp Thr Gln Arg Phe Ile Asn Ile Cys Val Gly Ala		80
	85	90
Pro Ile Gly Gln Gly Tyr Gly Leu Thr Glu Thr Cys Ala Gly Gly Thr		95
	100	105
Phe Ser Glu Phe Glu Asp Thr Ser Val Gly Arg Val Gly Ala Pro Leu		110
	115	120
Pro Cys Ser Phe Val Lys Leu Val Asp Trp Ala Glu Gly Gly Tyr Leu		125
	130	135
Thr Ser Asp Lys Pro Met Pro Arg Gly Glu Ile Val Ile Gly Gly Ser		140
145	150	155
Asn Ile Thr Leu Gly Tyr Phe Lys Asn Glu Lys Thr Lys Glu Val		160
	165	170
Tyr Lys Val Asp Glu Lys Gly Met Arg Trp Phe Tyr Thr Gly Asp Ile		175
	180	185
Gly Arg Phe His Pro Asp Gly Cys Leu Glu Ile Ile Asp Arg Lys Lys		190
	195	200
Asp Ile Val Lys Leu Gln His Gly Glu Tyr Val Ser Leu Gly Lys Val		205
	210	215
Glu Ala Ala Leu Ser Ile Ser Pro Tyr Val Glu Asn Ile Met Val His		220
225	230	235
Ala Asp Ser Phe Tyr Ser Tyr Cys Val Ala Leu Val Val Ala Ser Gln		240
	245	250
His Thr Val Glu Gly Trp Ala Ser Lys Xaa Gly Ile Xaa Phe Ala Asn		255
	260	265
Phe Glu Glu Leu Cys Thr Lys Glu Gln Ala Val Lys Glu Val Tyr Ala		270
	275	280
Tyr Leu Val Lys Ala Ala Lys Gln Ser Arg Leu Glu Lys Phe Glu Ile		285
	290	295
Xaa Ala Lys Ile Lys Leu Leu Ala Ser Pro Trp Thr Pro Glu Ser Gly		300
305	310	315
Leu Val Thr Ala Ala Leu Lys Leu Lys Arg Asp Val Ile Arg Arg Glu		320
	325	330
Phe Ser Glu Asp Leu Thr Lys Leu Tyr Ala		335
	340	345

(2) INFORMATION FOR SEQ ID NO:1060:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..197

(D) OTHER INFORMATION: / Ceres Seq. ID 1568874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

Met Pro Arg Gly	Glu Ile Val Ile Gly	Gly Ser Asn Ile Thr Leu Gly
1	5	10
Tyr Phe Lys Asn Glu Lys Thr Lys Glu Val Tyr Lys Val Asp Glu		15
	20	25
Lys Gly Met Arg Trp Phe Tyr Thr Gly Asp Ile Gly Arg Phe His Pro		30
	35	40
Asp Gly Cys Leu Glu Ile Ile Asp Arg Lys Lys Asp Ile Val Lys Leu		45
	50	55
Gln His Gly Glu Tyr Val Ser Leu Gly Lys Val Glu Ala Ala Leu Ser		60
65	70	75
Ile Ser Pro Tyr Val Glu Asn Ile Met Val His Ala Asp Ser Phe Tyr		80
	85	90
		95

Ser Tyr Cys Val Ala Leu Val Val Ala Ser Gln His Thr Val Glu Gly
100 105 110
Trp Ala Ser Lys Xaa Gly Ile Xaa Phe Ala Asn Phe Glu Glu Leu Cys
115 120 125
Thr Lys Glu Gln Ala Val Lys Glu Val Tyr Ala Tyr Leu Val Lys Ala
130 135 140
Ala Lys Gln Ser Arg Leu Glu Lys Phe Glu Ile Xaa Ala Lys Ile Lys
145 150 155 160
Leu Leu Ala Ser Pro Trp Thr Pro Glu Ser Gly Leu Val Thr Ala Ala
165 170 175
Leu Lys Leu Lys Arg Asp Val Ile Arg Arg Glu Phe Ser Glu Asp Leu
180 185 190
Thr Lys Leu Tyr Ala
195

(2) INFORMATION FOR SEQ ID NO:1061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1133

(D) OTHER INFORMATION: / Ceres Seq. ID 1568883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

gtgtctcaca	tctctttgtc	ttctccgcct	cctccgatct	cactccgatc	tctctacgat	60
tcattctctc	atggcttcac	ttgctacttc	tgtctctact	tctctccaa	ctcgtctctc	120
tcaactgggtg	attgggggcta	aacaagttaa	aagcttttagc	tatggaagca	gaagcaatct	180
ttcttttaat	cttgccacgc	ttctacccgc	cttgactgtt	tactgcgctg	caaaacctga	240
gacagtggac	aaggtgtgtg	cagttgtcag	aaagcaactc	tcaactaaa	aggctgacga	300
aattaccgtc	gccaccaaat	ttgctgcaat	tggtgctgat	tccttgata	cgttgagat	360
agttatggga	ttagaggaag	agtttgggat	tgaatggct	tcaacgatgt	ttctaaatta	420
cctgacttgg	aagagaagca	tgtctccaaa	ggggcacata	ccagaagcag	agattgcaaa	480
tgatctatcg	cataacaaga	tgtgtatgca	aggtcatgac	aagatgggtc	gacctatcgc	540
tgttgccatt	gggaacagac	ataacccttc	caaaaggcaac	cctgacgagt	tcaagcgttt	600
tgttgtctac	acgctcgaga	agatttggc	tagaatgcg	agaggtcaa	agaaattcgt	660
agcaattgga	gatctgcaag	gctggggata	ttctaattgt	gacatccgtg	gctaccttgc	720
tgctctttcc	actttgcagg	attgttacc	agagagatta	gggaacctct	atatagttca	780
tgcccccctac	attttcatga	cgcgatggaa	ggctcattat	ctctttatcg	acgcgcaaac	840
caagaaaaaag	attgtttttc	tgagagaaca	gaactcact	ccaacgctgc	ttagagacat	900
agacgaaagc	caactctccg	Gacatctacg	gaggcaaaAt	tgccacttgt	tcctattcag	960
gagacctgtat	tataggtcatt	actTaaggGc	ccacctctat	ttccaaatta	ttacttacta	1020
gtatctctttt	ttttatttga	ataaaatgaa	aaacatatgt	agtgtcgcca	aatgccaaca	1080
attatataatt	tactgtcaaa	gaagctaaaa	gatataatat	tgaatcacc	ttt	

(2) INFORMATION FOR SEQ ID NO:1062:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..339

(D) OTHER INFORMATION: / Ceres Seq. ID 1568884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:

Cys	Leu	Thr	Ser	Leu	Cys	Leu	Leu	Arg	Leu	Arg	Ser	His	Ser	Asp
1				5				10				15		
Leu	Ser	Thr	Ile	His	Ser	Ser	Met	Ala	Ser	Ile	Ala	Thr	Ser	Ala
				20				25				30		

Thr Ser Leu Gln Ala Arg Pro Arg Gln Leu Val Ile Gly Ala Lys Gln
35 40 45
Val Lys Ser Phe Ser Tyr Gly Ser Arg Ser Asn Leu Ser Phe Asn Leu
50 55 60
Arg Gln Leu Pro Thr Arg Leu Thr Val Tyr Cys Ala Ala Lys Pro Glu
65 70 75 80
Thr Val Asp Lys Val Cys Ala Val Val Arg Lys Gln Leu Ser Leu Lys
85 90 95
Glu Ala Asp Glu Ile Thr Ala Ala Thr Lys Phe Ala Ala Leu Gly Ala
100 105 110
Asp Ser Leu Asp Thr Val Glu Ile Val Met Gly Leu Glu Glu Glu Phe
115 120 125
Gly Ile Glu Met Ala Ser Thr Met Phe Leu Asn Tyr Leu Thr Trp Lys
130 135 140
Arg Ser Met Leu Pro Lys Gly His Ile Pro Glu Ala Glu Ile Ala Asn
145 150 155 160
Asp Leu Ser His Asn Lys Met Cys Met Gln Gly His Asp Lys Met Gly
165 170 175
Arg Pro Ile Ala Val Ala Ile Gly Asn Arg His Asn Pro Ser Lys Gly
180 185 190
Asn Pro Asp Glu Phe Lys Arg Phe Val Val Tyr Thr Leu Glu Lys Ile
195 200 205
Cys Ala Arg Met Pro Arg Gly Gln Glu Lys Phe Val Ala Ile Gly Asp
210 215 220
Leu Gln Gly Trp Gly Tyr Ser Asn Cys Asp Ile Arg Gly Tyr Leu Ala
225 230 235 240
Ala Leu Ser Thr Leu Gln Asp Cys Tyr Pro Glu Arg Leu Gly Lys Leu
245 250 255
Tyr Ile Val His Ala Pro Tyr Ile Phe Met Thr Ala Trp Lys Val Ile
260 265 270
Tyr Pro Phe Ile Asp Ala Asn Thr Lys Lys Lys Ile Val Phe Val Glu
275 280 285
Asn Lys Lys Leu Thr Pro Thr Leu Leu Glu Asp Ile Asp Glu Ser Gln
290 295 300
Leu Pro Gly His Leu Arg Arg Gln Asn Cys His Leu Phe Leu Phe Arg
305 310 315 320
Arg Pro Asp Tyr Arg Ser Tyr Leu Arg Ala His Leu Tyr Phe Gln Ile
325 330 335
Ile Thr Tyr

(2) INFORMATION FOR SEQ ID NO:1063:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..316

(D) OTHER INFORMATION: / Ceres Seq. ID 1568885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

Met Ala Ser Ile Ala Thr Ser Ala Ser Thr Ser Leu Gln Ala Arg Pro
1 5 10 15
Arg Gln Leu Val Ile Gly Ala Lys Gln Val Lys Ser Phe Ser Tyr Gly
20 25 30
Ser Arg Ser Asn Leu Ser Phe Asn Leu Arg Gln Leu Pro Thr Arg Leu
35 40 45
Thr Val Tyr Cys Ala Ala Lys Pro Glu Thr Val Asp Lys Val Cys Ala
50 55 60
Val Val Arg Lys Gln Leu Ser Leu Lys Glu Ala Asp Glu Ile Thr Ala

65		70		75		80
Ala Thr Lys Phe	Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr Val Glu					
	85			90		95
Ile Val Met Gly	Leu Glu Glu Glu Phe Gly Ile Glu Met Ala Ser Thr					
	100			105		110
Met Phe Leu Asn Tyr	Leu Thr Trp Lys Arg Ser Met Leu Pro Lys Gly					
	115			120		125
His Ile Pro Glu Ala	Glu Ile Ala Asn Asp Leu Ser His Asn Lys Met					
	130			135		140
Cys Met Gln Gly His	Asp Lys Met Gly Arg Pro Ile Ala Val Ala Ile					
	145			150		155
Gly Asn Arg His Asn	Pro Ser Lys Gly Asn Pro Asp Glu Phe Lys Arg					
	165			170		175
Phe Val Val Tyr Thr	Leu Glu Lys Ile Cys Ala Arg Met Pro Arg Gly					
	180			185		190
Gln Glu Lys Phe Val	Ala Ile Gly Asp Leu Gln Gly Trp Gly Tyr Ser					
	195			200		205
Asn Cys Asp Ile Arg	Gly Tyr Leu Ala Ala Leu Ser Thr Leu Gln Asp					
	210			215		220
Cys Tyr Pro Glu Arg	Leu Gly Lys Leu Tyr Ile Val His Ala Pro Tyr					
	225			230		235
Ile Phe Met Thr Ala	Trp Lys Val Ile Tyr Pro Phe Ile Asp Ala Asn					
	245			250		255
Thr Lys Lys Lys Ile	Val Phe Val Glu Asn Lys Lys Leu Thr Pro Thr					
	260			265		270
Leu Leu Glu Asp Ile	Asp Glu Ser Gln Leu Pro Gly His Leu Arg Arg					
	275			280		285
Gln Asn Cys His Leu	Phe Leu Phe Arg Arg Pro Asp Tyr Arg Ser Tyr					
	290			295		300
Leu Arg Ala His Leu	Tyr Phe Gln Ile Ile Thr Tyr					
	305			310		315

(2) INFORMATION FOR SEQ ID NO:1064:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..218

(D) OTHER INFORMATION: / Ceres Seq. ID 1568886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

Met Gly Leu Glu Glu Glu Phe Gly Ile Glu Met Ala Ser Thr Met Phe	
1	5 10 15
Leu Asn Tyr Leu Thr Trp Lys Arg Ser Met Leu Pro Lys Gly His Ile	
	20 25 30
Pro Glu Ala Glu Ile Ala Asn Asp Leu Ser His Asn Lys Met Cys Met	
	35 40 45
Gln Gly His Asp Lys Met Gly Arg Pro Ile Ala Val Ala Ile Gly Asn	
	50 55 60
Arg His Asn Pro Ser Lys Gly Asn Pro Asp Glu Phe Lys Arg Phe Val	
65	70 75 80
Val Tyr Thr Leu Glu Lys Ile Cys Ala Arg Met Pro Arg Gly Gln Glu	
	85 90 95
Lys Phe Val Ala Ile Gly Asp Leu Gln Gly Trp Gly Tyr Ser Asn Cys	
	100 105 110
Asp Ile Arg Gly Tyr Leu Ala Ala Leu Ser Thr Leu Gln Asp Cys Tyr	
	115 120 125
Pro Glu Arg Leu Gly Lys Leu Tyr Ile Val His Ala Pro Tyr Ile Phe	
	130 135 140

Met Thr Ala Trp Lys Val Ile Tyr Pro Phe Ile Asp Ala Asn Thr Lys
145 150 155 160
Lys Lys Ile Val Phe Val Glu Asn Lys Lys Leu Thr Pro Thr Leu Leu
165 170 175
Glu Asp Ile Asp Glu Ser Gln Leu Pro Gly His Leu Arg Arg Gln Asn
180 185 190
Cys His Leu Phe Leu Phe Arg Arg Pro Asp Tyr Arg Ser Tyr Leu Arg
195 200 205
Ala His Leu Tyr Phe Gln Ile Ile Thr Tyr
210 215

(2) INFORMATION FOR SEQ ID NO:1065:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1790 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1790

(D) OTHER INFORMATION: / Ceres Seq. ID 1568887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

ccctcgcgca	tcttcggtgc	tataaaacaa	actcacgact	agatcatctt	ggagtggagt	60
ttacgtttga	tagactacta	caatgaagga	gccaacgacg	gagatagaga	ttgaaacttc	120
agctgtcaca	acgactcctgc	ctccctcctct	tcctccgacg	cgctcacctc	atcaggcggt	180
gggtggagagg	ctcaaggatt	atggacagga	agatgttttc	tcctctctgg	atgaactctc	240
accggaagag	cgagatctcc	tcctccgaga	tatcgagaat	ttggatcttc	caaggataga	300
tcggatcatc	agatgctcac	ttcactcaca	aggggttgcca	gtggcgccaa	tagaacgggt	360
gcggagagaat	tgtgtgtcaa	cggtggagga	aagaactaag	gaagacagag	aaaaatgggt	420
gaaaatggga	ttaaaagcta	tctacgaagg	caaatgggtg	gtgggtgctt	tatctgggtg	480
acagggaaca	agacttggaa	gttcagatcc	aaaagggtgt	tataatatcg	gactgccatc	540
tgggaaatca	ctttttcaga	ttcaagctga	gaggatctta	tgtgtccaaa	ggcttgcttc	600
tcaggcaaat	agtgaaggcaa	gtccaaactcg	cccagttaca	atacagtggg	atataatgac	660
cagtcacatt	actcatgaac	caacacaaaa	attcttcgag	agtcacaaat	attttggcct	720
tgaaaccagat	caagtccact	ttttttcaac	aaggagctct	gccttgcat	tcaaaaggatg	780
gcaagtttat	catggagaca	cttttcagcc	tatccaaggc	gccggatggg	aacggggagg	840
tttatcacgc	tttaaaatct	tcaaggttat	tagaagatat	ggcttcgagg	gggattaaat	900
atgtggattg	ctatggtggt	gacaatgttc	tggttcgagt	agctgaccct	actttctctg	960
gatacttcatt	cgacaaaagt	gcagcttcag	ctgcacaaat	agtgcgcaag	gcataccac	1020
aggaaaaagt	tgaggatatt	gtaaggaggg	gaaaagggtg	gcctttgact	gtagtttagt	1080
acacagagct	tgaccagctt	atggctctct	caactaatca	acaaacagga	cgcttctcaat	1140
attgtctggg	taacgtgtgc	ttacacatgt	tcactctgga	tttccctaac	caagttgcga	1200
attggctgaa	aaagacagcg	tttaccattt	ggcgGagaag	aagataccgt	ctataaatgt	1260
cgacatagt	ggGactaaa	actagaacag	ttcatattcg	attgcttttc	ttatgctcct	1320
tcgactgcaac	tttttgaggt	gttgaggagg	gaagagtttg	caccgggtgaa	gaacgcacaa	1380
gggtgcgaatt	acgacacacc	ggaaaacgca	agactgttgg	ttctacagct	gcatacacgt	1440
tggtgtcatg	caagctgtgtg	attttcaaca	cattccgttg	cttttatatg	gactggtgtg	1500
gaagtgtcac	catgtgtctc	gtacgctgga	gaaaactctag	aagcgatttg	tcgggggaaga	1560
acctttcacg	caacatgtga	aatctccctc	taattcttct	ctttcttttt	cttatctatt	1620
cttgtaattt	tgtcattgtc	tttgcttttt	cttttggctt	ggttctctct	ttgtgttggg	1680
gtttgtgtct	tatatatgaa	ctgtaaactg	cggaggtggt	cagtagtctc	ttttcaatgt	1740
gttactcttc	attattgcga	caatagtga	gtctccgaaa	ttttggtggt		

(2) INFORMATION FOR SEQ ID NO:1066:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1568888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

Met Lys Glu Pro Thr Thr Glu Ile Glu Ile Glu Thr Ser Ala Val Thr
1 5 10 15
Thr Ile Leu Pro Pro Pro Leu Pro Pro Thr Ala Ser Pro His Gln Ala
20 25 30
Leu Val Glu Arg Leu Lys Asp Tyr Gly Gln Glu Asp Val Phe Ser Leu
35 40 45
Trp Asp Glu Leu Ser Pro Glu Glu Arg Asp Leu Leu Leu Arg Asp Ile
50 55 60
Glu Asn Leu Asp Leu Pro Arg Ile Asp Arg Ile Ile Arg Cys Ser Leu
65 70 75 80
His Ser Gln Gly Leu Pro Val Ala Ala Ile Glu Pro Val Pro Glu Asn
85 90 95
Cys Val Ser Thr Val Glu Glu Arg Thr Lys Glu Asp Arg Glu Lys Trp
100 105 110
Trp Lys Met Gly Leu Lys Ala Ile Tyr Glu Gly Lys Leu Gly Val Val
115 120 125
Leu Leu Ser Gly Gly Gln Gly Thr Arg Leu Gly Ser Ser Asp Pro Lys
130 135 140
Gly Cys Tyr Asn Ile Gly Leu Pro Ser Gly Lys Ser Leu Phe Gln Ile
145 150 155 160
Gln Ala Glu Arg Ile Leu Cys Val Gln Arg Leu Ala Ser Gln Ala Met
165 170 175
Ser Glu Ala Ser Pro Thr Arg Pro Val Thr Ile Gln Trp Tyr Ile Met
180 185 190
Thr Ser Pro Phe Thr His Glu Pro Thr Gln Lys Phe Phe Glu Ser His
195 200 205
Lys Tyr Phe Gly Leu Glu Pro Asp Gln Val Thr Phe Phe Ser Thr Arg
210 215 220
Ser Ser Ala Leu His Phe Lys Gly Trp Gln Val Tyr His Gly Asp Thr
225 230 235 240
Phe Gln Pro Ile Gln Gly Ala Gly Trp Glu Arg Gly Ser Leu Tyr Ser
245 250 255
Phe Lys Ile Phe Lys Val Ile Arg Arg Tyr Gly Phe Glu Gly Asp
260 265 270

(2) INFORMATION FOR SEQ ID NO:1067:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1568889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

Met Gly Leu Lys Ala Ile Tyr Glu Gly Lys Leu Gly Val Val Leu Leu
1 5 10 15
Ser Gly Gly Gln Gly Thr Arg Leu Gly Ser Ser Asp Pro Lys Gly Cys
20 25 30
Tyr Asn Ile Gly Leu Pro Ser Gly Lys Ser Leu Phe Gln Ile Gln Ala
35 40 45
Glu Arg Ile Leu Cys Val Gln Arg Leu Ala Ser Gln Ala Met Ser Glu
50 55 60
Ala Ser Pro Thr Arg Pro Val Thr Ile Gln Trp Tyr Ile Met Thr Ser
65 70 75 80
Pro Phe Thr His Glu Pro Thr Gln Lys Phe Phe Glu Ser His Lys Tyr
85 90 95

Phe Gly Leu Glu Pro Asp Gln Val Thr Phe Phe Ser Thr Arg Ser Ser
100 105 110
Ala Leu His Phe Lys Gly Trp Gln Val Tyr His Gly Asp Thr Phe Gln
115 120 125
Pro Ile Gln Gly Ala Gly Trp Glu Arg Gly Ser Leu Tyr Ser Phe Lys
130 135 140
Ile Phe Lys Val Ile Arg Arg Tyr Gly Phe Glu Gly Asp
145 150 155

(2) INFORMATION FOR SEQ ID NO:1068:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1568890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

Met Asn Gln His Lys Asn Ser Ser Arg Val Thr Ser Ile Leu Ala Leu
1 5 10 15
Asn Gln Ile Lys Ser Pro Phe Phe Gln Gln Gly Ala Leu Pro Cys Ile
20 25 30
Ser Lys Asp Gly Lys Phe Ile Met Glu Thr Pro Phe Ser Leu Ser Lys
35 40 45
Ala Pro Asp Gly Asn Gly Gly Val Tyr Thr Ala Leu Lys Ser Ser Arg
50 55 60
Leu Leu Glu Asp Met Ala Ser Arg Gly Ile Lys Tyr Val Asp Cys Tyr
65 70 75 80
Gly Val Asp Asn Val Leu Val Arg Val Ala Asp Pro Thr Phe Leu Gly
85 90 95
Tyr Phe Ile Asp Lys Ser Ala Ala Ser Ala Ala Lys Val Val Arg Lys
100 105 110
Ala Tyr Pro Gln Glu Lys Val Gly Val Phe Val Arg Arg Gly Lys Gly
115 120 125
Gly Pro Leu Thr Val Val Glu Tyr Thr Glu Leu Asp Gln Ser Met Ala
130 135 140
Ser Ala Thr Asn Gln Gln Thr Gly Arg Leu Gln Tyr Cys Trp Ser Asn
145 150 155 160
Val Cys Leu His Met Phe Thr Leu Asp Phe Leu Asn Gln Val Ala Asn
165 170 175
Gly Leu Lys Lys Thr Ala Phe Thr Ile Trp Arg Arg Arg Arg Tyr Arg
180 185 190
Leu

(2) INFORMATION FOR SEQ ID NO:1069:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1575 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1575

(D) OTHER INFORMATION: / Ceres Seq. ID 1568891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

aaagagcaaa actatctaat tccatggcgt tctccctct cttccaatt cctcaacctg	60
cctctctttt tttaactctc tccgcatta ccgtttctaa taatgcttcc tctctctctc	120
tctcccgctt ttactcttta tatcacccca aaggaaacct acgaaccaga accgcgacct	180

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cgtttttcgg agcttctggg aacttgagga ttgtttccat ggcggagaat aggcaattgg 240
ttttaggatt tgggtggcga gcCggCtgcg gaattggatg atattggatga aggtgaaatc 300
cagaggattg gaaatgaaga cgaagacgac gatgaattca tacaagtcca tgcataaatac 360
tcctctgctg ctctgcctga gagatgggat gttttgggtc tcggccaagc catggtagat 420
ttctctggag ttgtggatga tgagtttcta aagaaacttg gtttaaaaaa gggaacaagg 480
aaactgatta atcacgagga gaggggtaaa ttattacaag caatggatgg ttgtagctat 540
aaRgcgcagc ctggaggctc attgtccaaac actttagtgg ctctcgcaag attaggtttc 600
caatccatct gtgaccggcc ttgtaatgtg gcaatggcgt gcagtattgg aggtgaccct 660
ctcggtagct tttacgggac taaactacga cgagcaaatg taaattttct tctctgtcca 720
atcaaggacg gaacaacagg aacagtgata gtctccacaa ctctcgatgc acaacgtact 780
atgcttgcat atcagggaac atctctgtgc gttaattatg attctgtttt ggctagtattg 840
atagccaaga caaatgtctt ttgttgggaa ggctatttgt ttgagcttcc tgatactata 900
agaaccataa caaaagcctg cgaagaagcc cacagaaacg gggcacttgt tgctgtgaca 960
gcatcagatg tgtcctgcat agagaggcat tatgatgatt tctgggacat tgtggggaac 1020
tatgcggata ttgtatttgc aatatagcga gaagcaagag cgttttgtca cttttccgca 1080
gaggaagctc caatttcacg gacaagatac atgagccact ttgttccgtt tgtttctgtt 1140
accgatggaa tcaacgggtc atatattgga gtaaaaggag agggccatcta cattctccg 1200
tccccatgcg tgccagtgtg tacatgtgtg gctggagatg catatgtctc agggatctta 1260
tacggtagct tgagggggtg ctctgacttg aaaggaaatg gagatattgc tgcaacgatt 1320
cgagcaactg tgggtgggtca acaaggaacc aggccttaggg ttcaggagcg gggtgagctg 1380
gtcgtctcac atgccttcg tctcaatggt tctggtgttc gaacagatgt tgggtcttga 1440
tgaaacctct ttagcttggt atttttagct ttttgattca tctcttgtct tcatgtagta 1500
gtgcctttt caattgact gtaacttgt atgtaacatt ttagtatata gatatgttt 1560
cgcgaaagt ttgag

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(2) INFORMATION FOR SEQ ID NO:1070:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 385 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..385

(D) OTHER INFORMATION: / Ceres Seq. ID 1568892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:

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Met Asp Glu Gly Ile Gln Arg Ile Gly Asn Glu Asp Glu Asp Asp
1 5 10 15
Asp Glu Phe Ile Gln Val His Ala Asn Asn Ser Ser Ala Ala Ser Pro
20 25 30
Glu Arg Trp Asp Val Leu Gly Leu Gly Gln Ala Met Val Asp Phe Ser
35 40 45
Gly Val Val Asp Asp Glu Phe Leu Lys Lys Leu Gly Leu Lys Gly
50 55 60
Thr Arg Lys Leu Ile Asn His Glu Glu Arg Gly Lys Leu Leu Gln Ala
65 70 75 80
Met Asp Gly Cys Ser Tyr Xaa Ala Ala Ala Gly Gly Ser Leu Ser Asn
85 90 95
Thr Leu Val Ala Leu Ala Arg Leu Gly Ser Gln Ser Ile Cys Asp Arg
100 105 110
Pro Leu Asn Val Ala Met Ala Gly Ser Ile Gly Gly Asp Pro Leu Gly
115 120 125
Ser Phe Tyr Gly Thr Lys Leu Arg Arg Ala Asn Val Asn Phe Leu Ser
130 135 140
Ala Pro Ile Lys Asp Gly Thr Thr Gly Thr Val Ile Val Leu Thr Thr
145 150 155 160
Pro Asp Ala Gln Arg Thr Met Leu Ala Tyr Gln Gly Thr Ser Ser Val
165 170 175
Val Asn Tyr Asp Ser Cys Leu Ala Ser Leu Ile Ala Lys Thr Asn Val
180 185 190
Phe Val Val Glu Gly Tyr Leu Phe Glu Leu Pro Asp Thr Ile Arg Thr

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195	200	205
Ile Thr Lys Ala Cys Glu Glu Ala His Arg Asn Gly Ala Leu Val Ala		
210	215	220
Val Thr Ala Ser Asp Val Ser Cys Ile Glu Arg His Tyr Asp Asp Phe		
225	230	235
Trp Asp Ile Val Gly Asn Tyr Ala Asp Ile Val Phe Ala Asn Ser Asp		
245	250	255
Glu Ala Arg Ala Phe Cys His Phe Ser Ala Glu Glu Ser Pro Ile Ser		
260	265	270
Ala Thr Arg Tyr Met Ser His Phe Val Pro Phe Val Ser Val Thr Asp		
275	280	285
Gly Ile Asn Gly Ser Tyr Ile Gly Val Lys Gly Glu Ala Ile Tyr Ile		
290	295	300
Pro Pro Ser Pro Cys Val Pro Val Asp Thr Cys Gly Ala Gly Asp Ala		
305	310	315
Tyr Ala Ser Gly Ile Leu Tyr Gly Ile Leu Arg Gly Val Ser Asp Leu		
325	330	335
Lys Gly Met Gly Asp Met Ala Ala Thr Ile Ala Ala Thr Val Val Gly		
340	345	350
Gln Gln Gly Thr Arg Leu Arg Val Gln Asp Ala Val Glu Leu Ala Arg		
355	360	365
Ser His Ala Phe Arg Leu Asn Gly Ser Gly Val Arg Thr Asp Val Gly		
370	375	380

Ser
385

(2) INFORMATION FOR SEQ ID NO:1071:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..342

(D) OTHER INFORMATION: / Ceres Seq. ID 1568893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:

Met Val Asp Phe Ser Gly Val Val Asp Asp Glu Phe Leu Lys Lys Leu	
1	15
Gly Leu Lys Lys Gly Thr Arg Lys Leu Ile Asn His Glu Glu Arg Gly	
20	30
Lys Leu Leu Gln Ala Met Asp Gly Cys Ser Tyr Xaa Ala Ala Ala Gly	
35	45
Gly Ser Leu Ser Asn Thr Leu Val Ala Leu Ala Arg Leu Gly Ser Gln	
50	60
Ser Ile Cys Asp Arg Pro Leu Asn Val Ala Met Ala Gly Ser Ile Gly	
65	75
Gly Asp Pro Leu Gly Ser Phe Tyr Gly Thr Lys Leu Arg Arg Ala Asn	
85	95
Val Asn Phe Leu Ser Ala Pro Ile Lys Asp Gly Thr Thr Gly Thr Val	
100	110
Ile Val Leu Thr Thr Pro Asp Ala Gln Arg Thr Met Leu Ala Tyr Gln	
115	125
Gly Thr Ser Ser Val Val Asn Tyr Asp Ser Cys Leu Ala Ser Leu Ile	
130	140
Ala Lys Thr Asn Val Phe Val Val Glu Gly Tyr Leu Phe Glu Leu Pro	
145	155
Asp Thr Ile Arg Thr Ile Thr Lys Ala Cys Glu Glu Ala His Arg Asn	
165	175
Gly Ala Leu Val Ala Val Thr Ala Ser Asp Val Ser Cys Ile Glu Arg	
180	190

His Tyr Asp Asp Phe Trp Asp Ile Val Gly Asn Tyr Ala Asp Ile Val
195 200 205
Phe Ala Asn Ser Asp Glu Ala Arg Ala Phe Cys His Phe Ser Ala Glu
210 215 220
Glu Ser Pro Ile Ser Ala Thr Arg Tyr Met Ser His Phe Val Pro Phe
225 230 235 240
Val Ser Val Thr Asp Gly Ile Asn Gly Ser Tyr Ile Gly Val Lys Gly
245 250 255
Glu Ala Ile Tyr Ile Pro Pro Ser Pro Cys Val Pro Val Asp Thr Cys
260 265 270
Gly Ala Gly Asp Ala Tyr Ala Ser Gly Ile Leu Tyr Gly Ile Leu Arg
275 280 285
Gly Val Ser Asp Leu Lys Gly Met Gly Asp Met Ala Ala Thr Ile Ala
290 295 300
Ala Thr Val Val Gly Gln Gln Gly Thr Arg Leu Arg Val Gln Asp Ala
305 310 315 320
Val Glu Leu Ala Arg Ser His Ala Phe Arg Leu Asn Gly Ser Gly Val
325 330 335
Arg Thr Asp Val Gly Ser
340

(2) INFORMATION FOR SEQ ID NO:1072:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..305

(D) OTHER INFORMATION: / Ceres Seq. ID 1568894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

Met Asp Gly Cys Ser Tyr Xaa Ala Ala Ala Gly Gly Ser Leu Ser Asn
1 5 10 15
Thr Leu Val Ala Leu Ala Arg Leu Gly Ser Gln Ser Ile Cys Asp Arg
20 25 30
Pro Leu Asn Val Ala Met Ala Gly Ser Ile Gly Gly Asp Pro Leu Gly
35 40 45
Ser Phe Tyr Gly Thr Lys Leu Arg Arg Ala Asn Val Asn Phe Leu Ser
50 55 60
Ala Pro Ile Lys Asp Gly Thr Thr Gly Thr Val Ile Val Leu Thr Thr
65 70 75 80
Pro Asp Ala Gln Arg Thr Met Leu Ala Tyr Gln Gly Thr Ser Ser Val
85 90 95
Val Asn Tyr Asp Ser Cys Leu Ala Ser Leu Ile Ala Lys Thr Asn Val
100 105 110
Phe Val Val Glu Gly Tyr Leu Phe Glu Leu Pro Asp Thr Ile Arg Thr
115 120 125
Ile Thr Lys Ala Cys Glu Glu Ala His Arg Asn Gly Ala Leu Val Ala
130 135 140
Val Thr Ala Ser Asp Val Ser Cys Ile Glu Arg His Tyr Asp Asp Phe
145 150 155 160
Trp Asp Ile Val Gly Asn Tyr Ala Asp Ile Val Phe Ala Asn Ser Asp
165 170 175
Glu Ala Arg Ala Phe Cys His Phe Ser Ala Glu Glu Ser Pro Ile Ser
180 185 190
Ala Thr Arg Tyr Met Ser His Phe Val Pro Phe Val Ser Val Thr Asp
195 200 205
Gly Ile Asn Gly Ser Tyr Ile Gly Val Lys Gly Glu Ala Ile Tyr Ile
210 215 220
Pro Pro Ser Pro Cys Val Pro Val Asp Thr Cys Gly Ala Gly Asp Ala

225	230	235	240
Tyr Ala Ser Gly Ile Leu Tyr Gly Ile Leu Arg Gly Val Ser Asp Leu			
	245	250	255
Lys Gly Met Gly Asp Met Ala Ala Thr Ile Ala Ala Thr Val Val Gly			
	260	265	270
Gln Gln Gly Thr Arg Leu Arg Val Gln Asp Ala Val Glu Leu Ala Arg			
	275	280	285
Ser His Ala Phe Arg Leu Asn Gly Ser Gly Val Arg Thr Asp Val Gly			
	290	295	300

Ser
305

(2) INFORMATION FOR SEQ ID NO:1073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1374
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:

attatggtgta	atttctgctg	ccattgctgc	tcctctctcc	ggagatacaa	aggcgaaatct	60
gaccagtaag	aaagatggca	gtcgagatgg	ccctctcagtc	tcagggttttg	gtggaagaga	120
aatcgagtgt	tagaattcttg	acactaaaca	gaccaaaagca	gctgaatgct	ctgtcccttcc	180
acatgatctc	tcgattgctg	caactgttcc	ttgcatttga	ggaggaccct	agtgtgaaac	240
ttgtcatcct	aaagggtcat	gggagagcct	tttgtgctgg	tgccgatgtt	gcagctgttg	300
ttcgtgacat	caatcaaggt	aactggagac	tcggtgccaa	ttactttcca	ctgtaataca	360
tgctcaacta	tggtatggcc	acatatagca	aagctcaggt	ttcaactctg	aatgggtatcg	420
tcattggagg	cggagctggt	gtatccgtcc	atggtcgatt	tcgtattgca	actgagaaca	480
cgggtttttg	catgcctcag	acagctctgg	ggctctttcc	agatgtaggc	gcctctact	540
tcctgtcaag	gctccctggt	ttttttgggg	agtatgttgg	cctcacacga	gctagattag	600
atgggtgctga	aatgcttgct	tgtggccttg	caactcattt	tgttcctcca	acgaggttga	660
ctgcattaga	agcagatctt	tgacagaatta	attcaaatga	tcacaacttt	gcctcaacaa	720
ttctcgatgc	atacaccagc	catccgcgcc	tgaacacagca	gagtgcttac	cgcaggttag	780
atgttattga	taggtgtttc	tcaaggagaa	cagtcgaaga	aattatatct	gcacttgaga	840
gagagggcac	tcaagaagca	gatgggttga	tctcagctac	cattcaagca	ttgaagaagg	900
gttcaccagc	aagccttaaa	atctctctta	gatcgataag	ggaaggggcg	gtgcagggggg	960
tggggacagt	tccttatccg	gagtagagaa	tggtgtgtca	tgtgatgaag	ggagaataca	1020
gcaaaagtatt	tggtggagggg	tcagagagcca	tattgttaga	caaaagataa	aaccacaaat	1080
gggagccaa	gcgactggag	gacatgaagg	atagcatggt	ggagcagtag	ttcgagagag	1140
tggaacggga	ggatgatcta	aagcttccgc	caaggaaata	cttcgctgct	ttagggtatcg	1200
caaaagctgtg	aagtggagaa	ggtgatggag	cactattgtt	tacgtctgtg	ggaaagaaaa	1260
aagaaaaata	atgtaaacac	acttgtgttg	aataggactt	gcatacata	cataaatcat	1320
tattgtattt	gagaattgac	accaaagcag	cagagcagaa	tttgtttaag	attc	

(2) INFORMATION FOR SEQ ID NO:1074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..378
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

Met Ala Val Glu Met Ala Ser Gln Ser Gln Val Leu Val Glu Glu Lys			
1	5	10	15
Ser Ser Val Arg Ile Leu Thr Leu Asn Arg Pro Lys Gln Leu Asn Ala			

	20		25		30
Leu Ser Phe His Met Ile Ser Arg Leu Leu Gln Leu Phe Leu Ala Phe	35		40		45
Glu Glu Asp Pro Ser Val Lys Leu Val Ile Leu Lys Gly His Gly Arg	50		55		60
Ala Phe Cys Ala Gly Gly Asp Val Ala Ala Val Val Arg Asp Ile Asn	65		70		75
Gln Gly Asn Trp Arg Leu Gly Ala Asn Tyr Phe Ser Ser Glu Tyr Met	85		90		95
Leu Asn Tyr Val Met Ala Thr Tyr Ser Lys Ala Gln Val Ser Ile Leu	100		105		110
Asn Gly Ile Val Met Gly Gly Gly Ala Gly Val Ser Val His Gly Arg	115		120		125
Phe Arg Ile Ala Thr Glu Asn Thr Val Phe Ala Met Pro Glu Thr Ala	130		135		140
Leu Gly Leu Phe Pro Asp Val Gly Ala Ser Tyr Phe Leu Ser Arg Leu	145		150		155
Pro Gly Phe Phe Gly Glu Tyr Val Gly Leu Thr Arg Ala Arg Leu Asp	165		170		175
Gly Ala Glu Met Leu Ala Cys Gly Leu Ala Thr His Phe Val Pro Ser	180		185		190
Thr Arg Leu Thr Ala Leu Glu Ala Asp Leu Cys Arg Ile Asn Ser Asn	195		200		205
Asp Pro Thr Phe Ala Ser Thr Ile Leu Asp Ala Tyr Thr Gln His Pro	210		215		220
Arg Leu Lys Gln Gln Ser Ala Tyr Arg Arg Leu Asp Val Ile Asp Arg	225		230		235
Cys Phe Ser Arg Arg Thr Val Glu Glu Ile Ile Ser Ala Leu Glu Arg	245		250		255
Glu Ala Thr Gln Glu Ala Asp Gly Trp Ile Ser Ala Thr Ile Gln Ala	260		265		270
Leu Lys Lys Gly Ser Pro Ala Ser Leu Lys Ile Ser Leu Arg Ser Ile	275		280		285
Arg Glu Gly Arg Leu Gln Gly Val Gly Gln Cys Leu Ile Arg Glu Tyr	290		295		300
Arg Met Val Cys His Val Met Lys Gly Glu Ile Ser Lys Asp Phe Val	305		310		315
Glu Gly Cys Arg Ala Ile Leu Val Asp Lys Asp Lys Asn Pro Lys Trp	325		330		335
Glu Pro Arg Arg Leu Glu Asp Met Lys Asp Ser Met Val Glu Gln Tyr	340		345		350
Phe Glu Arg Val Glu Arg Glu Asp Asp Leu Lys Leu Pro Pro Arg Asn	355		360		365
Asn Leu Pro Ala Leu Gly Ile Ala Lys Leu	370		375		

(2) INFORMATION FOR SEQ ID NO:1075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..374
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

Met Ala Ser Gln Ser Gln Val Leu Val Glu Glu Lys Ser Ser Val Arg		
1	5	10
Ile Leu Thr Leu Asn Arg Pro Lys Gln Leu Asn Ala Leu Ser Phe His		
20	25	30

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Met Ile Ser Arg Leu Leu Gln Leu Phe Leu Ala Phe Glu Glu Asp Pro
    35          40          45
Ser Val Lys Leu Val Ile Leu Lys Gly His Gly Arg Ala Phe Cys Ala
    50          55          60
Gly Gly Asp Val Ala Ala Val Val Arg Asp Ile Asn Gln Gly Asn Trp
    65          70          75          80
Arg Leu Gly Ala Asn Tyr Phe Ser Ser Glu Tyr Met Leu Asn Tyr Val
    85          90          95
Met Ala Thr Tyr Ser Lys Ala Gln Val Ser Ile Leu Asn Gly Ile Val
    100          105          110
Met Gly Gly Gly Ala Gly Val Ser Val His Gly Arg Phe Arg Ile Ala
    115          120          125
Thr Glu Asn Thr Val Phe Ala Met Pro Glu Thr Ala Leu Gly Leu Phe
    130          135          140
Pro Asp Val Gly Ala Ser Tyr Phe Leu Ser Arg Leu Pro Gly Phe Phe
    145          150          155          160
Gly Glu Tyr Val Gly Leu Thr Arg Ala Arg Leu Asp Gly Ala Glu Met
    165          170          175
Leu Ala Cys Gly Leu Ala Thr His Phe Val Pro Ser Thr Arg Leu Thr
    180          185          190
Ala Leu Glu Ala Asp Leu Cys Arg Ile Asn Ser Asn Asp Pro Thr Phe
    195          200          205
Ala Ser Thr Ile Leu Asp Ala Tyr Thr Gln His Pro Arg Leu Lys Gln
    210          215          220
Gln Ser Ala Tyr Arg Arg Leu Asp Val Ile Asp Arg Cys Phe Ser Arg
    225          230          235          240
Arg Thr Val Glu Glu Ile Ile Ser Ala Leu Glu Arg Glu Ala Thr Gln
    245          250          255
Glu Ala Asp Gly Trp Ile Ser Ala Thr Ile Gln Ala Leu Lys Lys Gly
    260          265          270
Ser Pro Ala Ser Leu Lys Ile Ser Leu Arg Ser Ile Arg Glu Gly Arg
    275          280          285
Leu Gln Gly Val Gly Gln Cys Leu Ile Arg Glu Tyr Arg Met Val Cys
    290          295          300
His Val Met Lys Gly Glu Ile Ser Lys Asp Phe Val Glu Gly Cys Arg
    305          310          315          320
Ala Ile Leu Val Asp Lys Asp Lys Asn Pro Lys Trp Glu Pro Arg Arg
    325          330          335
Leu Glu Asp Met Lys Asp Ser Met Val Glu Gln Tyr Phe Glu Arg Val
    340          345          350
Glu Arg Glu Asp Asp Leu Lys Leu Pro Pro Arg Asn Asn Leu Pro Ala
    355          360          365
Leu Gly Ile Ala Lys Leu
    370

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(2) INFORMATION FOR SEQ ID NO:1076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..342
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

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Met Ile Ser Arg Leu Leu Gln Leu Phe Leu Ala Phe Glu Glu Asp Pro
1          5          10          15
Ser Val Lys Leu Val Ile Leu Lys Gly His Gly Arg Ala Phe Cys Ala
    20          25          30
Gly Gly Asp Val Ala Ala Val Val Arg Asp Ile Asn Gln Gly Asn Trp

```


35	40	45
Arg Leu Gly Ala Asn Tyr Phe Ser Ser Glu Tyr Met Leu Asn Tyr Val		
50	55	60
Met Ala Thr Tyr Ser Lys Ala Gln Val Ser Ile Leu Asn Gly Ile Val		
65	70	75
Met Gly Gly Gly Ala Gly Val Ser Val His Gly Arg Phe Arg Ile Ala		
85	90	95
Thr Glu Asn Thr Val Phe Ala Met Pro Glu Thr Ala Leu Gly Leu Phe		
100	105	110
Pro Asp Val Gly Ala Ser Tyr Phe Leu Ser Arg Leu Pro Gly Phe Phe		
115	120	125
Gly Glu Tyr Val Gly Leu Thr Arg Ala Arg Leu Asp Gly Ala Glu Met		
130	135	140
Leu Ala Cys Gly Leu Ala Thr His Phe Val Pro Ser Thr Arg Leu Thr		
145	150	155
Ala Leu Glu Ala Asp Leu Cys Arg Ile Asn Ser Asn Asp Pro Thr Phe		
165	170	175
Ala Ser Thr Ile Leu Asp Ala Tyr Thr Gln His Pro Arg Leu Lys Gln		
180	185	190
Gln Ser Ala Tyr Arg Arg Leu Asp Val Ile Asp Arg Cys Phe Ser Arg		
195	200	205
Arg Thr Val Glu Glu Ile Ile Ser Ala Leu Glu Arg Glu Ala Thr Gln		
210	215	220
Glu Ala Asp Gly Trp Ile Ser Ala Thr Ile Gln Ala Leu Lys Lys Gly		
225	230	235
Ser Pro Ala Ser Leu Lys Ile Ser Leu Arg Ser Ile Arg Glu Gly Arg		
245	250	255
Leu Gln Gly Val Gly Gln Cys Leu Ile Arg Glu Tyr Arg Met Val Cys		
260	265	270
His Val Met Lys Gly Glu Ile Ser Lys Asp Phe Val Glu Gly Cys Arg		
275	280	285
Ala Ile Leu Val Asp Lys Asp Lys Asn Pro Lys Trp Glu Pro Arg Arg		
290	295	300
Leu Glu Asp Met Lys Asp Ser Met Val Glu Gln Tyr Phe Glu Arg Val		
305	310	315
Glu Arg Glu Asp Asp Leu Lys Leu Pro Pro Arg Asn Asn Leu Pro Ala		
325	330	335
Leu Gly Ile Ala Lys Leu		
340		

(2) INFORMATION FOR SEQ ID NO:1077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1180

(D) OTHER INFORMATION: / Ceres Seq. ID 1568902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

aatatagtac	caactccatt	gaatgttaaa	actcagaaga	aagtggagtg	atcatataac	60
gacaatgaag	aattctcttta	acttgttctt	tatgttkttc	tttgcaatgc	caattctttc	120
actctccgag	aatccaacca	atttcagcga	gagttgcgaa	gacgggagtg	gagaaaccgg	180
ttcaagcttt	ggcatagggt	tcgatttggt	tcttgatttt	ggttataacc	ggaatagctg	240
ccccgaagca	gagtcctatcg	tctactcgtg	gggtggaacc	acggtgttag	aggatccaag	300
aatggctgct	tctctctctc	gtcttcattt	ccacgactgt	tttgtcaatg	gatgtgatgc	360
ttcgggtgtg	ttagatgaca	cagaaggact	ggttgggtgaa	aaaacggcgc	ctcctaattc	420
aaattctcta	cgagggttcg	aagtgatgta	ttcgataaag	tctgatattg	aattctgatg	480
tcacagagacc	gtctcatcgc	cagacattct	tgccatggct	gctagagatt	cagtcgtgtg	540
gtcgggtgga	ccaaggtggg	aggtggaagt	aggaagaaaa	gacagtagaa	cagcaagcaa	600

acaggcgacga acaaatggct tacccctcacc aaactcaacc gatatcaactc tcatctctac 660
tttccagaatt cttggccttt cacaaccgga catggctgct cttccgggtgacacatatt 720
gggaaaggca cggNgcAct cgttttacag ctgggttgca gccactgcaa actgggacaac 780
cagctaacca cggagacaac cttgagttcc tcgagtcact gcaacagtta tgctgcagct 840
ttggcccccag ttaggtatc actcagcttg acttggtgac tccatcaaca ttggacaacc 900
agtactatgt aaacctcctc tgggttgagg gattgcttcc atcagaccag gcttttagcgg 960
ttcaagaccc agggacaagg gcgattgttg agacctacgc aacagatcag tcgggttttt 1020
ttgaggattt taagaacgct atggttaaaa tgggagggat atccggtggt agtaaatagcg 1080
agattaggaa gaattgtaga atgattaaat aaaaataaaa gcccgactta ttgaatgata 1140
tctaattatc tatataaaaa ttaagaagt ccacctacgt

(2) INFORMATION FOR SEQ ID NO:1078:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1568903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

Met	Leu	Lys	Leu	Arg	Arg	Lys	Trp	Ser	Asp	His	Ile	Thr	Thr	Met	Lys
1			5						10					15	
Asn	Leu	Phe	Asn	Leu	Phe	Leu	Met	Xaa	Phe	Phe	Ala	Met	Pro	Ile	Leu
			20					25					30		
Ser	Leu	Ser	Glu	Asn	Pro	Thr	Asn	Phe	Ser	Glu	Ser	Cys	Glu	Asp	Gly
		35					40					45			
Ser	Gly	Glu	Thr	Gly	Ser	Ser	Phe	Gly	Ile	Gly	Phe	Asp	Leu	Val	Leu
		50				55				60					
Asp	Phe	Gly	Leu	Tyr	Arg	Asn	Ser	Cys	Pro	Glu	Ala	Glu	Ser	Ile	Val
65					70				75					80	
Tyr	Ser	Trp	Val	Glu	Thr	Thr	Val	Leu	Glu	Asp	Pro	Arg	Met	Ala	Ala
			85						90				95		
Ser	Leu	Leu	Arg	Leu	His	Phe	His	Asp	Cys	Phe	Val	Asn	Gly	Cys	Asp
			100					105					110		
Ala	Ser	Val	Leu	Leu	Asp	Asp	Thr	Glu	Gly	Leu	Val	Gly	Glu	Lys	Thr
			115				120					125			
Ala	Pro	Pro	Asn	Leu	Asn	Ser	Leu	Arg	Gly	Phe	Glu	Val	Ile	Asp	Ser
			130			135					140				
Ile	Lys	Ser	Asp	Ile	Glu	Ser	Val	Cys	Pro	Glu	Thr	Val	Ser	Cys	Ala
145				150					155					160	
Asp	Ile	Leu	Ala	Met	Ala	Ala	Arg	Asp	Ser	Val	Val	Val	Ser	Gly	Gly
			165					170					175		
Pro	Arg	Trp	Glu	Val	Glu	Val	Gly	Arg	Lys	Asp	Ser	Arg	Thr	Ala	Ser
			180				185						190		
Lys	Gln	Ala	Ala	Thr	Asn	Gly	Leu	Pro	Ser	Pro	Asn	Ser	Thr	Val	Ser
			195				200					205			
Thr	Leu	Ile	Ser	Thr	Phe	Gln	Asn	Leu	Gly	Leu	Ser	Gln	Thr	Asp	Met
			210			215					220				
Val	Ala	Leu	Ser	Gly	Gly	His	Thr	Leu	Gly	Lys	Ala	Arg	Xaa	His	Phe
225				230						235				240	
Val	Tyr	Ser	Ser	Val	Ala	Ala	Thr	Ala	Asn	Trp	Thr	Thr	Ser		
				245					250						

(2) INFORMATION FOR SEQ ID NO:1079:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..240

(D) OTHER INFORMATION: / Ceres Seq. ID 1568904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

Met	Lys	Asn	Leu	Phe	Asn	Leu	Phe	Leu	Met	Xaa	Phe	Phe	Ala	Met	Pro
1			5						10					15	
Ile	Leu	Ser	Leu	Ser	Glu	Asn	Pro	Thr	Asn	Phe	Ser	Glu	Ser	Cys	Glu
			20					25					30		
Asp	Gly	Ser	Gly	Glu	Thr	Gly	Ser	Ser	Phe	Gly	Ile	Gly	Phe	Asp	Leu
			35				40					45			
Val	Leu	Asp	Phe	Gly	Leu	Tyr	Arg	Asn	Ser	Cys	Pro	Glu	Ala	Glu	Ser
			50			55					60				
Ile	Val	Tyr	Ser	Trp	Val	Glu	Thr	Thr	Val	Leu	Glu	Asp	Pro	Arg	Met
65				70					75					80	
Ala	Ala	Ser	Leu	Leu	Arg	Leu	His	Phe	His	Asp	Cys	Phe	Val	Asn	Gly
			85					90						95	
Cys	Asp	Ala	Ser	Val	Leu	Leu	Asp	Asp	Thr	Glu	Gly	Leu	Val	Gly	Glu
			100					105					110		
Lys	Thr	Ala	Pro	Pro	Asn	Leu	Asn	Ser	Leu	Arg	Gly	Phe	Glu	Val	Ile
			115				120					125			
Asp	Ser	Ile	Lys	Ser	Asp	Ile	Glu	Ser	Val	Cys	Pro	Glu	Thr	Val	Ser
			130				135				140				
Cys	Ala	Asp	Ile	Leu	Ala	Met	Ala	Ala	Arg	Asp	Ser	Val	Val	Val	Ser
145				150					155						160
Gly	Gly	Pro	Arg	Trp	Glu	Val	Glu	Val	Gly	Arg	Lys	Asp	Ser	Arg	Thr
			165						170					175	
Ala	Ser	Lys	Gln	Ala	Ala	Thr	Asn	Gly	Leu	Pro	Ser	Pro	Asn	Ser	Thr
			180					185					190		
Val	Ser	Thr	Leu	Ile	Ser	Thr	Phe	Gln	Asn	Leu	Gly	Leu	Ser	Gln	Thr
			195				200					205			
Asp	Met	Val	Ala	Leu	Ser	Gly	Gly	His	Thr	Leu	Gly	Lys	Ala	Arg	Xaa
			210			215					220				
His	Phe	Val	Tyr	Ser	Ser	Val	Ala	Ala	Thr	Ala	Asn	Trp	Thr	Thr	Ser
225				230						235					240

(2) INFORMATION FOR SEQ ID NO:1080:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1568905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

Met	Xaa	Phe	Phe	Ala	Met	Pro	Ile	Leu	Ser	Leu	Ser	Glu	Asn	Pro	Thr
1				5						10				15	
Asn	Phe	Ser	Glu	Ser	Cys	Glu	Asp	Gly	Ser	Gly	Glu	Thr	Gly	Ser	Ser
			20					25					30		
Phe	Gly	Ile	Gly	Phe	Asp	Leu	Val	Leu	Asp	Phe	Gly	Leu	Tyr	Arg	Asn
			35				40					45			
Ser	Cys	Pro	Glu	Ala	Glu	Ser	Ile	Val	Tyr	Ser	Trp	Val	Glu	Thr	Thr
			50			55					60				
Val	Leu	Glu	Asp	Pro	Arg	Met	Ala	Ala	Ser	Leu	Leu	Arg	Leu	His	Phe
65				70					75					80	
His	Asp	Cys	Phe	Val	Asn	Gly	Cys	Asp	Ala	Ser	Val	Leu	Leu	Asp	Asp
			85						90					95	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

```

Met Gly Asn Leu Phe Cys Cys Val Gln Val Asp Gln Ser Thr Val Ala
1      5      10      15
Ile Lys Glu Thr Phe Gly Lys Phe Glu Asp Val Leu Glu Pro Gly Cys
20      25      30
His Phe Leu Pro Trp Cys Leu Gly Ser Gln Val Ala Gly Tyr Leu Ser
35      40      45
Leu Arg Val Gln Gln Leu Asp Val Arg Cys Glu Thr Lys Thr Lys Asp
50      55      60
Asn Val Phe Val Asn Val Val Ala Ser Ile Gln Tyr Arg Ala Leu Ala
65      70      75      80
Asn Lys Ala Asn Asp Ala Tyr Tyr Lys Leu Ser Asn Thr Arg Gly Gln
85      90      95
Ile Gln Ala Tyr Val Phe Asp Val Ile Arg Ala Ser Val Pro Lys Leu
100      105      110
Leu Leu Asp Asp Val Phe Glu Gln Lys Asn Asp Ile Ala Lys Ala Val
115      120      125
Glu Glu Glu Leu Glu Lys Ala Met Ser Ala Tyr Gly Tyr Glu Ile Val
130      135      140
Gln Thr Leu Ile Val Asp Ile Glu Pro Asp Glu His Val Lys Arg Ala
145      150      155      160
Met Asn Glu Ile Asn Ala Ala Ala Arg Met Arg Leu Ala Ala Asn Glu
165      170      175
Lys Ala Glu Ala Glu Lys Ile Leu Gln Ile Lys Arg Ala Glu Gly Glu
180      185      190
Ala Glu Ser Lys Tyr Leu Ser Gly Leu Gly Ile Ala Arg Gln Arg Gln
195      200      205
Ala Ile Val Asp Gly Leu Arg Asp Ser Val Leu Gly Phe Ala Val Asn
210      215      220
Val Pro Gly Thr Thr Ala Lys Asp Val Met Asp Met Val Leu Val Thr
225      230      235      240
Gln Tyr Phe Asp Thr Met Lys Glu Ile Gly Ala Ser Ser Lys Ser Ser
245      250      255
Ala Val Phe Ile Pro His Gly Pro Gly Ala Val Arg Asp Val Ala Ser
260      265      270
Gln Ile Arg Asp Gly Leu Leu Gln Gly Ser Ser Ala Asn Leu
275      280      285

```

(2) INFORMATION FOR SEQ ID NO:1083:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

```

Met Ser Ala Tyr Gly Tyr Glu Ile Val Gln Thr Leu Ile Val Asp Ile
1      5      10      15
Glu Pro Asp Glu His Val Lys Arg Ala Met Asn Glu Ile Asn Ala Ala
20      25      30
Ala Arg Met Arg Leu Ala Ala Asn Glu Lys Ala Glu Ala Glu Lys Ile
35      40      45
Leu Gln Ile Lys Arg Ala Glu Gly Glu Ala Glu Ser Lys Tyr Leu Ser
50      55      60
Gly Leu Gly Ile Ala Arg Gln Arg Gln Ala Ile Val Asp Gly Leu Arg
65      70      75      80
Asp Ser Val Leu Gly Phe Ala Val Asn Val Pro Gly Thr Thr Ala Lys
85      90      95
Asp Val Met Asp Met Val Leu Val Thr Gln Tyr Phe Asp Thr Met Lys

```

100 105 110
Glu Ile Gly Ala Ser Ser Lys Ser Ser Ala Val Phe Ile Pro His Gly
115 120 125
Pro Gly Ala Val Arg Asp Val Ala Ser Gln Ile Arg Asp Gly Leu Leu
130 135 140
Gln Gly Ser Ser Ala Asn Leu
145 150

(2) INFORMATION FOR SEQ ID NO:1084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1391
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

```

gaaaaagaga ggcagcgatg aacagtatct tctccattga cgatttctcc gatcctttct 60
gggaaactcc tccgattcct ctcaatcctg acttctctaa gccgtgttac gcggtatgaag 120
ttagccagag tcacaccggaa tggactttcg agatgtttct cgaagagatt tcttcgtcgg 180
cggtgagctc tgagccactt ggtaacaaca acaacgcgat cgtcggtgtt tcttcggcgc 240
aatctcttcc tctgttttcc ggacagaatg atttcgagga tgatagtcga ttctgtgatc 300
gcgattcggg aaatttggat tgtgtcgtc ccatgacgac gaagacgggt attgttgatt 360
ccgatgatta tcgtcgtgtt ttaagaaca agcttgagac tgagtgcgct acgtgtgttt 420
ctcttcgggt tgggtctgtg aagcctgaag attcgactag tctccagaaa actcaacttc 480
aaccagttca atocagtcct ctactcaag gagaacttgg gtgtacttct tcttaccag 540
ctgaggtGaa aaaaactggg gtatcaatga agcaggttac tagtgatcg tcgagagaat 600
attctgata cgaggacctt gatgaagaga atgaaccac cggttccttg aagccagagg 660
acgttaaaaa acttagaagg atgctgtcaa atcgtgagtc agctaggcga tctagaagga 720
gaaagcagga gcaaacaaat gacctcgaaa cacagggttaa tgatctaaaa ggtgagcatt 780
catcacttct taacaacactg agcaacatga atcacaagta tgacgaggct gctgttgcca 840
atagaatact aaaggctgac attgagacat taagagctaa ggtgaaaatg gcggaagaaa 900
ccgtgaagag agtaacagga atgaatccga tgcttctcgg aagatcaagt ggacataaag 960
acaacaacag aatgccaaata actggttaaca acaggatgga tctctctagc attattccag 1020
cttatcaacc acactcaaac ctaaacacaca tgtcaaacca aaacatcggg attaccaacca 1080
ttctactctc aagactcggg aacaatttgc ctgctctccc atcccaaac agctctctct 1140
tgcaagaaat tagaataagg caaaatcacc atgtttactcc aagcgccaac ccgatggct 1200
ggcaatccga actcagaac gattcagcat ggccgaaaaa atgcgtggac tgatcaaaaa 1260
agaagcgggt ttgcactat attaatgtct atgcactctg aatttgaag ttattataag 1320
ttacgaatca tgagaaaaaa tcttgtgaaa atacagttct atgcttata tatatataag 1380
ctctgtctta t

```

(2) INFORMATION FOR SEQ ID NO:1085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..416
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

```

Lys Arg Glu Arg Ala Met Asn Ser Ile Phe Ser Ile Asp Asp Phe Ser
1 5 10 15
Asp Pro Phe Trp Glu Thr Pro Pro Ile Pro Leu Asn Pro Asp Ser Ser
20 25 30
Lys Pro Val Thr Ala Asp Glu Val Ser Gln Ser Gln Pro Glu Trp Thr
35 40 45

```

```

Phe Glu Met Phe Leu Glu Glu Ile Ser Ser Ser Ala Val Ser Ser Glu
  50          55          60
Pro Leu Gly Asn Asn Asn Asn Ala Ile Val Gly Val Ser Ser Ala Gln
  65          70          75          80
Ser Leu Pro Ser Val Ser Gly Gln Asn Asp Phe Glu Asp Asp Ser Arg
          85          90          95
Phe Arg Asp Arg Asp Ser Gly Asn Leu Asp Cys Ala Ala Pro Met Thr
          100          105          110
Thr Lys Thr Val Ile Val Asp Ser Asp Asp Tyr Arg Arg Val Leu Lys
          115          120          125
Asn Lys Leu Glu Thr Glu Cys Ala Thr Val Val Ser Leu Arg Val Gly
          130          135          140
Ser Val Lys Pro Glu Asp Ser Thr Ser Ser Pro Glu Thr Gln Leu Gln
          145          150          155          160
Pro Val Gln Ser Ser Pro Leu Thr Gln Gly Glu Leu Gly Val Thr Ser
          165          170          175
Ser Leu Pro Ala Glu Val Lys Lys Thr Gly Val Ser Met Lys Gln Val
          180          185          190
Thr Ser Gly Ser Ser Arg Glu Tyr Ser Ser Asp Asp Glu Asp Leu Asp Glu
          195          200          205
Glu Asn Glu Thr Thr Gly Ser Leu Lys Pro Glu Asp Val Lys Lys Ser
          210          215          220
Arg Arg Met Leu Ser Asn Arg Glu Ser Ala Arg Arg Ser Arg Arg Arg
          225          230          235          240
Lys Gln Glu Gln Thr Ser Asp Leu Glu Thr Gln Val Asn Asp Leu Lys
          245          250          255
Gly Glu His Ser Ser Leu Leu Lys Gln Leu Ser Asn Met Asn His Lys
          260          265          270
Tyr Asp Glu Ala Ala Val Gly Asn Arg Ile Leu Lys Ala Asp Ile Glu
          275          280          285
Thr Leu Arg Ala Lys Val Lys Met Ala Glu Glu Thr Val Lys Arg Val
          290          295          300
Thr Gly Met Asn Pro Met Leu Leu Gly Arg Ser Ser Gly His Asn Asn
          305          310          315          320
Asn Asn Arg Met Pro Ile Thr Gly Asn Asn Arg Met Asp Ser Ser Ser
          325          330          335
Ile Ile Pro Ala Tyr Gln Pro His Ser Asn Leu Asn His Met Ser Asn
          340          345          350
Gln Asn Ile Gly Ile Pro Thr Ile Leu Pro Pro Arg Leu Gly Asn Asn
          355          360          365
Phe Ala Ala Pro Pro Ser Gln Thr Ser Ser Pro Leu Gln Arg Ile Arg
          370          375          380
Asn Gly Gln Asn His His Val Thr Pro Ser Ala Asn Pro Tyr Gly Trp
          385          390          395          400
Asn Thr Glu Pro Gln Asn Asp Ser Ala Trp Pro Lys Lys Cys Val Asp
          405          410          415

```

(2) INFORMATION FOR SEQ ID NO:1086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..411
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

Met Asn Ser Ile Phe Ser Ile Asp Asp Phe Ser Asp Pro Phe Trp Glu

1	5	10	15
Thr Pro Pro Ile Pro Leu Asn Pro Asp Ser Ser Lys Pro Val Thr Ala	20	25	30
Asp Glu Val Ser Gln Ser Gln Pro Glu Trp Thr Phe Glu Met Phe Leu	35	40	45
Glu Glu Ile Ser Ser Ser Ala Val Ser Ser Glu Pro Leu Gly Asn Asn	50	55	60
Asn Asn Ala Ile Val Gly Val Ser Ser Ala Gln Ser Leu Pro Ser Val	65	70	75
Ser Gly Gln Asn Asp Phe Glu Asp Asp Ser Arg Phe Arg Asp Arg Asp	80	85	90
Ser Gly Asn Leu Asp Cys Ala Ala Pro Met Thr Thr Lys Thr Val Ile	100	105	110
Val Asp Ser Asp Asp Tyr Arg Arg Val Leu Lys Asn Lys Leu Glu Thr	115	120	125
Glu Cys Ala Thr Val Val Ser Leu Arg Val Gly Ser Val Lys Pro Glu	130	135	140
Asp Ser Thr Ser Ser Pro Glu Thr Gln Leu Gln Pro Val Gln Ser Ser	145	150	155
Pro Leu Thr Gln Gly Glu Leu Gly Val Thr Ser Ser Leu Pro Ala Glu	160	165	170
Val Lys Lys Thr Gly Val Ser Met Lys Gln Val Thr Ser Gly Ser Ser	175	180	185
Arg Glu Tyr Ser Asp Asp Glu Asp Leu Asp Glu Glu Asn Glu Thr Thr	190	195	200
Gly Ser Leu Lys Pro Glu Asp Val Lys Lys Ser Arg Arg Met Leu Ser	205	210	215
Asn Arg Glu Ser Ala Arg Arg Ser Arg Arg Lys Lys Gln Glu Gln Thr	220	225	230
Ser Asp Leu Glu Thr Gln Val Asn Asp Leu Lys Gly Glu His Ser Ser	235	240	245
Leu Leu Lys Gln Leu Ser Asn Met Asn His Lys Tyr Asp Glu Ala Ala	250	255	260
Val Gly Asn Arg Ile Leu Lys Ala Asp Ile Glu Thr Leu Arg Ala Lys	265	270	275
Val Lys Met Ala Glu Glu Thr Val Lys Arg Val Thr Gly Met Asn Pro	280	285	290
Met Leu Leu Gly Arg Ser Ser Gly His Asn Asn Asn Asn Arg Met Pro	295	300	305
Ile Thr Gly Asn Asn Arg Met Asp Ser Ser Ser Ile Ile Pro Ala Tyr	310	315	320
Gln Pro His Ser Asn Leu Asn His Met Ser Asn Gln Asn Ile Gly Ile	325	330	335
Pro Thr Ile Leu Pro Pro Arg Leu Gly Asn Asn Phe Ala Ala Pro Pro	340	345	350
Ser Gln Thr Ser Ser Pro Leu Gln Arg Ile Arg Asn Gly Gln Asn His	355	360	365
His Val Thr Pro Ser Ala Asn Pro Tyr Gly Trp Asn Thr Glu Pro Gln	370	375	380
His Val Thr Pro Ser Ala Asn Pro Tyr Gly Trp Asn Thr Glu Pro Gln	385	390	395
Asn Asp Ser Ala Trp Pro Lys Lys Cys Val Asp	400	405	410

(2) INFORMATION FOR SEQ ID NO:1087:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..366

(D) OTHER INFORMATION: / Ceres Seq. ID 1568931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

```
Met Phe Leu Glu Ile Ser Ser Ser Ala Val Ser Ser Glu Pro Leu
1      5      10      15
Gly Asn Asn Asn Asn Ala Ile Val Gly Val Ser Ser Ala Gln Ser Leu
20      25      30
Pro Ser Val Ser Gly Gln Asn Asp Phe Glu Asp Asp Ser Arg Phe Arg
35      40      45
Asp Arg Asp Ser Gly Asn Leu Asp Cys Ala Ala Pro Met Thr Thr Lys
50      55      60
Thr Val Ile Val Asp Ser Asp Asp Tyr Arg Arg Val Leu Lys Asn Lys
65      70      75      80
Leu Glu Thr Glu Cys Ala Thr Val Val Ser Leu Arg Val Gly Ser Val
85      90      95
Lys Pro Glu Asp Ser Thr Ser Ser Pro Glu Thr Gln Leu Gln Pro Val
100      105      110
Gln Ser Ser Pro Leu Thr Gln Gly Glu Leu Gly Val Thr Ser Ser Leu
115      120      125
Pro Ala Glu Val Lys Lys Thr Gly Val Ser Met Lys Gln Val Thr Ser
130      135      140
Gly Ser Ser Arg Glu Tyr Ser Asp Asp Glu Asp Leu Asp Glu Glu Asn
145      150      155      160
Glu Thr Thr Gly Ser Leu Lys Pro Glu Asp Val Lys Lys Ser Arg Arg
165      170      175
Met Leu Ser Asn Arg Glu Ser Ala Arg Arg Ser Arg Arg Arg Lys Gln
180      185      190
Glu Gln Thr Ser Asp Leu Glu Thr Gln Val Asn Asp Leu Lys Gly Glu
195      200      205
His Ser Ser Leu Leu Lys Gln Leu Ser Asn Met Asn His Lys Tyr Asp
210      215      220
Glu Ala Ala Val Gly Asn Arg Ile Leu Lys Ala Asp Ile Glu Thr Leu
225      230      235      240
Arg Ala Lys Val Lys Met Ala Glu Glu Thr Val Lys Arg Val Thr Gly
245      250      255
Met Asn Pro Met Leu Leu Gly Arg Ser Ser Gly His Asn Asn Asn Asn
260      265      270
Arg Met Pro Ile Thr Gly Asn Asn Arg Met Asp Ser Ser Ser Ile Ile
275      280      285
Pro Ala Tyr Gln Pro His Ser Asn Leu Asn His Met Ser Asn Gln Asn
290      295      300
Ile Gly Ile Pro Thr Ile Leu Pro Pro Arg Leu Gly Asn Asn Phe Ala
305      310      315      320
Ala Pro Pro Ser Gln Thr Ser Ser Pro Leu Gln Arg Ile Arg Asn Gly
325      330      335
Gln Asn His His Val Thr Pro Ser Ala Asn Pro Tyr Gly Trp Asn Thr
340      345      350
Glu Pro Gln Asn Asp Ser Ala Trp Pro Lys Lys Cys Val Asp
355      360      365
```

(2) INFORMATION FOR SEQ ID NO:1088:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1213

(D) OTHER INFORMATION: / Ceres Seq. ID 1568944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

gtctcctttc cagaacaatc taacgctttc tgaacatct tctctctctt cttctctcgaa

attatttttc	cagtgatcaa	tttcttctct	tctagatttt	tacaggaact	aattttctgc	120
tctgaggtat	cagatgagta	gccgatggaa	tcgtacgac	tacgttggtga	atttgctctg	180
agatattcgc	aagtgtgag	ttgaagatct	ctctacaag	tatggaccaa	ttgtggacat	240
tgatttgaag	attccaccga	gacctctctg	ttatgctctt	gtcagatttg	aagatccctg	300
tgatgcagac	gatgcaattt	atggacgtga	tggttatgat	tttgatgggt	gtcgactctg	360
ggttgagatt	gcacatgggt	gtcgtagatt	ttcaccatca	gttgataggt	acagcagcag	420
ctacagtgcg	agccgtgcac	cttcaagacg	ctctgactat	cgcgtgcttg	tgaccggatt	480
accgctctct	gcttctgtgc	aggaccttaa	ggatcacatg	cgcaaaagctg	gagatgctct	540
cttctctgaa	gttttccctg	accgtaaaag	catgtctctg	gttgctggatt	atagcaacta	600
tgatgatgat	aagtacgcaa	taaggaaact	tgatgccact	gaatttcgaa	atgctttctc	660
tgatgcttat	agtcagggtga	gggaatatga	gtcgaggagt	gtgagtcgaa	gccagcatga	720
ttctaagaag	tatagaagca	ggagtcggag	ccgtggtcca	agctgtagct	atagtagcaa	780
gagcaggagt	gtgtcacctg	ctagatccat	ttcccccggt	tcacggcccc	ttagtctgtc	840
tcgtctgccca	tacagctctc	ttctcaaggct	ccaatcaaga	tcaaaatcaa	gatCAACAYc	900
aGgatcaaga	tcgaattctc	cagtttcacc	gtgtatatct	ggatgaaaaa	gaaaactggc	960
cactggctgt	accggaatct	ttctcaagctt	ctcaggtctc	actgctaata	gaatttgatt	1020
ccgattttgg	attattatac	tggtcttctt	gtatgggaag	accaatatgt	ctttctagtt	1080
ctagtgttga	acctggaatt	ggtctgttat	tggtctcatta	aaaagccgga	aactctgtct	1140
cggctgcata	ataaagtcca	ctcagcgttg	tggtgggtgt	ggtgaggttt	ttccatacat	1200
atacatttac	att					

(2) INFORMATION FOR SEQ ID NO:1089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..270
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

Met	Ser	Ser	Arg	Trp	Asn	Arg	Thr	Ile	Tyr	Val	Gly	Asn	Leu	Pro	Gly
1			5						10					15	
Asp	Ile	Arg	Lys	Cys	Glu	Val	Glu	Asp	Leu	Phe	Tyr	Lys	Tyr	Gly	Pro
			20						25				30		
Ile	Val	Asp	Ile	Asp	Leu	Lys	Ile	Pro	Pro	Arg	Pro	Pro	Gly	Tyr	Ala
			35				40					45			
Phe	Val	Glu	Phe	Glu	Asp	Pro	Arg	Asp	Ala	Asp	Asp	Ala	Ile	Tyr	Gly
			50				55				60				
Arg	Asp	Gly	Tyr	Asp	Phe	Asp	Gly	Cys	Arg	Leu	Arg	Val	Glu	Ile	Ala
					70					75				80	
His	Gly	Gly	Arg	Arg	Phe	Ser	Pro	Ser	Val	Asp	Arg	Tyr	Ser	Ser	Ser
					85					90				95	
Tyr	Ser	Ala	Ser	Arg	Ala	Pro	Ser	Arg	Arg	Ser	Asp	Tyr	Arg	Val	Leu
					100					105				110	
Val	Thr	Gly	Leu	Pro	Pro	Ser	Ala	Ser	Trp	Gln	Asp	Leu	Lys	Asp	His
					115					120				125	
Met	Arg	Lys	Ala	Gly	Asp	Val	Cys	Phe	Ser	Glu	Val	Phe	Pro	Asp	Arg
							135					140			
Lys	Gly	Met	Ser	Gly	Val	Val	Asp	Tyr	Ser	Asn	Tyr	Asp	Asp	Met	Lys
							150				155				160
Tyr	Ala	Ile	Arg	Lys	Leu	Asp	Ala	Thr	Glu	Phe	Arg	Asn	Ala	Phe	Ser
							165				170				175
Ser	Ala	Tyr	Ile	Arg	Val	Arg	Glu	Tyr	Glu	Ser	Arg	Ser	Val	Ser	Arg
							185						190		
Ser	Pro	Asp	Asp	Ser	Lys	Ser	Tyr	Arg	Ser	Arg	Ser	Arg	Ser	Arg	Gly
							200					205			
Pro	Ser	Cys	Ser	Tyr	Ser	Ser	Lys	Ser	Arg	Ser	Val	Ser	Pro	Ala	Arg
							215					220			
Ser	Ile	Ser	Pro	Arg	Ser	Arg	Pro	Leu	Ser	Arg	Ser	Arg	Ser	Pro	Tyr

(2) INFORMATION FOR SEQ ID NO:1090:

(A) LENGTH: 142 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(1x) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..142
(D) OTHER INFORMATION
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Lys | Ala | Gly | Asp | Val | Cys | Phe | Ser | Glu | Val | Phe | Pro | Asp | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Gly | Met | Ser | Gly | Val | Val | Asp | Tyr | Ser | Asn | Tyr | Asp | Asp | Met | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Ala | Ile | Arg | Lys | Leu | Asp | Ala | Thr | Glu | Phe | Arg | Asn | Ala | Phe | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ser | Ala | Tyr | Ile | Arg | Val | Arg | Glu | Tyr | Glu | Ser | Arg | Ser | Val | Ser | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Pro | Asp | Asp | Ser | Lys | Ser | Tyr | Arg | Ser | Arg | Ser | Arg | Ser | Arg | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Ser | Cys | Ser | Tyr | Ser | Ser | Lys | Ser | Arg | Ser | Val | Ser | Pro | Ala | Arg |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Ile | Ser | Pro | Arg | Ser | Arg | Pro | Leu | Ser | Arg | Ser | Arg | Ser | Pro | Tyr |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Ser | Val | Ser | Arg | Ser | Gln | Ser | Arg | Ser | Lys | Ser | Arg | Ser | Thr | Xaa |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Ser | Arg | Ser | Asn | Ser | Pro | Val | Ser | Pro | Val | Ile | Ser | Gly |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

```
(ix) FEATURE:
```

- (A) NAME/KEY: -  
(B) LOCATION: 1..1204  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568962

|             |             |            |             |             |            |     |
|-------------|-------------|------------|-------------|-------------|------------|-----|
| atataaaaaa  | accatatctc  | tcactctctc | ttctctctct  | ttcttatcaat | attctgcgat | 60  |
| tttcccctct  | ctgtgtgttat | agaagatctc | ggcgagctagc | gtcaaccaaa  | aagaacaacc | 120 |
| agtatctgtc  | tcagaatgag  | agtttttoca | gaagacaaaa  | gtcatttcga  | tgcgtaacag | 180 |
| tcacaaacag  | tatctaacag  | cagacgcaga | tgaagaaacc  | gattctcaaa  | accgtaacgg | 240 |
| attaccaaa   | aacgttcgat  | ggcgcgtcga | accggttgat  | gatctttctc  | atgtttatga | 300 |
| tctttaaagc  | ttgttcagta  | agttactatc | cgctcttaac  | gacgcgttct  | tgctcggagc | 360 |
| tcacgggaag  | aagtagattc  | agttgaaact | gactggcgggt | gattctctgt  | ttgagtggga | 420 |
| acogggttaga | gaagtagctc  | agattaaagt | taggactaga  | ttgtgtaact  | attaccgagg | 480 |
| taagtggagt  | cttctctctt  | ggataaacct | ggtcacacac  | gaocgttctc  | atttgtctgc | 540 |
| tactacgat   | tcgattttct  | ggagttgtga | tgttgttgag  | atcttgactg  | attccgaatt | 600 |
| ccagacggag  | ttctcgaaag  | cgcgcgcacc | gaagacgacg  | ttctccaccg  | cgcctacggg | 660 |
| accgcagagt  | tcgccgttgt  | cgcgtcgact | tccaagacGt  | tcgtttcttc  | tttcagacag | 720 |
| atccgattca  | gactcggttg  | agcttcgcgc | taaatctgat  | ggacgaacca  | tatatatcca | 780 |
| ttctcgtgac  | gaggaacgac  | acgttggaga | tgaacaaccc  | tgttgatgat  | cttccagttt | 840 |

|            |             |            |            |            |             |      |
|------------|-------------|------------|------------|------------|-------------|------|
| taaaggaat  | agcgtggcgg  | agctgactca | gacattgcga | gaagaaacgt | gcattggaaga | 900  |
| cgctgtggtg | tgtacttgta  | gtcctttaaa | cggaagctg  | tttctcttc  | gtttgcaact  | 960  |
| tcctctaac  | aacggaaacat | tgcatgtcat | tttactaccc | tccagcgca  | gcctctagaa  | 1020 |
| tcgaccggag | acaattagaa  | atgagtgatt | gtttgtgtaa | gcatagttta | tgagtcattt  | 1080 |
| tactaccctc | cagcgcgagc  | ctctagaatc | gaccogagac | aattagaaat | gagtgattgt  | 1140 |
| gtgattgttt | gggtgaagcat | atgttatgaa | cogtataaga | agatagtaag | agttggtagt  | 1200 |
| tggt       |             |            |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:1092:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 338 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..338

(D) OTHER INFORMATION: / Ceres Seq. ID 1568963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Lys | Ile | Thr | Ile | Ser | Leu | Thr | Ser | Ser | Ser | Ser | Ser | Ser | Tyr | His |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Tyr | Ser | Leu | Ile | Ser | Pro | Ser | Leu | Leu | Gln | Lys | Ser | Thr | Ala | Ser |     |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ser | Phe | Asn | Gln | Lys | Glu | Thr | Pro | Val | Ser | Val | Ser | Ala | Met | Glu | Phe |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Gln | Lys | Ala | Lys | Ala | Ile | Arg | Met | Arg | Asn | Ser | His | Asn | Lys | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Thr | Ala | Asp | Asp | Asp | Glu | Glu | Thr | Val | Thr | Gln | Asn | Arg | Asn | Gly |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Thr | Lys | Asn | Val | Arg | Trp | Thr | Val | Glu | Pro | Val | Arg | Asp | Ser | Phe |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| His | Val | Ile | Arg | Leu | Lys | Ser | Cys | Tyr | Gly | Lys | Tyr | Leu | Thr | Ala | Ser |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Asn | Glu | Arg | Phe | Leu | Leu | Gly | Ala | Thr | Gly | Lys | Lys | Val | Ile | Gln | Leu |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Lys | Leu | Ser | Arg | Val | Asp | Ser | Ser | Val | Glu | Trp | Glu | Pro | Val | Arg | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Ser | Lys | Ile | Lys | Leu | Arg | Thr | Arg | Ser | Gly | Asn | Tyr | Leu | Arg | Gly |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Asn | Gly | Gly | Leu | Pro | Pro | Trp | Arg | Asn | Ser | Val | Thr | His | Asp | Val | Pro |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |
| His | Leu | Ser | Ala | Thr | Gln | Asp | Ser | Ile | Ser | Trp | Asp | Val | Asp | Val | Val |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Glu | Ile | Leu | Thr | Asp | Ser | Glu | Phe | Gln | Thr | Glu | Ser | Ala | Lys | Ala | Pro |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Pro | Pro | Lys | Thr | Thr | Ser | Pro | Pro | Pro | His | Arg | Arg | Pro | Thr | Ser | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Pro | Leu | Ser | Ala | Glu | Ser | Pro | Arg | Thr | Ser | Ser | Ser | Leu | Ser | Asp | Arg |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Ser | Asp | Ser | Asp | Ser | Val | Glu | Ser | Pro | Pro | Lys | Ser | Asp | Gly | Arg | Thr |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Ile | Tyr | Tyr | His | Val | Ala | Asp | Glu | Glu | Gly | His | Val | Glu | Asp | Glu | Thr |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Thr | Val | Gly | Tyr | Ala | Phe | Thr | Phe | Lys | Gly | Asn | Ser | Val | Ala | Glu | Leu |
|     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Thr | Gln | Thr | Leu | Arg | Glu | Glu | Thr | Cys | Met | Glu | Asp | Ala | Val | Val | Cys |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Thr | Arg | Ser | Pro | Leu | Asn | Gly | Lys | Leu | Phe | Pro | Leu | Arg | Leu | Gln | Leu |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |
| Pro | Pro | Asn | Asn | Gly | Thr | Leu | His | Val | Ile | Leu | Leu | Pro | Ser | Ser | Ala |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     | 335 |     |     |

Ser Leu

(2) INFORMATION FOR SEQ ID NO:1093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..293
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Phe | Phe | Gln | Lys | Ala | Lys | Ala | Ile | Arg | Met | Arg | Asn | Ser | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Lys | Tyr | Leu | Thr | Ala | Asp | Asp | Asp | Glu | Glu | Thr | Val | Thr | Gln | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Asn | Gly | Ser | Thr | Lys | Asn | Val | Arg | Trp | Thr | Val | Glu | Pro | Val | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ser | Phe | His | Val | Ile | Arg | Leu | Lys | Ser | Cys | Tyr | Gly | Lys | Tyr | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Thr | Ala | Ser | Asn | Glu | Arg | Phe | Leu | Leu | Gly | Ala | Thr | Gly | Lys | Lys | Val |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Gln | Leu | Lys | Leu | Ser | Arg | Val | Asp | Ser | Ser | Val | Glu | Trp | Glu | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Arg | Glu | Gly | Ser | Lys | Ile | Lys | Leu | Arg | Thr | Arg | Ser | Gly | Asn | Tyr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Arg | Gly | Asn | Gly | Gly | Leu | Pro | Pro | Trp | Arg | Asn | Ser | Val | Thr | His |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Val | Pro | His | Leu | Ser | Ala | Thr | Gln | Asp | Ser | Ile | Ser | Trp | Asp | Val |
|     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Asp | Val | Val | Glu | Ile | Leu | Thr | Asp | Ser | Glu | Phe | Gln | Thr | Glu | Ser | Ala |
|     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Lys | Ala | Pro | Pro | Pro | Lys | Thr | Thr | Ser | Pro | Pro | Pro | His | Arg | Arg | Pro |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Thr | Ser | Ser | Pro | Leu | Ser | Ala | Glu | Ser | Pro | Arg | Thr | Ser | Ser | Ser | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Asp | Arg | Ser | Asp | Ser | Asp | Ser | Val | Glu | Ser | Pro | Pro | Lys | Ser | Asp |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Arg | Thr | Ile | Tyr | Tyr | His | Val | Ala | Asp | Glu | Glu | Gly | His | Val | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asp | Glu | Thr | Thr | Val | Gly | Tyr | Ala | Phe | Thr | Phe | Lys | Gly | Asn | Ser | Val |
|     | 225 |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Ala | Glu | Leu | Thr | Gln | Thr | Leu | Arg | Glu | Glu | Thr | Cys | Met | Glu | Asp | Ala |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Val | Val | Cys | Thr | Arg | Ser | Pro | Leu | Asn | Gly | Lys | Leu | Phe | Pro | Leu | Arg |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Leu | Gln | Leu | Pro | Pro | Asn | Asn | Gly | Thr | Leu | His | Val | Ile | Leu | Leu | Pro |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |

Ser Ser Ala Ser Leu  
290

(2) INFORMATION FOR SEQ ID NO:1094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..282

(D) OTHER INFORMATION: / Ceres Seq. ID 1568965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

```
Met Arg Asn Ser His Asn Lys Tyr Leu Thr Ala Asp Asp Asp Glu Glu
1 5 10 15
Thr Val Thr Gln Asn Arg Asn Gly Ser Thr Lys Asn Val Arg Trp Thr
20 25 30
Val Glu Pro Val Arg Asp Ser Phe His Val Ile Arg Leu Lys Ser Cys
35 40 45
Tyr Gly Lys Tyr Leu Thr Ala Ser Asn Glu Arg Phe Leu Leu Gly Ala
50 55 60
Thr Gly Lys Lys Val Ile Gln Leu Lys Leu Ser Arg Val Asp Ser Ser
65 70 75 80
Val Glu Trp Glu Pro Val Arg Glu Gly Ser Lys Ile Lys Leu Arg Thr
85 90 95
Arg Ser Gly Asn Tyr Leu Arg Gly Asn Gly Gly Leu Pro Trp Arg
100 105 110
Asn Ser Val Thr His Asp Val Pro His Leu Ser Ala Thr Gln Asp Ser
115 120 125
Ile Ser Trp Asp Val Asp Val Val Glu Ile Leu Thr Asp Ser Glu Phe
130 135 140
Gln Thr Glu Ser Ala Lys Ala Pro Pro Lys Thr Thr Ser Pro Pro
145 150 155 160
Pro His Arg Arg Pro Thr Ser Ser Pro Leu Ser Ala Glu Ser Pro Arg
165 170 175
Thr Ser Ser Ser Leu Ser Asp Arg Ser Asp Ser Asp Ser Val Glu Ser
180 185 190
Pro Pro Lys Ser Asp Gly Arg Thr Ile Tyr Tyr His Val Ala Asp Glu
195 200 205
Glu Gly His Val Glu Asp Glu Thr Thr Val Gly Tyr Ala Phe Thr Phe
210 215 220
Lys Gly Asn Ser Val Ala Glu Leu Thr Gln Thr Leu Arg Glu Glu Thr
225 230 235 240
Cys Met Glu Asp Ala Val Val Cys Thr Arg Ser Pro Leu Asn Gly Lys
245 250 255
Leu Phe Pro Leu Arg Leu Gln Leu Pro Pro Asn Asn Gly Thr Leu His
260 265 270
Val Ile Leu Leu Pro Ser Ser Ala Ser Leu
275 280
```

(2) INFORMATION FOR SEQ ID NO:1095:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1043 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1043

(D) OTHER INFORMATION: / Ceres Seq. ID 1568966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

```
aaaagtgtggc cactaagtgg tgtaagaata ataaattgtc aatatcaatt gactgattct 60
tattgttcat atacggacac aaatcttttc gttaagttag tgttttgatac aaaaaaagt 120
gaaaacttta aagccatgcc atcacttttg tctaacgaat ccgatggatac attacgagag 180
catcttgtgg atgtgttgtt gtctgtttca gaaccaaaga ttccgggtaca tgactgacc 240
cgagtcgccg atgatggatc tcggatcttg aaaggagtta cgtatagatat accaaaaggt 300
atgatcgctt gtgtgattgg acctagtgga agtgaaagt caacgttttt gagatctctg 360
aatcgtcttt ggggaaccac ggagtcgaact gtgtctcttg accggtgaaga taaaaccaac 420
gttgatgtta ttgctctctg tcgtagagtt ggaatgcctt tcagctctcc tgttcttttt 480
caagggaactg ttgcggataa tgtgagatat ggtccgaatt tgagagggga gaaactaagt 540
gacgaagaggg ttataagctt gctaagctct gcagacacttg atgcttctct tgctaagaag 600
```

```

actgggtgcag agttatctgt gggtaacgt caacgagtag cacttgcaag gactctagcc 660
aacgagcctg aggtgttctt gctcgatgaa caacaacgtg ctcttgatcc gatatcgaca 720
gagaaacatt aggatgttat agtgaaactg aagaagcaga gagggattac tactgtgatt 780
gtttctcaca gtatcaagca gattcagaaa gttgctgata tcgtttgcct tgttctcgac 840
ggagagattg ttgaagttct taaaccaagt gagctttcgc acgCtacgca tccaatggca 900
cagaggtttc ttcaactcag ttcttgagac catctttctca ttgattggttc ctgcaagtta 960
tttgctatct tgcttgaaac ttaataatct ctttcaagag aggaacaaaat gctgggtgaa 1020
tgtaacaaca cctttcatgg ttt

```

(2) INFORMATION FOR SEQ ID NO:1096:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..263

(D) OTHER INFORMATION: / Ceres Seq. ID 1568967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

```

Met Pro Ser Leu Trp Ser Asn Glu Ser Asp Gly Ser Leu Arg Glu His
1 5 10 15
Leu Val Asp Val Val Ser Gly Ser Glu Pro Lys Ile Arg Val His
20 25 30
Asp Leu Thr Arg Val Ala Asp Asp Gly Ser Arg Ile Leu Lys Gly Val
35 40 45
Thr Ile Asp Ile Pro Lys Gly Met Ile Val Gly Val Ile Gly Pro Ser
50 55 60
Gly Ser Gly Lys Ser Thr Phe Leu Arg Ser Leu Asn Arg Leu Trp Glu
65 70 75 80
Pro Pro Glu Ser Thr Val Phe Leu Asp Gly Glu Asp Ile Thr Asn Val
85 90 95
Asp Val Ile Ala Leu Arg Arg Arg Val Gly Met Leu Phe Gln Leu Pro
100 105 110
Val Leu Phe Gln Gly Thr Val Ala Asp Asn Val Arg Tyr Gly Pro Asn
115 120 125
Leu Arg Gly Glu Lys Leu Ser Asp Glu Glu Val Tyr Lys Leu Leu Ser
130 135 140
Leu Ala Asp Leu Asp Ala Ser Phe Ala Lys Lys Thr Gly Ala Glu Leu
145 150 155
Ser Val Gly Gln Ala Gln Arg Val Ala Leu Ala Arg Thr Leu Ala Asn
160 165 170 175
Glu Pro Glu Val Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Pro
180 185 190
Ile Ser Thr Glu Asn Ile Glu Asp Val Ile Val Lys Leu Lys Lys Gln
195 200 205
Arg Gly Ile Thr Thr Val Ile Val Ser His Ser Ile Lys Gln Ile Gln
210 215 220
Lys Val Ala Asp Ile Val Cys Leu Val Val Asp Gly Glu Ile Val Glu
225 230 235 240
Val Leu Lys Pro Ser Glu Leu Ser His Ala Thr His Pro Met Ala Gln
245 250 255
Arg Phe Leu Gln Leu Ser Ser
260

```

(2) INFORMATION FOR SEQ ID NO:1097:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 1568968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

```
Met Ile Val Gly Val Ile Gly Pro Ser Gly Ser Gly Lys Ser Thr Phe
1 5 10 15
Leu Arg Ser Leu Asn Arg Leu Trp Glu Pro Pro Glu Ser Thr Val Phe
 20 25 30
Leu Asp Gly Glu Asp Ile Thr Asn Val Asp Val Ile Ala Leu Arg Arg
 35 40 45
Arg Val Gly Met Leu Phe Gln Leu Pro Val Leu Phe Gln Gly Thr Val
 50 55 60
Ala Asp Asn Val Arg Tyr Gly Pro Asn Leu Arg Gly Glu Lys Leu Ser
 65 70 75 80
Asp Glu Glu Val Tyr Lys Leu Leu Ser Leu Ala Asp Leu Asp Ala Ser
 85 90 95
Phe Ala Lys Lys Thr Gly Ala Glu Leu Ser Val Gly Gln Ala Gln Arg
 100 105 110
Val Ala Leu Ala Arg Thr Leu Ala Asn Glu Pro Glu Val Leu Leu Leu
 115 120 125
Asp Glu Pro Thr Ser Ala Leu Asp Pro Ile Ser Thr Glu Asn Ile Glu
 130 135 140
Asp Val Ile Val Lys Leu Lys Lys Gln Arg Gly Ile Thr Thr Val Ile
 145 150 155 160
Val Ser His Ser Ile Lys Gln Ile Gln Lys Val Ala Asp Ile Val Cys
 165 170 175
Leu Val Val Asp Gly Glu Ile Val Glu Val Leu Lys Pro Ser Glu Leu
 180 185 190
Ser His Ala Thr His Pro Met Ala Gln Arg Phe Leu Gln Leu Ser Ser
 195 200 205
```

(2) INFORMATION FOR SEQ ID NO:1098:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1568969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

```
Met Leu Phe Gln Leu Pro Val Leu Phe Gln Gly Thr Val Ala Asp Asn
1 5 10 15
Val Arg Tyr Gly Pro Asn Leu Arg Gly Glu Lys Leu Ser Asp Glu Glu
 20 25 30
Val Tyr Lys Leu Leu Ser Leu Ala Asp Leu Asp Ala Ser Phe Ala Lys
 35 40 45
Lys Thr Gly Ala Glu Leu Ser Val Gly Gln Ala Gln Arg Val Ala Leu
 50 55 60
Ala Arg Thr Leu Ala Asn Glu Pro Glu Val Leu Leu Leu Asp Glu Pro
 65 70 75 80
Thr Ser Ala Leu Asp Pro Ile Ser Thr Glu Asn Ile Glu Asp Val Ile
 85 90 95
Val Lys Leu Lys Lys Gln Arg Gly Ile Thr Thr Val Ile Val Ser His
 100 105 110
Ser Ile Lys Gln Ile Gln Lys Val Ala Asp Ile Val Cys Leu Val Val
 115 120 125
```



Asp Gly Glu Ile Val Glu Val Leu Lys Pro Ser Glu Leu Ser His Ala  
130 135 140  
Thr His Pro Met Ala Gln Arg Phe Leu Gln Leu Ser Ser  
145 150 155

(2) INFORMATION FOR SEQ ID NO:1099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1218
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:

|             |            |            |            |            |            |      |
|-------------|------------|------------|------------|------------|------------|------|
| atgttcacca  | cttcacctct | ctctctcttt | cttctccact | gtaacctccc | aattcaaaaa | 60   |
| caattataaa  | ccaaacttga | ttaatatata | tttctttatc | atcatctctt | cgaatgcaa  | 120  |
| gatattcatg  | attttcccat | gaacggagtt | ggtggtgggg | gaggaggagg | agggagggtt | 180  |
| ttcgggtggag | gaatcgccgg | cggaggaggt | ggtgatcgaa | ggatgagagc | tcatcagaac | 240  |
| aatatactta  | accatcatca | atctctcaag | tgtcctcggt | gtaattctct | taacacaaag | 300  |
| ttctgttact  | acaacaattt | caatctttct | cagcctcgct | acttttgcaa | gaactgtcgt | 360  |
| cgttactcga  | ctaaagggtg | tgttctcgt  | aacgttccc  | tcggagggtg | ttgccggaaa | 420  |
| gctaaacggt  | cgaaaaacaa | acaggttccg | tctgtctcat | cagccgacaa | accaacgacg | 480  |
| acgcaagatg  | atcatcacgt | ggaggagaaa | tcgagtcacg | gatctcaact | tagcagcgag | 540  |
| agctctcttc  | tcacgcgttc | taactctacc | acgtgctccg | ccgtctccgt | caccgcggcg | 600  |
| gcggaagtgt  | cttcgctcgt | tattccaggt | tttgatagtc | ctaataatga | aatttacggt | 660  |
| aacgggatcg  | agtgtcgac  | gttacttgga | caaggctcat | cggccgggtg | tgttttctcg | 720  |
| gagatcggtg  | gttttccggc | ggtttcagct | attgaaacta | caccgttttg | attcgggggt | 780  |
| aaattcgtaa  | atcaaatgta | tcactcgaag | tagaagggtg | aaactgtaca | gcagcaacag | 840  |
| tttggaacgt  | gaacggctca | ggttgagttt | caagggaagt | cttcgatcc  | gaatatggga | 900  |
| tttgaacgtg  | tggattgggg | aagtgccggt | ggagatcaaa | cactgtttga | tttaaccagt | 960  |
| accgttgatc  | atgcatactg | gagtcacaa  | caatggacgt | cgtctgacca | agatcagagt | 1020 |
| ggtctctacc  | ttccttgatt | ctgatcatag | cttcttcttc | tttaaccaaa | aatatatatt | 1080 |
| ttatacacat  | aaggtaaagt | tcgatgaagt | ggttttttwa | attttTattt | gatggGtCta | 1140 |
| aaAcgggatt  | Tattatataa | ttatatgact | gottgtaaat | ttttTccca  | aatatacaat | 1200 |
| ttacctctct  | tttttttt   |            |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:1100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..307
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Asp | Ile | His | Asp | Phe | Ser | Met | Asn | Gly | Val | Gly | Gly | Gly | Gly |
| 1   |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |     |
| Gly | Gly | Gly | Gly | Arg | Phe | Phe | Gly | Gly | Gly | Ile | Gly | Gly | Gly | Gly | Gly |
|     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Gly | Asp | Arg | Arg | Met | Arg | Ala | His | Gln | Asn | Asn | Ile | Leu | Asn | His | His |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gln | Ser | Leu | Lys | Cys | Pro | Arg | Cys | Asn | Ser | Leu | Asn | Thr | Lys | Phe | Cys |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Tyr | Tyr | Asn | Asn | Tyr | Asn | Leu | Ser | Gln | Pro | Arg | His | Phe | Cys | Lys | Asn |
|     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Cys | Arg | Arg | Tyr | Trp | Thr | Lys | Gly | Gly | Val | Leu | Arg | Asn | Val | Pro | Val |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |

Tyr Leu Pro  
305

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Gly | Val | Gly | Gly | Gly | Gly | Gly | Gly | Gly | Gly | Arg | Phe | Phe | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Gly | Ile | Gly | Gly | Gly | Gly | Gly | Asp | Arg | Arg | Met | Arg | Ala | His |     |
|     |     | 20  |     |     |     |     |     | 25  |     |     | 30  |     |     |     |     |
| Gln | Asn | Asn | Ile | Leu | Asn | His | Gln | Ser | Leu | Lys | Cys | Pro | Arg | Cys |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Asn | Ser | Leu | Asn | Thr | Lys | Phe | Cys | Tyr | Tyr | Asn | Asn | Tyr | Asn | Leu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gln | Pro | Arg | His | Phe | Cys | Lys | Asn | Cys | Arg | Arg | Tyr | Trp | Thr | Lys | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Val | Leu | Arg | Asn | Val | Pro | Val | Gly | Gly | Gly | Cys | Arg | Lys | Ala | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Ser | Lys | Thr | Lys | Gln | Val | Pro | Ser | Ser | Ser | Ser | Ala | Asp | Lys | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Thr | Thr | Gln | Asp | Asp | His | His | Val | Glu | Glu | Lys | Ser | Ser | Thr | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | His | Ser | Ser | Ser | Glu | Ser | Ser | Ser | Leu | Thr | Ala | Ser | Asn | Ser | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Val | Ala | Ala | Val | Ser | Val | Thr | Ala | Ala | Ala | Glu | Val | Ala | Ser | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Val | Ile | Pro | Gly | Phe | Asp | Met | Pro | Asn | Met | Lys | Ile | Tyr | Gly | Asn | Gly |

(2) INFORMATION FOR SEQ ID NO:1102:

(A) LENGTH: 271 amino acids

(A) LENGTH: 271 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1568977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ala | His | Gln | Asn | Asn | Ile | Leu | Asn | His | His | Gln | Ser | Leu | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Cys | Pro | Arg | Cys | Asn | Ser | Leu | Asn | Thr | Lys | Phe | Cys | Tyr | Tyr | Asn | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Asn | Leu | Ser | Gln | Pro | Arg | His | Phe | Cys | Lys | Asn | Cys | Arg | Arg | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Trp | Thr | Lys | Gly | Val | Leu | Arg | Asn | Val | Pro | Val | Gly | Gly | Gly | Cys |     |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Arg | Lys | Ala | Lys | Arg | Ser | Lys | Thr | Lys | Gln | Val | Pro | Ser | Ser | Ser | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Asp | Lys | Pro | Thr | Thr | Gln | Asp | Asp | His | His | Val | Glu | Glu | Lys |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Ser | Thr | Gly | Ser | His | Ser | Ser | Ser | Glu | Ser | Ser | Ser | Leu | Thr | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Asn | Ser | Thr | Thr | Val | Ala | Ala | Val | Ser | Val | Thr | Ala | Ala | Ala | Glu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Ala | Ser | Ser | Val | Ile | Pro | Gly | Phe | Asp | Met | Pro | Asn | Met | Lys | Ile |
|     |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     |     |
| Tyr | Gly | Asn | Gly | Ile | Glu | Trp | Ser | Thr | Leu | Leu | Gly | Gln | Gly | Ser | Ser |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Ala | Gly | Gly | Val | Phe | Ser | Glu | Ile | Gly | Gly | Phe | Pro | Ala | Val | Ser | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Glu | Thr | Thr | Pro | Phe | Gly | Phe | Gly | Gly | Lys | Phe | Val | Asn | Gln | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | His | Leu | Lys | Leu | Glu | Gly | Glu | Thr | Val | Gln | Gln | Gln | Gln | Gly |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asp | Arg | Thr | Ala | Gln | Val | Glu | Phe | Gln | Gly | Arg | Ser | Ser | Asp | Pro | Asn |
|     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Met | Gly | Phe | Glu | Pro | Leu | Asp | Trp | Gly | Ser | Gly | Gly | Gly | Asp | Gln | Thr |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Leu | Phe | Asp | Leu | Thr | Ser | Thr | Val | Asp | His | Ala | Tyr | Trp | Ser | Gln | Ser |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |

Gln Trp Thr Ser Ser Asp Gln Asp Gln Ser Gly Leu Tyr Leu Pro  
260 265 270

(2) INFORMATION FOR SEQ ID NO:1103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1484
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

|             |             |             |             |            |             |      |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| acgggtcaat  | ttgatttgga  | taataattct  | ctttttctct  | ggaaagtctg | aatttttttt  | 60   |
| tgtttggaag  | ctctggagaa  | atattatact  | cttctcattg  | aatgatcaat | ttacaaatcc  | 120  |
| tcatttgatc  | gatctttgtc  | atttttgaaa  | aaaaaaatct  | gaactttgag | aaagatttat  | 180  |
| gagttttgat  | atctgtcggg  | catggtttga  | ttgtggctgt  | tgggtaagac | aacaaattag  | 240  |
| ggtttttgaa  | tagttttgtg  | attgaagatt  | gtctgaaatg  | gaagcagcta | ttactcagag  | 300  |
| gattcagtac  | ccatcatggg  | ttgattgtag  | aaaagttaga  | tgtaaagcgc | agcgtgggtc  | 360  |
| attgcggtat  | ttctcagcag  | ttaaaggtaga | tgaaggtttt  | agaggtcttt | ctttggctcg  | 420  |
| cttgcacact  | gaagaagaaa  | ttgatcaacg  | aagacagatt  | ttctcagcgg | ttctcgtgtc  | 480  |
| tgataaacct  | ttctcagcgt  | ttgtggagac  | tggaaagtgt  | tatccatttg | atgaagatat  | 540  |
| ttcacaagaga | aaagcagaag  | aggttaaacc  | gtatttgaat  | ggacgatcta | tgtaccttgt  | 600  |
| cggaaatgat  | gggtcttgga  | aaacaactgt  | gggaaagtta  | atgtccaaag | tgctcggtta  | 660  |
| tacgttcttt  | gactgcgaca  | ctttgattga  | gggcgatgaa  | tggaaactct | gttgacagaga | 720  |
| tatttgttca  | tcacggagag  | aattttttta  | gaggaaagga  | gaccgatcgc | cttaagaagc  | 780  |
| ttcttctcag  | ttatcaagtt  | gttgtttcca  | caggtggagg  | tgacgttata | agacccatta  | 840  |
| actggaagta  | tatgcataaa  | ggaatcacga  | tttggtctaga | tgtgcctcta | gaagcattag  | 900  |
| cccatagaa   | cgtctgtgtt  | ggaactgatt  | cacgaccact  | gtacacagat | gaatcaggag  | 960  |
| atgcatactc  | agtgctcttc  | aaacgtctct  | cggctatttg  | ggacgagcgc | ggtagaagcat | 1020 |
| acacaaacgc  | aaatgccaga  | ttctccttag  | aaaataattg  | agcaaaagct | ggctataaaa  | 1080 |
| atgtctcaga  | ttctcacacca | actgaaattt  | gtatcgaggc  | cttcagacaa | gttctgagct  | 1140 |
| ttctagagaa  | agaagaaaact | atggagatcc  | cagacggcga  | ctctaatatt | ccacgccttc  | 1200 |
| tgttctcogt  | ctcttcattt  | atctgtttta  | tcaactaaac  | gaagcaatca | ctcatcacca  | 1260 |
| ggccattgag  | caagttcaga  | gacaaagaag  | acctctagtt  | actggttccg | gttcatttga  | 1320 |
| gcttacacga  | gcctaatttt  | gactggaaact | atggtttatt  | aaaagaagat | tcaatacatg  | 1380 |
| tatatataaa  | atataatact  | ttttttttgt  | ttcagtatca  | ttctttctct | cttttccctta | 1440 |
| caataagaat  | taaggaaaa   | tagccgtgtt  | tgtaacatg   | ggcc       |             |      |

(2) INFORMATION FOR SEQ ID NO:1104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Ala | Ala | Ile | Thr | Gln | Arg | Ile | Gln | Tyr | Pro | Ser | Trp | Val | Asp |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Cys | Arg | Lys | Val | Glu | Cys | Lys | Pro | Gln | Arg | Gly | Ser | Leu | Arg | Tyr | Ser |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Gln | Gln | Val | Lys | Val | Asp | Arg | Arg | Phe | Arg | Gly | Leu | Ser | Leu | Ala | Arg |  |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |  |
| Leu | Gln | Pro | Glu | Arg | Arg | Ile | Asp | Gln | Arg | Arg | Ala | Val | Ser | Pro | Ala |  |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |  |
| Val | Ser | Cys | Ser | Asp | Asn | Asn | Ser | Ser | Ala | Leu | Leu | Glu | Thr | Gly | Ser |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Pro | Phe | Asp | Glu | Asp | Ile | Leu | Lys | Arg | Lys | Ala | Glu | Glu | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Pro | Tyr | Leu | Asn | Gly | Arg | Ser | Met | Tyr | Leu | Val | Gly | Met | Met | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Gly | Lys | Thr | Thr | Val | Gly | Lys | Leu | Met | Ser | Lys | Val | Leu | Gly | Tyr |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Thr | Phe | Phe | Asp | Cys | Asp | Thr | Leu | Ile | Glu | Gly | Asp | Glu | Trp | Asn | Phe |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Cys | Cys | Arg | Asp | Ile | Cys | Ser | Ser | Arg | Arg | Glu | Phe | Phe |     |     |     |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1568980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Gly | Thr | Ser | Val | Ala | Glu | Ile | Phe | Val | His | His | Gly | Glu | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Phe | Arg | Gly | Lys | Glu | Thr | Asp | Ala | Leu | Lys | Lys | Leu | Ser | Ser | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Gln | Val | Val | Val | Ser | Thr | Gly | Gly | Gly | Ala | Val | Ile | Arg | Pro | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Trp | Lys | Tyr | Met | His | Lys | Gly | Ile | Ser | Ile | Trp | Leu | Asp | Val | Pro |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Glu | Ala | Leu | Ala | His | Arg | Ile | Ala | Ala | Val | Gly | Thr | Asp | Ser | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Leu | Leu | His | Asp | Glu | Ser | Gly | Asp | Ala | Tyr | Ser | Val | Ala | Phe | Lys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Arg | Leu | Ser | Ala | Ile | Trp | Asp | Glu | Arg | Gly | Glu | Ala | Tyr | Thr | Asn | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Ala | Arg | Val | Ser | Leu | Glu | Asn | Ile | Ala | Ala | Lys | Arg | Gly | Tyr | Lys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Val | Ser | Asp | Leu | Thr | Pro | Thr | Glu | Ile | Cys | Ile | Glu | Ala | Phe | Glu |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Val | Leu | Ser | Phe | Leu | Glu | Lys | Glu | Glu | Thr | Met | Glu | Ile | Pro | Asp |
|     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Gly | Asp | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1568981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Lys | Gly | Ile | Ser | Ile | Trp | Leu | Asp | Val | Pro | Leu | Glu | Ala | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | His | Arg | Ile | Ala | Ala | Val | Gly | Thr | Asp | Ser | Arg | Pro | Leu | Leu | His |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Asp | Glu | Ser | Gly | Asp | Ala | Tyr | Ser | Val | Ala | Phe | Lys | Arg | Leu | Ser | Ala |

(2) INFORMATION FOR SEQ ID NO:1107:

(A) LENGTH: 1196 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1569006

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| tccaacaattc | gtctctcccca | acagtttttct | tctctctctc | ttcttttggtg | gtctccctcca | 60   |
| ccaacggcgag | aaatagattt  | ggctaatctct | tcccctctct | ctctgatctct | ctgatcgccg  | 120  |
| cgcgggaagac | tcaattttccc | gtgttagtcca | caaaaaaaa  | actctccggt  | tttatttttc  | 180  |
| cccttttttcc | acccgttgga  | gtttcccgag  | atggtgtcac | ccgaataacg  | taattggatt  | 240  |
| tgctgacttga | tcgatgtctg  | taacggaggt  | ttcaacaatc | acgtctctgt  | ttctctctgt  | 300  |
| ccgtgtcaagc | aacctatgga  | gtttctctct  | aactccagtg | ctggagttda  | tggctcggct  | 360  |
| ggaactcagc  | aagctagcaa  | agaaacttga  | tcctaaaaga | ggggagagtg  | tgaatcatcc  | 420  |
| ttctgccatac | tcgctgaagc  | atgtagaagc  | aagcagcgac | gggaacagtg  | gaatgacaa   | 480  |
| tttatggaa   | tggttggaat  | tttggagcct  | ggaaatctct | ccaaaacaga  | caagctgtgt  | 540  |
| atctttggtg  | atgtctgtcc  | catgtgtgaa  | cagctacggg | cgcaggccca  | gaagctgaag  | 600  |
| gcctccaatt  | caagtcttca  | gagacaatac  | aaagatttaa | agactctaaa  | aaacgcagctg | 660  |
| cgagatgaga  | aacagaggct  | gaagacagag  | aaagaaaagc | tggagacaga  | gctgaaagct  | 720  |
| attaatgtctc | ctcaaccaag  | tttttttcca  | ggcccacata | tgatgctcac  | tgttttaagc  | 780  |
| tcagcggcaag | gccaaagctc  | tggaaacaa   | atggtgccaa | tcatcagtta  | cccaggagtt  | 840  |
| gcgatctggc  | agttcatgcc  | ctctcgtctc  | gtcgataact | ctcaggaata  | tgtctctcgt  | 900  |
| ctctcgttgt  | cttaaacatc  | aaaaatcatc  | aaacggtttg | cttcttgtct  | cgccttaaaa  | 960  |
| gaaagactct  | catttgtttt  | gcctctctct  | ctttctgaag | tttctctatc  | ttatctcttt  | 1020 |
| gctgttgctg  | gtttatcatg  | taactgtctt  | ctgttgaaac | atgatataac  | attgtaaact  | 1080 |
| ccaattgctt  | cgcgcaatgt  | tatctatata  | catgtaaat  | taagtagatg  | ttagcgagatc | 1140 |
| gtctctcact  | ttatgttttc  | ttacatatta  | acatagaatg | tggttacttc  | ctctgcc     |      |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1569007

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ser | Val | Pro | Glu | Asn | Ala | Asn | Trp | Ile | Cys | Asp | Leu | Ile | Asp | Ala |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Tyr | Gly | Ser | Phe | Thr | Ile | Gln | Gly | Pro | Gly | Phe | Ser | Trp | Pro | Val |     |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gln | Gln | Pro | Ile | Gly | Val | Ser | Ser | Asn | Ser | Ser | Ala | Gly | Val | Asp | Gly |     |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Ser | Ala | Gly | Asn | Ser | Glu | Ala | Ser | Lys | Glu | Pro | Gly | Ser | Lys | Lys | Arg |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |

Gly Arg Cys Glu Ser Ser Ser Ala Thr Ser Ser Lys Ala Cys Arg Glu  
65 70 75 80  
Lys Gln Arg Arg Asp Arg Leu Asn Asp Lys Phe Met Glu Leu Gly Ala  
85 90 95  
Ile Leu Glu Pro Gly Asn Pro Pro Lys Thr Asp Lys Ala Ala Ile Leu  
100 105 110  
Val Asp Ala Val Arg Met Val Thr Gln Leu Arg Gly Glu Ala Gln Lys  
115 120 125  
Leu Lys Asp Ser Asn Ser Ser Leu Gln Asp Lys Ile Lys Glu Leu Lys  
130 135 140  
Thr Glu Lys Asn Glu Leu Arg Asp Glu Lys Gln Arg Leu Lys Thr Glu  
145 150 155 160  
Lys Glu Lys Leu Glu Gln Gln Leu Lys Ala Ile Asn Ala Pro Gln Pro  
165 170 175  
Ser Phe Phe Pro Ala Pro Pro Met Met Pro Thr Ala Phe Ala Ser Ala  
180 185 190  
Gln Gly Gln Ala Pro Gly Asn Lys Met Val Pro Ile Ile Ser Tyr Pro  
195 200 205  
Gly Val Ala Met Trp Gln Phe Met Pro Pro Ala Ser Val Asp Thr Ser  
210 215 220  
Gln Asp His Val Leu Arg Pro Pro Val Ala  
225 230

(2) INFORMATION FOR SEQ ID NO:1109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1569008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

Met Glu Leu Gly Ala Ile Leu Glu Pro Gly Asn Pro Pro Lys Thr Asp  
1 5 10 15  
Lys Ala Ala Ile Leu Val Asp Ala Val Arg Met Val Thr Gln Leu Arg  
20 25 30  
Gly Glu Ala Gln Lys Leu Lys Asp Ser Asn Ser Ser Leu Gln Asp Lys  
35 40 45  
Ile Lys Glu Leu Lys Thr Glu Lys Asn Glu Leu Arg Asp Glu Lys Gln  
50 55 60  
Arg Leu Lys Thr Glu Lys Glu Lys Leu Glu Gln Gln Leu Lys Ala Ile  
65 70 75 80  
Asn Ala Pro Gln Pro Ser Phe Phe Pro Ala Pro Pro Met Met Pro Thr  
85 90 95  
Ala Phe Ala Ser Ala Gln Gly Gln Ala Pro Gly Asn Lys Met Val Pro  
100 105 110  
Ile Ile Ser Tyr Pro Gly Val Ala Met Trp Gln Phe Met Pro Pro Ala  
115 120 125  
Ser Val Asp Thr Ser Gln Asp His Val Leu Arg Pro Pro Val Ala  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1569009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

```
Met Val Thr Gln Leu Arg Gly Glu Ala Gln Lys Leu Lys Asp Ser Asn
1 5 10 15
Ser Ser Leu Gln Asp Lys Ile Lys Glu Leu Lys Thr Glu Lys Asn Glu
20 25 30
Leu Arg Asp Glu Lys Gln Arg Leu Lys Thr Glu Lys Glu Lys Leu Glu
35 40 45
Gln Gln Leu Lys Ala Ile Asn Ala Pro Gln Pro Ser Phe Phe Pro Ala
50 55 60
Pro Pro Met Met Pro Thr Ala Phe Ala Ser Ala Gln Gly Gln Ala Pro
65 70 75 80
Gly Asn Lys Met Val Pro Ile Ile Ser Tyr Pro Gly Val Ala Met Trp
85 90 95
Gln Phe Met Pro Pro Ala Ser Val Asp Thr Ser Gln Asp His Val Leu
100 105 110
Arg Pro Pro Val Ala
115
```

(2) INFORMATION FOR SEQ ID NO:1111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1936 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1936

(D) OTHER INFORMATION: / Ceres Seq. ID 1569025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

```
gaagtagatg ttctgtaaca acaatggcca aaacacagag gtcttgtgtt ctctgcaacg 60
ctctaatacgc tatagctttt ttggcgacag Cccatttgtg tgaagctggc ttgtctcaga 120
aagaacagga caaggtctcg aaattgccctg tgcagaattt ttgtctcaact 180
actctggggt ttgtctact aatgagcaat tgggaagagc tctcttttac tggttatttg 240
aagccgttga agatgctaag tctaagcctc ttgttctctg gctcaatgga ggaccaggat 300
gttcattctgt tgcataatgg gaagcagaag agataggacc atttcacatt aaggcagatg 360
ggaaaactct ttaccttaat caatattctt ggaacaaagc tgcaaatatt ttgttctctg 420
atgcacctgt ttgagttggg tattcatact caaacacctc gtctgatttg aagagcaatg 480
gtgataaaa aactgcggaa gactcactga aatttctgct gaaatggggt gagcggtttc 540
cggaatacaa aggaagggac ttttatatag taggggagag ctatgcagga cattacattc 600
ctcagcttga tgaagccatt taaaacata accaaggttc tgacaaaaac agtataaatc 660
tgaagggtta catgttagga aatgggctga tggacgattt ccatgacagg cttggtcttt 720
tccaatatat ttggtcgttg ggttttatat ctgacaaaac atacagctta ctgcaacttc 780
aatgcgggtt cgaatcggtt attcactctt ccaaacagtg taacaagatt ctggagatag 840
cggacaaaaga aataggtaac atagaccaat acagtgtctt caacccagct tgtgttgcca 900
atgcttcocca gtcaaatatg ttgtctaaaga aaagacctat gactagccgc gtgagcgaa 960
agtatgatcc ttgtacggag aaacacacta cagtttattt caactctcca gaggtctcaa 1020
aagccctcca ttgtccaccca ggaacttgac catcaaaatg ggataacttg agtgatgtg 1080
tgagtgtaaa ctggaaatgac tctcttctct cggttctaaa catttaccac gaggttatag 1140
ctgctggggtc tcgtatctgg gtttctcagt gggagcgaga tgccgttgta ccagtcacat 1200
caaccgggta cagtatcgat gcactaaacc ttgctctctt ggggtgcctat ggtccttggt 1260
acttagatgc acaggtggga ggggtggatc agcagtatgc tggctcgaac ttgtgacag 1320
tgagaggtgc aggcocatga gttctcttgc acagaccgga gcaagctctt cgcctctcca 1380
aggcttttat atctggaact ccaattgtcca cacatgagaa cagcatcagc cgcgacatgt 1440
ctgaactcgt tagtgactca taattgagttc tgatttgatg taatgtgtga ttgtattct 1500
caatcaaaaaa cttccacatc aggcggttga aataagaaga gggaagaga ataatcaat 1560
gttttaagtgc atcagttcaa tgcttctctt tctcttggtt gtttgttgtt ttggataaac 1620
atttgtcgtc ttgaattctaa taaaagaagt ttctaccatt tgcagcacat agcatccttg 1680
aataacaaca acatattctt gtgtaatgag aaagtgaagt ctgatctgtg atgtatagga 1740
ctgggtatta atctggtaac ggtataataa ctggggtaga aaatgaatt tagactagta 1800
```



ttgggggtct aaacgaatt atacagaagc attgggcttg acttggccca tgagacctaa 1860  
gcccataattt taaagaatta ggggtttctt ctctctttgt ctgttcaaat tgaagaaaacc 1920  
tggttttttt tatttc

(2) INFORMATION FOR SEQ ID NO:1112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..486

(D) OTHER INFORMATION: / Ceres Seq. ID 1569026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ile | Val | Ser | Val | Thr | Thr | Met | Ala | Lys | Thr | Arg | Gly | Ser | Cys | Cys |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Val | Asn | Ala | Leu | Ile | Ala | Ile | Ala | Phe | Leu | Ala | Thr | Ala | His | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Glu | Ala | Gly | Leu | Ser | Gln | Lys | Glu | Gln | Asp | Lys | Val | Ser | Lys | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Gly | Gln | Asn | Phe | Asn | Val | Ser | Phe | Ala | His | Tyr | Ser | Gly | Phe | Val |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Thr | Asn | Glu | Gln | Leu | Gly | Arg | Ala | Leu | Phe | Tyr | Trp | Leu | Phe | Glu |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Val | Glu | Asp | Ala | Lys | Ser | Lys | Pro | Leu | Val | Leu | Trp | Leu | Asn | Gly |
|     |     |     |     |     | 85  |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Pro | Gly | Cys | Ser | Ser | Val | Ala | Tyr | Gly | Glu | Ala | Glu | Glu | Ile | Gly |
|     |     |     |     |     |     | 100 |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Phe | His | Ile | Lys | Ala | Asp | Gly | Lys | Thr | Leu | Tyr | Leu | Asn | Gln | Tyr |
|     |     |     |     |     |     | 115 |     | 120 |     |     |     | 125 |     |     |     |
| Ser | Trp | Asn | Gln | Ala | Ala | Asn | Ile | Leu | Phe | Leu | Asp | Ala | Pro | Val | Gly |
|     |     |     |     |     |     | 130 |     | 135 |     |     | 140 |     |     |     |     |
| Val | Gly | Tyr | Ser | Tyr | Ser | Asn | Thr | Ser | Ser | Asp | Leu | Lys | Ser | Asn | Gly |
|     |     |     |     |     |     | 145 |     | 150 |     | 155 |     |     |     |     | 160 |
| Asp | Lys | Arg | Thr | Ala | Glu | Asp | Ser | Leu | Lys | Phe | Leu | Leu | Lys | Trp | Val |
|     |     |     |     |     | 165 |     |     | 170 |     |     |     |     |     | 175 |     |
| Glu | Arg | Phe | Pro | Glu | Tyr | Lys | Gly | Arg | Asp | Phe | Tyr | Ile | Val | Gly | Glu |
|     |     |     |     |     | 180 |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Tyr | Ala | Gly | His | Tyr | Ile | Pro | Gln | Leu | Ser | Glu | Ala | Ile | Val | Lys |
|     |     |     |     |     | 195 |     | 200 |     |     |     |     | 205 |     |     |     |
| His | Asn | Gln | Gly | Ser | Asp | Lys | Asn | Ser | Ile | Asn | Leu | Lys | Gly | Tyr | Met |
|     |     |     |     |     |     | 210 |     | 215 |     |     |     | 220 |     |     |     |
| Val | Gly | Asn | Gly | Leu | Met | Asp | Asp | Phe | His | Asp | Arg | Leu | Gly | Leu | Phe |
|     |     |     |     |     | 225 |     | 230 |     |     | 235 |     |     |     |     | 240 |
| Gln | Tyr | Ile | Trp | Ser | Leu | Gly | Phe | Ile | Ser | Asp | Gln | Thr | Tyr | Ser | Leu |
|     |     |     |     |     | 245 |     |     | 250 |     |     |     |     |     | 255 |     |
| Leu | Gln | Leu | Gln | Cys | Gly | Phe | Glu | Ser | Phe | Ile | His | Ser | Ser | Lys | Gln |
|     |     |     |     |     | 260 |     |     | 265 |     |     |     |     |     | 270 |     |
| Cys | Asn | Lys | Ile | Leu | Glu | Ile | Ala | Asp | Lys | Glu | Ile | Gly | Asn | Ile | Asp |
|     |     |     |     |     | 275 |     |     | 280 |     |     |     | 285 |     |     |     |
| Gln | Tyr | Ser | Val | Phe | Thr | Pro | Ala | Cys | Val | Ala | Asn | Ala | Ser | Gln | Ser |
|     |     |     |     |     |     | 290 |     | 295 |     |     | 300 |     |     |     |     |
| Asn | Met | Leu | Leu | Lys | Lys | Arg | Pro | Met | Thr | Ser | Arg | Val | Ser | Glu | Gln |
|     |     |     |     |     |     | 305 |     | 310 |     | 315 |     |     |     |     | 320 |
| Tyr | Asp | Pro | Cys | Thr | Glu | Lys | His | Thr | Thr | Val | Tyr | Phe | Asn | Leu | Pro |
|     |     |     |     |     | 325 |     |     | 330 |     |     |     |     | 335 |     |     |
| Glu | Val | Gln | Lys | Ala | Leu | His | Val | Pro | Pro | Gly | Leu | Ala | Pro | Ser | Lys |
|     |     |     |     |     | 340 |     |     | 345 |     |     |     |     | 350 |     |     |
| Trp | Asp | Thr | Cys | Ser | Asp | Val | Val | Ser | Glu | His | Trp | Asn | Asp | Ser | Pro |
|     |     |     |     |     | 355 |     |     | 360 |     |     |     |     | 365 |     |     |

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Ser Ser Val Leu Asn Ile Tyr His Glu Leu Ile Ala Ala Gly Leu Arg
370 375 380
Ile Trp Val Phe Ser Gly Asp Ala Asp Ala Val Val Pro Val Thr Ser
385 390 395 400
Thr Arg Tyr Ser Ile Asp Ala Leu Asn Leu Arg Pro Leu Gly Ala Tyr
405 410 415
Gly Pro Trp Tyr Leu Asp Gly Gln Val Gly Gly Trp Ser Gln Gln Tyr
420 425 430
Ala Gly Leu Asn Phe Val Thr Val Arg Gly Ala Gly His Glu Val Pro
435 440 445
Leu His Arg Pro Lys Gln Ala Leu Ala Leu Phe Lys Ala Phe Ile Ser
450 455 460
Gly Thr Pro Leu Ser Thr His Glu Asn Ser Ile Ser Arg Asp Met Ser
465 470 475 480
Glu Leu Val Ser Asp Ser
485

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(2) INFORMATION FOR SEQ ID NO:1113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..479
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

```

Met Ala Lys Thr Arg Gly Ser Cys Cys Leu Val Asn Ala Leu Ile Ala
1 5 10 15
Ile Ala Phe Leu Ala Thr Ala His Leu Cys Glu Ala Gly Leu Ser Gln
20 25 30
Lys Glu Gln Asp Lys Val Ser Lys Leu Pro Gly Gln Asn Phe Asn Val
35 40 45
Ser Phe Ala His Tyr Ser Gly Phe Val Ala Thr Asn Glu Gln Leu Gly
50 55 60
Arg Ala Leu Phe Tyr Trp Leu Phe Glu Ala Val Glu Asp Ala Lys Ser
65 70 75 80
Lys Pro Leu Val Leu Trp Leu Asn Gly Gly Pro Gly Cys Ser Ser Val
85 90 95
Ala Tyr Gly Glu Ala Glu Glu Ile Gly Pro Phe His Ile Lys Ala Asp
100 105 110
Gly Lys Thr Leu Tyr Leu Asn Gln Tyr Ser Trp Asn Gln Ala Ala Asn
115 120 125
Ile Leu Phe Leu Asp Ala Pro Val Gly Val Gly Tyr Ser Tyr Ser Asn
130 135 140
Thr Ser Ser Asp Leu Lys Ser Asn Gly Asp Lys Arg Thr Ala Glu Asp
145 150 155 160
Ser Leu Lys Phe Leu Leu Lys Trp Val Glu Arg Phe Pro Glu Tyr Lys
165 170 175
Gly Arg Asp Phe Tyr Ile Val Gly Glu Ser Tyr Ala Gly His Tyr Ile
180 185 190
Pro Gln Leu Ser Glu Ala Ile Val Lys His Asn Gln Gly Ser Asp Lys
195 200 205
Asn Ser Ile Asn Leu Lys Gly Tyr Met Val Gly Asn Gly Leu Met Asp
210 215 220
Asp Phe His Asp Arg Leu Gly Leu Phe Gln Tyr Ile Trp Ser Leu Gly
225 230 235 240
Phe Ile Ser Asp Gln Thr Tyr Ser Leu Leu Gln Leu Gln Cys Gly Phe
245 250 255
Glu Ser Phe Ile His Ser Ser Lys Gln Cys Asn Lys Ile Leu Glu Ile

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260 265 270  
Ala Asp Lys Glu Ile Gly Asn Ile Asp Gln Tyr Ser Val Phe Thr Pro  
275 280 285  
Ala Cys Val Ala Asn Ala Ser Gln Ser Asn Met Leu Leu Lys Lys Arg  
290 295 300  
Pro Met Thr Ser Arg Val Ser Glu Gln Tyr Asp Pro Cys Thr Glu Lys  
305 310 315  
His Thr Thr Val Tyr Phe Asn Leu Pro Glu Val Gln Lys Ala Leu His  
325 330 335  
Val Pro Pro Gly Leu Ala Pro Ser Lys Trp Asp Thr Cys Ser Asp Val  
340 345 350  
Val Ser Glu His Trp Asn Asp Ser Pro Ser Ser Val Leu Asn Ile Tyr  
355 360 365  
His Glu Leu Ile Ala Ala Gly Leu Arg Ile Trp Val Phe Ser Gly Asp  
370 375 380  
Ala Asp Ala Val Val Pro Val Thr Ser Thr Arg Tyr Ser Ile Asp Ala  
385 390 395  
Leu Asn Leu Arg Pro Leu Gly Ala Tyr Gly Pro Trp Tyr Leu Asp Gly  
405 410 415  
Gln Val Gly Gly Trp Ser Gln Gln Tyr Ala Gly Leu Asn Phe Val Thr  
420 425 430  
Val Arg Gly Ala Gly His Glu Val Pro Leu His Arg Pro Lys Gln Ala  
435 440 445  
Leu Ala Leu Phe Lys Ala Phe Ile Ser Gly Thr Pro Leu Ser Thr His  
450 455 460  
Glu Asn Ser Ile Ser Arg Asp Met Ser Glu Leu Val Ser Asp Ser  
465 470 475

(2) INFORMATION FOR SEQ ID NO:1114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..263
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

Met Val Gly Asn Gly Leu Met Asp Asp Phe His Asp Arg Leu Gly Leu  
1 5 10 15  
Phe Gln Tyr Ile Trp Ser Leu Gly Phe Ile Ser Asp Gln Thr Tyr Ser  
20 25 30  
Leu Leu Gln Leu Gln Cys Gly Phe Glu Ser Phe Ile His Ser Ser Lys  
35 40 45  
Gln Cys Asn Lys Ile Leu Glu Ile Ala Asp Lys Glu Ile Gly Asn Ile  
50 55 60  
Asp Gln Tyr Ser Val Phe Thr Pro Ala Cys Val Ala Asn Ala Ser Gln  
65 70 75 80  
Ser Asn Met Leu Leu Lys Lys Arg Pro Met Thr Ser Arg Val Ser Glu  
85 90 95  
Gln Tyr Asp Pro Cys Thr Glu Lys His Thr Thr Val Tyr Phe Asn Leu  
100 105 110  
Pro Glu Val Gln Lys Ala Leu His Val Pro Pro Gly Leu Ala Pro Ser  
115 120 125  
Lys Trp Asp Thr Cys Ser Asp Val Val Ser Glu His Trp Asn Asp Ser  
130 135 140  
Pro Ser Ser Val Leu Asn Ile Tyr His Glu Leu Ile Ala Ala Gly Leu  
145 150 155 160  
Arg Ile Trp Val Phe Ser Gly Asp Ala Val Val Pro Val Thr  
165 170 175

Ser Thr Arg Tyr Ser Ile Asp Ala Leu Asn Leu Arg Pro Leu Gly Ala  
180 185 190  
Tyr Gly Pro Trp Tyr Leu Asp Gly Gln Val Gly Gly Trp Ser Gln Gln  
195 200 205  
Tyr Ala Gly Leu Asn Phe Val Thr Val Arg Gly Ala Gly His Glu Val  
210 215 220  
Pro Leu His Arg Pro Lys Gln Ala Leu Ala Leu Phe Lys Ala Phe Ile  
225 230 235 240  
Ser Gly Thr Pro Leu Ser Thr His Glu Asn Ser Ile Ser Arg Asp Met  
245 250 255  
Ser Glu Leu Val Ser Asp Ser  
260

(2) INFORMATION FOR SEQ ID NO:1115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1666
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| ctgattacga | tccaatcctc | tccgatcggt | ggcctcctgt | ttccgtttta | ctcgacatcg | 60   |
| ttccgacgac | ttttgacctg | gaatcgacgc | agtgaattca | attcaactat | tcacattggt | 120  |
| ttgttgga   | tggaacaaag | agcacctcct | agtaattttg | tgaatgatgg | gtcatttcag | 180  |
| gaaagattca | gacagcttca | acaggagaaa | gataaagaca | aggataaggt | tgccaagtt  | 240  |
| gaggattcta | agcccggtga | gattatatca | aatcccaaac | ctgctgtcaa | taaaatttcc | 300  |
| attggattaa | agcccaatga | tgcccagaag | aaagggtgga | agcttgcttt | cagcttgaag | 360  |
| caaaagtcta | agctctttgc | acctcctgtg | aagcttggtg | cagaagaaga | tgaggatgat | 420  |
| gaggatgtta | aacatgaaca | aggcttttga | tcogtaaaag | gtcaaaagt  | agagcagaga | 480  |
| gacacacctg | taaagtcaag | aaaagtatcg | gatgttgac  | cacctccgcc | cagtgatcgt | 540  |
| actgtgaaga | aagtgtctga | taaaactaga | agttttgtg  | ctaagcatgt | aaggccattt | 600  |
| gagcacatta | cacggcaaaa | gaatcctggg | gatacaccat | ttaaatttct | ttttgacgag | 660  |
| aactgtgcgg | actacaagta | ctatgtattc | aggctggctg | aagaggaaaa | attaatttca | 720  |
| caaaccaagg | attctggtgt | acttcacagt | ggtgatgcag | gctcggaacc | gtccacagca | 780  |
| gcaatccctt | tgcaaaagcc | agcttatcaa | caaacaggat | atcagatccc | tgctccagct | 840  |
| ctctatgata | ctcctgtgga | acctggagct | tcctctagat | ctgctcaggc | atcaattaga | 900  |
| agaccagcgc | acagtgactc | ctttagtggg | ccgaggggtg | cagaccctct | atcaatagat | 960  |
| gagcttttca | tgaagaaggg | tgcccagaag | gagaaataga | gagcttctag | cagctcaaaa | 1020 |
| gagcaaatgc | ctccaccagc | ttcccttcaa | ggcccatctg | aaacttcctc | caagaccctc | 1080 |
| ggaagaagag | gtcatcacat | gggtgattat | atcccacttg | AGgagctaga | taagtctcct | 1140 |
| tcaaagtgca | atgacgcagc | tgacacaaaa | gccacaaaag | aggctgctga | gaaagcgaag | 1200 |
| atccagcag  | ataatgttgg | acataaactc | ttgtcaaaaa | tggtgtgaaa | agaaggtgaa | 1260 |
| gggtattgaa | gctccagaaa | gggtatggca | gacctataaa | tgccaggcga | tgtaaagaca | 1320 |
| aacaaacttg | gagttggtgc | ttccgctcca | ggagaagtca | agcctgagga | tgatatatac | 1380 |
| gagcagta   | agaagcggat | gatgctgggt | tacaaacaca | gaccacatcc | actgggaaat | 1440 |
| ccaggaaggg | cgtattacta | aggatcaaat | caatgtgtta | tgcgcaatta | ttatctttgg | 1500 |
| ttcacctcag | cacgctctga | gctttgcttt | tctattataa | agaattgtca | agcttttaga | 1560 |
| ttactgat   | attgaagtgt | tggtatgc   | tgaatttgcg | tttcagtggt | caaatagatc | 1620 |
| tccttgacag | acatatcagt | tgaaatacaa | tggattttgt | attgcc     |            |      |

(2) INFORMATION FOR SEQ ID NO:1116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..486

(D) OTHER INFORMATION: / Ceres Seq. ID 1569030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Thr | Ile | Gln | Ser | Ser | Pro | Ile | Val | Gly | Leu | Leu | Phe | Pro | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Ser | Thr | Ser | Phe | Arg | Arg | Leu | Leu | Thr | Trp | Asn | Arg | Arg | Ser | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Asn | Ser | Thr | Ile | Ala | Leu | Gly | Leu | Ala | Met | Asp | Lys | Gly | Ala |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Pro | Pro | Ser | Ile | Phe | Val | Asn | Asp | Gly | Ser | Phe | Met | Glu | Arg | Phe | Arg |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Leu | Gln | Gln | Glu | Lys | Asp | Lys | Asp | Lys | Val | Val | Gln | Val |     |     |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |     |
| Glu | Asp | Ser | Lys | Pro | Val | Lys | Ile | Ile | Ser | Asn | Pro | Lys | Pro | Ala | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |     |
| Asn | Lys | Ile | Ser | Ile | Gly | Leu | Lys | Pro | Asn | Asp | Ala | Gln | Lys | Lys | Gly |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Gly | Lys | Leu | Ala | Phe | Ser | Leu | Lys | Gln | Lys | Ser | Lys | Leu | Leu | Ala | Pro |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Val | Lys | Leu | Gly | Thr | Glu | Glu | Asp | Glu | Asp | Asp | Glu | Asp | Val | Lys |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| His | Glu | Gln | Gly | Phe | Gly | Ser | Val | Lys | Arg | Gln | Lys | Leu | Glu | Gln | Arg |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Asp | Thr | Pro | Val | Lys | Ser | Ala | Lys | Val | Ser | Asp | Val | Ala | Pro | Pro | Pro |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Pro | Ser | Asp | Pro | Thr | Val | Lys | Lys | Val | Ala | Asp | Lys | Leu | Ala | Ser | Phe |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Val | Ala | Lys | His | Gly | Arg | Pro | Phe | Glu | His | Ile | Thr | Arg | Gln | Lys | Asn |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Gly | Asp | Thr | Pro | Phe | Lys | Phe | Leu | Phe | Asp | Glu | Asn | Cys | Ala | Asp |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Tyr | Lys | Tyr | Tyr | Val | Phe | Arg | Leu | Ala | Glu | Glu | Glu | Lys | Leu | Ile | Ser |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Gln | Thr | Lys | Asp | Ser | Gly | Val | Leu | His | Ser | Gly | Asp | Ala | Gly | Ser | Arg |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Thr | Ser | Thr | Ala | Ala | Ile | Pro | Leu | Gln | Lys | Pro | Ala | Tyr | Gln | Gln | Thr |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Gly | Tyr | Gln | Ile | Pro | Ala | Ser | Ala | Leu | Tyr | Asp | Thr | Pro | Val | Glu | Pro |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Ala | Ser | Ser | Arg | Ser | Ala | Gln | Ala | Ser | Ile | Thr | Arg | Pro | Ser | Asp |
|     |     |     | 290 |     |     | 295 |     |     |     |     |     | 300 |     |     |     |
| Ser | Asp | Ser | Phe | Ser | Gly | Pro | Arg | Gly | Ala | Asp | Pro | Leu | Ser | Met | Met |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     | 320 |
| Glu | Phe | Tyr | Met | Lys | Lys | Ala | Ala | Gln | Glu | Glu | Lys | Met | Arg | Arg | Pro |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     | 335 |     |     |     |
| Arg | Gln | Ser | Lys | Asp | Glu | Met | Pro | Pro | Pro | Ala | Ser | Leu | Gln | Gly | Pro |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Ser | Glu | Thr | Ser | Ser | Thr | Asp | Pro | Gly | Lys | Arg | Gly | His | His | Met | Gly |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Asp | Tyr | Ile | Pro | Leu | Glu | Glu | Leu | Asp | Lys | Phe | Leu | Ser | Lys | Cys | Asn |
|     |     |     | 370 |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Asp | Ala | Ala | Ala | Gln | Lys | Ala | Thr | Lys | Glu | Ala | Ala | Glu | Lys | Ala | Lys |
| 385 |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |     |
| Ile | Gln | Ala | Asp | Asn | Val | Gly | His | Lys | Leu | Leu | Ser | Lys | Met | Gly | Trp |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |     |
| Lys | Glu | Gly | Glu | Gly | Ile | Gly | Ser | Arg | Lys | Gly | Met | Ala | Asp | Pro |     |
|     |     |     | 420 |     |     |     | 425 |     |     |     |     | 430 |     |     |     |
| Ile | Met | Ala | Gly | Asp | Val | Lys | Thr | Asn | Asn | Leu | Gly | Val | Gly | Ala | Ser |
|     |     |     | 435 |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Ala | Pro | Gly | Glu | Val | Lys | Pro | Glu | Asp | Asp | Ile | Tyr | Glu | Gln | Tyr | Lys |
|     |     |     | 450 |     |     | 455 |     |     |     |     |     | 460 |     |     |     |

Lys Arg Met Met Leu Gly Tyr Lys His Arg Pro Asn Pro Leu Gly Asn  
465 470 475 480  
Pro Arg Lys Ala Tyr Tyr  
485

(2) INFORMATION FOR SEQ ID NO:1117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..443
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Lys | Gly | Ala | Pro | Pro | Ser | Ile | Phe | Val | Asn | Asp | Gly | Ser | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Glu | Arg | Phe | Arg | Gln | Leu | Gln | Gln | Glu | Lys | Asp | Lys | Asp | Lys | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Val | Val | Gln | Val | Glu | Asp | Ser | Lys | Pro | Val | Lys | Ile | Ile | Ser | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Lys | Pro | Ala | Ala | Asn | Lys | Ile | Ser | Ile | Gly | Leu | Lys | Pro | Asn | Asp |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Gln | Lys | Lys | Gly | Gly | Lys | Leu | Ala | Phe | Ser | Leu | Lys | Gln | Lys | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Leu | Leu | Ala | Pro | Pro | Val | Lys | Leu | Gly | Thr | Glu | Glu | Asp | Glu | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Asp | Glu | Asp | Val | Lys | His | Glu | Gln | Gly | Phe | Gly | Ser | Val | Lys | Arg | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Leu | Glu | Gln | Arg | Asp | Thr | Pro | Val | Lys | Ser | Ala | Lys | Val | Ser | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Ala | Pro | Pro | Pro | Pro | Ser | Asp | Pro | Thr | Val | Lys | Lys | Val | Ala | Asp |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Leu | Ala | Ser | Phe | Val | Ala | Lys | His | Gly | Arg | Pro | Phe | Glu | His | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Arg | Gln | Lys | Asn | Pro | Gly | Asp | Thr | Pro | Phe | Lys | Phe | Leu | Phe | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Asn | Cys | Ala | Asp | Tyr | Lys | Tyr | Tyr | Val | Phe | Arg | Leu | Ala | Glu | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Lys | Leu | Ile | Ser | Gln | Thr | Lys | Asp | Ser | Gly | Val | Leu | His | Ser | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asp | Ala | Gly | Ser | Arg | Thr | Ser | Thr | Ala | Ala | Ile | Pro | Leu | Gln | Lys | Pro |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Tyr | Gln | Gln | Thr | Gly | Tyr | Gln | Ile | Pro | Ala | Ser | Ala | Leu | Tyr | Asp |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Thr | Pro | Val | Glu | Pro | Gly | Ala | Ser | Ser | Arg | Ser | Ala | Gln | Ala | Ser | Ile |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Arg | Pro | Ser | Asp | Ser | Asp | Ser | Phe | Ser | Gly | Pro | Arg | Gly | Ala | Asp |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Pro | Leu | Ser | Met | Met | Glu | Phe | Tyr | Met | Lys | Lys | Ala | Ala | Gln | Glu | Glu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Lys | Met | Arg | Arg | Pro | Arg | Gln | Ser | Lys | Asp | Glu | Met | Pro | Pro | Pro | Ala |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ser | Leu | Gln | Gly | Pro | Ser | Glu | Thr | Ser | Ser | Thr | Asp | Pro | Gly | Lys | Arg |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Gly | His | His | Met | Gly | Asp | Tyr | Ile | Pro | Leu | Glu | Glu | Leu | Asp | Lys | Phe |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Ser | Lys | Cys | Asn | Asp | Ala | Ala | Ala | Gln | Lys | Ala | Thr | Lys | Glu | Ala |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ala | Glu | Lys | Ala | Lys | Ile | Gln | Ala | Asp | Asn | Val | Gly | His | Lys | Leu | Leu |

(2) INFORMATION FOR SEQ ID NO:1118:

(A) LENGTH: 427 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..427

(D) OTHER INFORMATION: / Ceres Seq. ID 1569032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Glu<br>1   | Arg<br>1   | Phe<br>1   | Arg<br>5   | Gln<br>1   | Leu<br>1   | Gln<br>1   | Gln<br>10  | Lys<br>1   | Asp<br>1   | Lys<br>1   | Asp<br>1   | Lys<br>15  | Asp<br>1   |
| Lys<br>1   | Val<br>1   | Val<br>1   | Gln<br>20  | Val<br>20  | Glu<br>1   | Asp<br>1   | Ser<br>1   | Lys<br>25  | Pro<br>1   | Val<br>1   | Lys<br>1   | Ile<br>30  | Ile<br>30  | Asn<br>1   |
| Pro<br>1   | Lys<br>35  | Pro<br>35  | Ala<br>1   | Ala<br>1   | Asn<br>1   | Lys<br>40  | Ile<br>40  | Ser<br>1   | Ile<br>1   | Gly<br>1   | Leu<br>45  | Lys<br>45  | Pro<br>1   | Asn<br>1   |
| Ala<br>50  | Gln<br>50  | Lys<br>1   | Lys<br>1   | Gly<br>1   | Gly<br>55  | Lys<br>55  | Leu<br>1   | Ala<br>1   | Phe<br>1   | Ser<br>60  | Leu<br>60  | Lys<br>1   | Gln<br>1   | Ser<br>1   |
| Lys<br>65  | Leu<br>65  | Leu<br>1   | Ala<br>1   | Pro<br>70  | Pro<br>70  | Val<br>1   | Lys<br>1   | Leu<br>1   | Gly<br>75  | Thr<br>75  | Glu<br>1   | Asp<br>1   | Glu<br>80  | Asp<br>1   |
| Asp<br>1   | Glu<br>1   | Asp<br>1   | Val<br>85  | Lys<br>85  | His<br>1   | Glu<br>1   | Gln<br>1   | Gly<br>90  | Phe<br>90  | Gly<br>1   | Ser<br>1   | Val<br>1   | Lys<br>95  | Arg<br>1   |
| Lys<br>1   | Leu<br>100 | Glu<br>100 | Gln<br>1   | Arg<br>1   | Asp<br>1   | Thr<br>1   | Pro<br>105 | Val<br>105 | Lys<br>1   | Ser<br>1   | Ala<br>1   | Lys<br>110 | Val<br>110 | Asp<br>1   |
| Val<br>1   | Ala<br>115 | Pro<br>115 | Pro<br>1   | Pro<br>1   | Ser<br>1   | Ser<br>120 | Asp<br>120 | Pro<br>1   | Thr<br>1   | Val<br>1   | Lys<br>125 | Lys<br>125 | Val<br>1   | Ala<br>1   |
| Lys<br>130 | Leu<br>130 | Ala<br>1   | Ser<br>1   | Phe<br>1   | Val<br>135 | Ala<br>135 | Lys<br>1   | His<br>1   | Gly<br>1   | Arg<br>140 | Pro<br>140 | Phe<br>1   | Glu<br>1   | Ile<br>1   |
| Thr<br>145 | Arg<br>145 | Gln<br>1   | Lys<br>1   | Asn<br>150 | Pro<br>150 | Gly<br>1   | Asp<br>1   | Thr<br>1   | Pro<br>1   | Phe<br>155 | Lys<br>1   | Phe<br>1   | Leu<br>1   | Asp<br>160 |
| Glu<br>1   | Asn<br>165 | Cys<br>165 | Ala<br>1   | Asp<br>165 | Tyr<br>1   | Lys<br>1   | Tyr<br>1   | Tyr<br>170 | Val<br>170 | Phe<br>1   | Arg<br>1   | Leu<br>175 | Ala<br>175 | Glu<br>1   |
| Glu<br>1   | Lys<br>180 | Leu<br>180 | Ile<br>1   | Ser<br>180 | Gln<br>1   | Thr<br>1   | Lys<br>1   | Asp<br>185 | Ser<br>185 | Gly<br>1   | Val<br>1   | Leu<br>190 | His<br>190 | Ser<br>1   |
| Asp<br>1   | Ala<br>195 | Gly<br>195 | Ser<br>1   | Arg<br>1   | Thr<br>1   | Ser<br>200 | Thr<br>200 | Ala<br>1   | Ala<br>1   | Ile<br>1   | Pro<br>205 | Leu<br>205 | Gln<br>1   | Pro<br>1   |
| Ala<br>210 | Tyr<br>210 | Gln<br>1   | Gln<br>1   | Thr<br>215 | Gly<br>215 | Tyr<br>215 | Gln<br>1   | Ile<br>1   | Pro<br>220 | Ala<br>220 | Ser<br>220 | Ala<br>1   | Leu<br>225 | Asp<br>1   |
| Thr<br>225 | Pro<br>225 | Val<br>230 | Glu<br>230 | Pro<br>230 | Gly<br>230 | Ala<br>1   | Ser<br>235 | Ser<br>235 | Arg<br>235 | Ser<br>235 | Ala<br>235 | Gln<br>240 | Ala<br>240 | Ile<br>240 |
| Thr<br>1   | Arg<br>245 | Pro<br>245 | Ser<br>245 | Ser<br>245 | Asp<br>250 | Ser<br>250 | Phe<br>250 | Ser<br>250 | Gly<br>250 | Pro<br>255 | Arg<br>255 | Gly<br>255 | Ala<br>255 | Asp<br>1   |
| Pro<br>1   | Leu<br>260 | Ser<br>260 | Met<br>260 | Met<br>260 | Glu<br>265 | Phe<br>265 | Tyr<br>265 | Lys<br>265 | Lys<br>265 | Ala<br>270 | Ala<br>270 | Gln<br>270 | Glu<br>270 | Glu<br>1   |
| Lys<br>1   | Met<br>275 | Arg<br>275 | Arg<br>280 | Pro<br>280 | Arg<br>280 | Gln<br>280 | Ser<br>280 | Lys<br>280 | Asp<br>285 | Glu<br>285 | Met<br>285 | Pro<br>285 | Pro<br>290 | Ala<br>1   |
| Ser<br>290 | Leu<br>290 | Gln<br>1   | Gly<br>1   | Pro<br>295 | Ser<br>295 | Glu<br>295 | Thr<br>295 | Ser<br>300 | Ser<br>300 | Thr<br>300 | Asp<br>300 | Pro<br>300 | Gly<br>290 | Arg<br>1   |

Gly His His Met Gly Asp Tyr Ile Pro Leu Glu Glu Leu Asp Lys Phe  
305 310 315 320  
Leu Ser Lys Cys Asn Asp Ala Ala Ala Gln Lys Ala Thr Lys Glu Ala  
325 330 335  
Ala Glu Lys Ala Lys Ile Gln Ala Asp Asn Val Gly His Lys Leu Leu  
340 345 350  
Ser Lys Met Gly Trp Lys Glu Gly Glu Gly Ile Gly Ser Ser Arg Lys  
355 360 365  
Gly Met Ala Asp Pro Ile Met Ala Gly Asp Val Lys Thr Asn Asn Leu  
370 375 380  
Gly Val Gly Ala Ser Ala Pro Gly Glu Val Lys Pro Glu Asp Asp Ile  
385 390 395 400  
Tyr Glu Gln Tyr Lys Lys Arg Met Met Leu Gly Tyr Lys His Arg Pro  
405 410 415  
Asn Pro Leu Gly Asn Pro Arg Lys Ala Tyr Tyr  
420 425

(2) INFORMATION FOR SEQ ID NO:1119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1316
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| aaaaaccaaa  | attcgcgcaga | gagaaagtatg | tccgaagaCgc | tggtgcaacc  | ggtagggcaa  | 60   |
| aagaggttga  | ctaattgtgc  | agtggttcgt  | ctcaaaaagc  | aaggccaatcg | cttcgcagatc | 120  |
| gcttggtaca  | agaataaagt  | ccatttcacg  | cggtctggcg  | tggaagaagga | atagatagaa  | 180  |
| gtgctacagt  | cgataactgt  | ttattcaaat  | gtttcgaaag  | gagttcttgc  | aaaatcgaaa  | 240  |
| gacttgatga  | agtcgtttgg  | atcagatgat  | catcacgaaa  | tatgcacga   | tattttggag  | 300  |
| aaaggagagc  | ttcaagttgc  | tggaaaagaa  | agagaatcac  | agttctcaag  | ccaggtttcgg | 360  |
| gatatagcaa  | cgattgttat  | gcagaaaact  | atcaaccctg  | aaacacaaag  | accattatacc | 420  |
| atcagcatgg  | tagagcgctc  | aatgcacgaa  | attcattttg  | ctgttgatcc  | tcatagtaat  | 480  |
| tccaagaagc  | aggcacttga  | tgtcatccgt  | gagctgcaaa  | agcacttccc  | tataaagcgt  | 540  |
| tctccaatga  | gactgcgtct  | tactgttcct  | gttcaaaatt  | tcccctcgct  | tctggagaag  | 600  |
| ctaaaagaat  | gggatggtag  | tgttgtctcc  | aaagacgaat  | ctggaacaca  | gatgtccact  | 660  |
| gtctgcgaga  | tggaaacccgg | ccattatccga | gagtgatgat  | cccattgtgag | gagtatccag  | 720  |
| ggaagactag  | aaataactgc  | tgtatcagtt  | catgcagaag  | gtgacacaag  | catggatcat  | 780  |
| tacgatgaagc | atgatgatat  | ggcattgcaa  | accacaaagc  | cggtgttacc  | tgctgagact  | 840  |
| gagactaagg  | atttgaccga  | tcccgtcggt  | gaacttagca  | agaaaactgca | gaagcaagag  | 900  |
| ataagtacta  | catagatacac | aaagcaagaa  | ggtggagaag  | aaaagaaggg  | gaccaagtgc  | 960  |
| agcacttgca  | acacgttcgt  | ttggagagct  | aagcaataca  | gagagcactg  | taagagtgtat | 1020 |
| tgccacaaca  | acaacottaa  | tcgttaagact | cggaaactcc  | ctccattatg  | tgctgcagcaa | 1080 |
| tgcattctcg  | agattgacat  | ggacgactct  | agagcagatt  | tgaagaacta  | ctctttctga  | 1140 |
| aactacaatt  | ttctcctttt  | gtgcttttaa  | ttttgtcaat  | gtgttaaatc  | tcgtagtcat  | 1200 |
| atgtgagtat  | gaatacacaa  | aacttgtgga  | atgaaatttt  | gcgcataact  | taagagtgaaa | 1260 |
| aacttgtgtt  | taagagacaa  | gcttggtgat  | ttggtatttt  | attaataact  | gtgacc      |      |

(2) INFORMATION FOR SEQ ID NO:1120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..379
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569042

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asn | Gln | Asn | Ser | Arg | Glu | Arg | Ser | Met | Ser | Lys | Thr | Leu | Val | Gln |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Pro | Val | Gly | Gln | Lys | Arg | Leu | Thr | Asn | Val | Ala | Val | Val | Arg | Leu | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Gln | Gly | Asn | Arg | Phe | Glu | Ile | Ala | Cys | Tyr | Lys | Asn | Lys | Val | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Trp | Arg | Ser | Gly | Val | Glu | Lys | Asp | Ile | Asp | Glu | Val | Leu | Gln | Ser |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His | Thr | Val | Tyr | Ser | Asn | Val | Ser | Lys | Gly | Val | Leu | Ala | Lys | Ser | Lys |
|     |     |     | 65  |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Leu | Met | Lys | Ser | Phe | Gly | Ser | Asp | Asp | His | Thr | Lys | Ile | Cys | Ile |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Asp | Ile | Leu | Glu | Lys | Gly | Glu | Leu | Gln | Val | Ala | Gly | Lys | Glu | Arg | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Gln | Phe | Ser | Ser | Gln | Phe | Arg | Asp | Ile | Ala | Thr | Ile | Val | Met | Gln |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Thr | Ile | Asn | Pro | Glu | Thr | Gln | Arg | Pro | Tyr | Thr | Ile | Ser | Met | Val |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Arg | Leu | Met | His | Glu | Ile | His | Phe | Ala | Val | Asp | Pro | His | Ser | Asn |
|     |     |     | 145 |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Ser | Lys | Lys | Gln | Ala | Leu | Asp | Val | Ile | Arg | Glu | Leu | Gln | Lys | His | Phe |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Ile | Lys | Arg | Ser | Pro | Met | Arg | Leu | Arg | Leu | Thr | Val | Pro | Val | Gln |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Asn | Phe | Pro | Ser | Leu | Leu | Glu | Lys | Leu | Lys | Glu | Trp | Asp | Gly | Ser | Val |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Ser | Lys | Asp | Glu | Ser | Gly | Thr | Gln | Met | Ser | Thr | Val | Cys | Glu | Met |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Pro | Gly | Leu | Phe | Arg | Glu | Cys | Asp | Ser | His | Val | Arg | Ser | Ile | Gln |
|     |     |     | 225 |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Gly | Arg | Leu | Glu | Ile | Leu | Ala | Val | Ser | Val | His | Ala | Glu | Gly | Asp | Thr |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Ser | Met | Asp | His | Tyr | Asp | Glu | His | Asp | Asp | Met | Ala | Leu | Gln | Thr | His |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Lys | Pro | Leu | Leu | Pro | Ala | Glu | Thr | Glu | Thr | Lys | Asp | Leu | Thr | Asp | Pro |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Val | Val | Glu | Leu | Ser | Lys | Lys | Leu | Gln | Lys | Gln | Glu | Ile | Ser | Thr | Thr |
|     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asp | Asn | Thr | Lys | Gln | Glu | Gly | Gly | Glu | Glu | Lys | Lys | Gly | Thr | Lys | Cys |
|     |     |     | 305 |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ser | Thr | Cys | Asn | Thr | Phe | Val | Gly | Glu | Ala | Lys | Gln | Tyr | Arg | Glu | His |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Cys | Lys | Ser | Asp | Trp | His | Lys | His | Asn | Leu | Asn | Arg | Lys | Thr | Arg | Lys |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Leu | Pro | Pro | Ile | Ser | Ala | Asp | Glu | Cys | Met | Ser | Glu | Ile | Asp | Met | Asp |
|     |     |     | 355 |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Asp | Ser | Arg | Ala | Asp | Leu | Lys | Asp | Tyr | Ser | Phe |     |     |     |     |     |
|     |     |     | 370 |     |     | 375 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..370
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

Met Ser Lys Thr Leu Val Gln Pro Val Gly Gln Lys Arg Leu Thr Asn  
1 5 10 15  
Val Ala Val Val Arg Leu Lys Lys Gln Gly Asn Arg Phe Glu Ile Ala  
20 25 30  
Cys Tyr Lys Asn Lys Val Leu Ser Trp Arg Ser Gly Val Glu Lys Asp  
35 40 45  
Ile Asp Glu Val Leu Gln Ser His Thr Val Tyr Ser Asn Val Ser Lys  
50 55 60  
Gly Val Leu Ala Lys Ser Lys Asp Leu Met Lys Ser Phe Gly Ser Asp  
65 70 75 80  
Asp His Thr Lys Ile Cys Ile Asp Ile Leu Glu Lys Gly Glu Leu Gln  
85 90 95  
Val Ala Gly Lys Glu Arg Glu Ser Gln Phe Ser Ser Gln Phe Arg Asp  
100 105 110  
Ile Ala Thr Ile Val Met Gln Lys Thr Ile Asn Pro Glu Thr Gln Arg  
115 120 125  
Pro Tyr Thr Ile Ser Met Val Glu Arg Leu Met His Glu Ile His Phe  
130 135 140  
Ala Val Asp Pro His Ser Asn Ser Lys Lys Gln Ala Leu Asp Val Ile  
145 150 155 160  
Arg Glu Leu Gln Lys His Phe Pro Ile Lys Arg Ser Pro Met Arg Leu  
165 170 175  
Arg Leu Thr Val Pro Val Gln Asn Phe Pro Ser Leu Leu Glu Lys Leu  
180 185 190  
Lys Glu Trp Asp Gly Ser Val Val Ser Lys Asp Glu Ser Gly Thr Gln  
195 200 205  
Met Ser Thr Val Cys Glu Met Glu Pro Gly Leu Phe Arg Glu Cys Asp  
210 215 220  
Ser His Val Arg Ser Ile Gln Gly Arg Leu Glu Ile Leu Ala Val Ser  
225 230 235 240  
Val His Ala Glu Gly Asp Thr Ser Met Asp His Tyr Asp Glu His Asp  
245 250 255  
Asp Met Ala Leu Gln Thr His Lys Pro Leu Leu Pro Ala Glu Thr Glu  
260 265 270  
Thr Lys Asp Leu Thr Asp Pro Val Val Glu Leu Ser Lys Lys Leu Gln  
275 280 285  
Lys Gln Glu Ile Ser Thr Thr Asp Asn Thr Lys Gln Glu Gly Gly Glu  
290 295 300  
Glu Lys Lys Gly Thr Lys Cys Ser Thr Cys Asn Thr Phe Val Gly Glu  
305 310 315 320  
Ala Lys Gln Tyr Arg Glu His Cys Lys Ser Asp Trp His Lys His Asn  
325 330 335  
Leu Asn Arg Lys Thr Arg Lys Leu Pro Pro Ile Ser Ala Asp Glu Cys  
340 345 350  
Met Ser Glu Ile Asp Met Asp Asp Ser Arg Ala Asp Leu Lys Asp Tyr  
355 360 365  
Ser Phe  
370

(2) INFORMATION FOR SEQ ID NO:1122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..297

(D) OTHER INFORMATION: / Ceres Seq. ID 1569044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

Met Lys Ser Phe Gly Ser Asp Asp His Thr Lys Ile Cys Ile Asp Ile

|                 |                 |                     |             |
|-----------------|-----------------|---------------------|-------------|
| 1               | 5               | 10                  | 15          |
| Leu Glu Lys Gly | Glu Leu Gln Val | Ala Gly Lys Glu Arg | Glu Ser Gln |
| 20              | 25              | 30                  |             |
| Phe Ser Ser Gln | Phe Arg Asp     | Ile Ala Thr         | Ile Val Met |
| 35              | 40              | 45                  |             |
| Ile Asn Pro Glu | Thr Gln Arg     | Pro Tyr Thr         | Ile Ser Met |
| 50              | 55              | 60                  |             |
| Leu Met His Glu | Ile His Phe     | Ala Val Asp         | Pro His Ser |
| 65              | 70              | 75                  |             |
| Lys Gln Ala Leu | Asp Val Ile     | Arg Glu Leu         | Gln Lys His |
| 85              | 90              | 95                  |             |
| Lys Arg Ser Pro | Met Arg Leu     | Arg Leu Thr         | Val Pro Val |
| 100             | 105             | 110                 |             |
| Pro Ser Leu Leu | Glu Lys Leu     | Lys Glu Trp         | Asp Gly Ser |
| 115             | 120             | 125                 |             |
| Lys Asp Glu Ser | Gly Thr Gln     | Met Ser Thr         | Val Cys Glu |
| 130             | 135             | 140                 |             |
| Gly Leu Phe Arg | Glu Cys Asp     | Ser His Val         | Arg Ser Ile |
| 145             | 150             | 155                 |             |
| Leu Glu Ile Leu | Ala Val Ser     | Val His Ala         | Glu Gly Asp |
| 165             | 170             | 175                 |             |
| Asp His Tyr Asp | Glu His Asp     | Asp Met Ala         | Leu Gln Thr |
| 180             | 185             | 190                 |             |
| Leu Leu Pro Ala | Glu Thr Glu     | Thr Lys Asp         | Leu Thr Asp |
| 195             | 200             | 205                 |             |
| Glu Leu Ser Lys | Lys Leu Gln     | Lys Glu Ile         | Ser Thr Thr |
| 210             | 215             | 220                 |             |
| Thr Lys Gln Glu | Gly Gly Glu     | Lys Lys Gly         | Thr Lys Cys |
| 225             | 230             | 235                 |             |
| Cys Asn Thr Phe | Val Gly Glu     | Ala Lys Gln         | Tyr Arg Glu |
| 245             | 250             | 255                 |             |
| Ser Asp Trp His | Lys His Asn     | Leu Asn Arg         | Lys Thr Arg |
| 260             | 265             | 270                 |             |
| Pro Ile Ser Ala | Asp Glu Cys     | Met Ser Glu         | Ile Asp Met |
| 275             | 280             | 285                 |             |
| Arg Ala Asp Leu | Lys Asp Tyr     | Ser Phe             |             |
| 290             | 295             |                     |             |

(2) INFORMATION FOR SEQ ID NO:1123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1314

(D) OTHER INFORMATION: / Ceres Seq. ID 1569049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

|             |             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| aaaaaaagac  | gtctcacaca  | aaaaagctgc  | tagaggaaga  | agacgattca  | cttctttTcc  | 60  |
| cgccacatttc | actatcttct  | ccggttggtga | gcaaaagatgt | tgtgggtcga  | caagtacagg  | 120 |
| ccgaaatacac | tcgacaagggt | catagtctcat | gaagatatcg  | cccaaaaaact | caagaaatttg | 180 |
| gtttccgagc  | aagattgtcc  | acatttgcctc | ttttatgggc  | cgtcagggttc | tggtaaagaaa | 240 |
| accctaatta  | tgctcttctc  | caagcagata  | tatggggccca | gtgcagagaa  | ggtgaaagtgt | 300 |
| gagaaacagg  | catggaaagt  | tgatgctggg  | agtagaacta  | ttgatctgga  | gctcactaca  | 360 |
| ttatcaagca  | ccaatcatgt  | ggaaacttact | ccaagtgtatg | caggcttttca | ggacagatat  | 420 |
| attgttcagg  | agataattaa  | agaaattggcc | aagaacagac  | caattgacac  | gaaagaaaag  | 480 |
| aagggatata  | aggtgttgtt  | attaaatgag  | gttgacaagc  | tctcacgaga  | agctcaacat  | 540 |
| tctctgcgga  | gaacaatgga  | gaaatacagc  | tcactcttgc  | gtctcatctt  | atgctgcaac  | 600 |
| agctcttcga  | aggttaccca  | agccattaag  | tctcgtttgc  | tcaatgtgcg  | cataaatgca  | 660 |
| ccttcgcagg  | aagagatagt  | gaaagtgttg  | gagttcgttg  | caagaaaaga  | aagtctgcaa  | 720 |

|            |            |            |            |             |            |      |
|------------|------------|------------|------------|-------------|------------|------|
| ctgccccagg | gttttgctgc | tcgtattgct | gaaaaatcaa | atcgcgactct | aagaagagct | 780  |
| attttgtcac | ttgaaacttg | tcgtgtccaa | aactatccgt | tcacaggttaa | ccaagtgata | 840  |
| tctccatcag | attgggaaga | gtatgttgct | gaaatagcaa | ctgacatgat  | gaaagaacaa | 900  |
| agcccaaaaa | agttatttca | ggtgctgga  | aaggtgtacg | aattactagt  | taattgtatt | 960  |
| ccaccagaag | tcatttcaaa | gagactcctt | catgaattgc | tgaagaaact  | ggactcagag | 1020 |
| ctaaagcttg | aagtctgcc  | ctgggctgca | tattatgaac | atcggtatg   | attaggtcag | 1080 |
| aaagccatat | ttcacataga | agcatttggt | gccaaagtta | tgacatata   | caaaacttc  | 1140 |
| ctcatttcaa | cgtttgggta | gagaagagag | gcttcaaatc | gaggaaaaga  | agatagactt | 1200 |
| gcacttgtac | tgttattttt | atgcgtgac  | cggtgttctg | aagttaaagt  | ttctgtttag | 1260 |
| tggtctgtct | taacttttga | tgtttgaatt | tgtttccttc | aacttgactg  | tctt       |      |

(2) INFORMATION FOR SEQ ID NO:1124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..354

(D) OTHER INFORMATION: / Ceres Seq. ID 1569050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Trp | Val | Asp | Lys | Tyr | Arg | Pro | Lys | Ser | Leu | Asp | Lys | Val | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | His | Glu | Asp | Ile | Ala | Gln | Lys | Leu | Lys | Lys | Leu | Val | Ser | Glu | Gln |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Asp | Cys | Pro | His | Leu | Leu | Phe | Tyr | Gly | Pro | Ser | Gly | Ser | Gly | Lys | Lys |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Thr | Leu | Ile | Met | Ala | Leu | Leu | Lys | Gln | Ile | Tyr | Gly | Ala | Ser | Ala | Glu |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |
| Lys | Val | Lys | Val | Glu | Asn | Arg | Ala | Trp | Lys | Val | Asp | Ala | Gly | Ser | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Ile | Asp | Leu | Glu | Leu | Thr | Thr | Leu | Ser | Ser | Thr | Asn | His | Val | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Thr | Pro | Ser | Asp | Ala | Gly | Phe | Gln | Asp | Arg | Tyr | Ile | Val | Gln | Glu |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Ile | Ile | Lys | Glu | Met | Ala | Lys | Asn | Arg | Pro | Ile | Asp | Thr | Lys | Gly | Lys |
|     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |
| Lys | Gly | Tyr | Lys | Val | Leu | Val | Leu | Asn | Glu | Val | Asp | Lys | Leu | Ser | Arg |
|     |     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |
| Glu | Ala | Gln | His | Ser | Leu | Arg | Arg | Thr | Met | Glu | Lys | Tyr | Ser | Ser | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Cys | Arg | Leu | Ile | Leu | Cys | Cys | Asn | Ser | Ser | Ser | Lys | Val | Thr | Glu | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Lys | Ser | Arg | Cys | Leu | Asn | Val | Arg | Ile | Asn | Ala | Pro | Ser | Gln | Glu |
|     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |
| Glu | Ile | Val | Lys | Val | Leu | Glu | Phe | Val | Ala | Lys | Lys | Glu | Ser | Leu | Gln |
|     |     |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |
| Leu | Pro | Gln | Gly | Phe | Ala | Ala | Arg | Ile | Ala | Glu | Lys | Ser | Asn | Arg | Ser |
|     |     |     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |
| Leu | Arg | Arg | Ala | Ile | Leu | Ser | Leu | Glu | Thr | Cys | Arg | Val | Gln | Asn | Tyr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Pro | Phe | Thr | Gly | Asn | Gln | Val | Ile | Ser | Pro | Met | Asp | Trp | Glu | Glu | Tyr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Ala | Glu | Ile | Ala | Thr | Asp | Met | Met | Lys | Glu | Gln | Ser | Pro | Lys | Lys |
|     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |
| Leu | Phe | Gln | Val | Arg | Gly | Lys | Val | Tyr | Glu | Leu | Leu | Val | Asn | Cys | Ile |
|     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |
| Pro | Pro | Glu | Val | Ile | Leu | Lys | Arg | Leu | Leu | His | Glu | Leu | Leu | Lys | Lys |
|     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |
| Leu | Asp | Ser | Glu | Leu | Lys | Leu | Glu | Val | Cys | His | Trp | Ala | Ala | Tyr | Tyr |

305 310 315 320  
Glu His Arg Met Arg Leu Gly Gln Lys Ala Ile Phe His Ile Glu Ala  
325 330 335  
Phe Val Ala Lys Phe Met Ser Ile Tyr Lys Asn Phe Leu Ile Ser Thr  
340 345 350  
Phe Gly

(2) INFORMATION FOR SEQ ID NO:1125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..303
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

Met Ala Leu Leu Lys Gln Ile Tyr Gly Ala Ser Ala Glu Lys Val Lys  
1 5 10 15  
Val Glu Asn Arg Ala Trp Lys Val Asp Ala Gly Ser Arg Thr Ile Asp  
20 25 30  
Leu Glu Leu Thr Thr Leu Ser Ser Thr Asn His Val Glu Leu Thr Pro  
35 40 45  
Ser Asp Ala Gly Phe Gln Asp Arg Tyr Ile Val Gln Glu Ile Ile Lys  
50 55 60  
Glu Met Ala Lys Asn Arg Pro Ile Asp Thr Lys Gly Lys Lys Gly Tyr  
65 70 75 80  
Lys Val Leu Val Leu Asn Glu Val Asp Lys Leu Ser Arg Glu Ala Gln  
85 90 95  
His Ser Leu Arg Arg Thr Met Glu Lys Tyr Ser Ser Ser Cys Arg Leu  
100 105 110  
Ile Leu Cys Asn Ser Ser Ser Lys Val Thr Glu Ala Ile Lys Ser  
115 120 125  
Arg Cys Leu Asn Val Arg Ile Asn Ala Pro Ser Gln Glu Glu Ile Val  
130 135 140  
Lys Val Leu Glu Phe Val Ala Lys Lys Glu Ser Leu Gln Leu Pro Gln  
145 150 155 160  
Gly Phe Ala Ala Arg Ile Ala Glu Lys Ser Asn Arg Ser Leu Arg Arg  
165 170 175  
Ala Ile Leu Ser Leu Glu Thr Cys Arg Val Gln Asn Tyr Pro Phe Thr  
180 185 190  
Gly Asn Gln Val Ile Ser Pro Met Asp Trp Glu Glu Tyr Val Ala Glu  
195 200 205  
Ile Ala Thr Asp Met Met Lys Glu Gln Ser Pro Lys Lys Leu Phe Gln  
210 215 220  
Val Arg Gly Lys Val Tyr Glu Leu Leu Val Asn Cys Ile Pro Pro Glu  
225 230 235 240  
Val Ile Leu Lys Arg Leu Leu His Glu Leu Leu Lys Lys Leu Asp Ser  
245 250 255  
Glu Leu Lys Leu Glu Val Cys His Trp Ala Tyr Tyr Glu His Arg  
260 265 270  
Met Arg Leu Gly Gln Lys Ala Ile Phe His Ile Glu Ala Phe Val Ala  
275 280 285  
Lys Phe Met Ser Ile Tyr Lys Asn Phe Leu Ile Ser Thr Phe Gly  
290 295 300

(2) INFORMATION FOR SEQ ID NO:1126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..238  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569052

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Asn | Arg | Pro | Ile | Asp | Thr | Lys | Gly | Lys | Lys | Gly | Thr | Lys |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Val | Leu | Val | Leu | Asn | Glu | Val | Asp | Lys | Leu | Ser | Arg | Glu | Ala | Gln | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Leu | Arg | Arg | Thr | Met | Glu | Lys | Tyr | Ser | Ser | Ser | Cys | Arg | Leu | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Cys | Cys | Asn | Ser | Ser | Ser | Lys | Val | Thr | Glu | Ala | Ile | Lys | Ser | Arg |
|     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Cys | Leu | Asn | Val | Arg | Ile | Asn | Ala | Pro | Ser | Gln | Glu | Glu | Ile | Val | Lys |
|     |     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Leu | Glu | Phe | Val | Ala | Lys | Lys | Glu | Ser | Leu | Gln | Leu | Pro | Gln | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Ala | Ala | Arg | Ile | Ala | Glu | Lys | Ser | Asn | Arg | Ser | Leu | Arg | Arg | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Leu | Ser | Leu | Glu | Thr | Cys | Arg | Val | Gln | Asn | Tyr | Pro | Phe | Thr | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Gln | Val | Ile | Ser | Pro | Met | Asp | Trp | Glu | Glu | Tyr | Val | Ala | Glu | Ile |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Ala | Thr | Asp | Met | Met | Lys | Glu | Gln | Ser | Pro | Lys | Lys | Leu | Phe | Gln | Val |
|     |     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Arg | Gly | Lys | Val | Tyr | Glu | Leu | Leu | Val | Asn | Cys | Ile | Pro | Pro | Glu | Val |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Leu | Lys | Arg | Leu | Leu | His | Glu | Leu | Leu | Lys | Lys | Leu | Asp | Ser | Glu |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Leu | Lys | Leu | Glu | Val | Cys | His | Trp | Ala | Ala | Tyr | Tyr | Glu | His | Arg | Met |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| Arg | Leu | Gly | Gln | Lys | Ala | Ile | Phe | His | Ile | Glu | Ala | Phe | Val | Ala | Lys |
|     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Phe | Met | Ser | Ile | Tyr | Lys | Asn | Phe | Leu | Ile | Ser | Thr | Phe | Gly |     |     |
|     |     | 225 |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:1127:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1148 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..1148  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569061

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

|              |             |            |             |            |            |     |
|--------------|-------------|------------|-------------|------------|------------|-----|
| actatctatt   | tcttctttca  | tcatcatcat | catcatcatc  | atcactctct | cttcttcttc | 60  |
| tctctattcc   | aKggcttttag | tacgtgaacg | tctcagctca  | aatctcgcgt | tctctcttcc | 120 |
| tccaatctcc   | gaccgcgcgt  | tctccacctc | ttctctctca  | gccaccacca | ccaccgtcgc | 180 |
| tggtctgaac   | ggaatctccg  | cttgtgatct | cgagaaactc  | aacgtttctc | gatgcggaaa | 240 |
| cggtcggtgatt | gtttacaaag  | tccgtcataa | aaccacatcg  | gagatctacg | ctttgaaaaa | 300 |
| agtttaacgg   | gacatgggat  | cgattttcac | aagacagtgt  | atgcgagaga | tggagattct | 360 |
| ccgacgtata   | gattcacctg  | acgtcgttaa | atgtcacgga  | atcttcgaga | aacctgtcgt | 420 |
| cggtgaagta   | tcgattctaa  | tgagtatata | ggacggcgga  | accctagaat | cactacgcgg | 480 |
| cggtgttaac   | gagcaaaaac  | tcgcgggatt | cgctaaaacg  | atctttaaag | gattaaagta | 540 |
| tttacacgct   | cttaagatcg  | ttcatcgtga | tataaaacc   | gcgaatcttc | ttctcaattc | 600 |
| gaaaaacgaa   | gttaaaatcg  | cgcatttcgg | agtttagtaag | atattagtcc | gatcattaga | 660 |

(2) INFORMATION FOR SEQ ID NO:1128:

(A) LENGTH: 333 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY:  $\text{lin}$

MOLECULE TYPE: peptide

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(11) MOLECULE TYPE: peptide
(12) FEATURE:
```

(1X) FEATURE:  
(7X) NAME:

(A) NAME/KEY: peptide  
(B) LOCATION: 1-222

(B) LOCATION: 1..333

(D) OTHER INFORMATION: / Ceres Seq. ID 1569062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Ile | Ser | Ser | Phe | Ile | Ile | Ile | Ile | Ile | Ile | Ile | Thr | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ser | Ser | Ser | Leu | Tyr | Ser | Xaa | Ala | Leu | Val | Arg | Glu | Arg | Gln |
| 1   |     |     |     | 20  |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Asn | Leu | Arg | Leu | Pro | Leu | Pro | Pro | Ile | Ser | Asp | Arg | Arg | Phe |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     | Ser |
| Thr | Ser | Ser | Ser | Ser | Ala | Thr | Thr | Thr | Thr | Val | Ala | Gly | Cys | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     | Gly |
| Ile | Ser | Ala | Cys | Asp | Leu | Glu | Lys | Leu | Asn | Val | Leu | Gly | Cys | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Gly | Gly | Ile | Val | Tyr | Lys | Val | Arg | His | Lys | Thr | Thr | Ser | Glu | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |
| Ala | Leu | Lys | Thr | Val | Asn | Gly | Asp | Met | Asp | Pro | Ile | Phe | Thr | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 | Gln |
| Leu | Met | Arg | Glu | Met | Glu | Ile | Leu | Arg | Arg | Thr | Asp | Ser | Pro | Tyr |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     | Val |
| Val | Lys | Cys | His | Gly | Ile | Phe | Glu | Lys | Pro | Val | Val | Gly | Glu | Val |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     | Ser |
| Ile | Leu | Met | Glu | Tyr | Met | Asp | Gly | Gly | Thr | Leu | Glu | Ser | Leu | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Gly | Val | Thr | Glu | Gln | Lys | Leu | Ala | Gly | Phe | Ala | Lys | Gln | Ile | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |
| Gly | Leu | Ser | Tyr | Leu | His | Ala | Leu | Lys | Ile | Val | His | Arg | Asp | Ile |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 | Lys |
| Pro | Ala | Asn | Leu | Leu | Leu | Asn | Ser | Lys | Asn | Glu | Val | Lys | Ile | Ala |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     | Asp |
| Phe | Gly | Val | Ser | Lys | Ile | Leu | Val | Arg | Ser | Leu | Asp | Ser | Cys | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     | Ser |
| Tyr | Val | Gly | Thr | Cys | Ala | Tyr | Met | Ser | Pro | Glu | Arg | Phe | Asp | Ser |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | Glu |
| Ser | Ser | Gly | Gly | Ser | Ser | Asp | Ile | Tyr | Ala | Gly | Asp | Ile | Trp | Ser |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |
| Gly | Leu | Met | Met | Leu | Glu | Leu | Leu | Val | Gly | His | Phe | Pro | Leu | Pro |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |
| Pro | Gly | Gln | Arg | Pro | Asp | Trp | Ala | Thr | Leu | Met | Cys | Ala | Val | Cys |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     | Phe |
| Gly | Glu | Pro | Pro | Arg | Ala | Pro | Glu | Gly | Cys | Ser | Glu | Glu | Phe | Arg |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     | Ser |
| Phe | Val | Glu | Cys | Cys | Leu | Arg | Lys | Asp | Ser | Ser | Lys | Arg | Trp | Thr |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |

Pro Gln Leu Leu Ala His Pro Phe Leu Arg Glu Asp Leu  
325 330

(2) INFORMATION FOR SEQ ID NO:1129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..229
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:

Met Asp Pro Ile Phe Thr Arg Gln Leu Met Arg Glu Met Glu Ile Leu  
1 5 10 15  
Arg Arg Thr Asp Ser Pro Tyr Val Val Lys Cys His Gly Ile Phe Glu  
20 25 30  
Lys Pro Val Val Gly Glu Val Ser Ile Leu Met Glu Tyr Met Asp Gly  
35 40 45  
Gly Thr Leu Glu Ser Leu Arg Gly Gly Val Thr Glu Gln Lys Leu Ala  
50 55 60  
Gly Phe Ala Lys Gln Ile Leu Lys Gly Leu Ser Tyr Leu His Ala Leu  
65 70 75 80  
Lys Ile Val His Arg Asp Ile Lys Pro Ala Asn Leu Leu Leu Asn Ser  
85 90 95  
Lys Asn Glu Val Lys Ile Ala Asp Phe Gly Val Ser Lys Ile Leu Val  
100 105 110  
Arg Ser Leu Asp Ser Cys Asn Ser Tyr Val Gly Thr Cys Ala Tyr Met  
115 120 125  
Ser Pro Glu Arg Phe Asp Ser Glu Ser Ser Gly Gly Ser Ser Asp Ile  
130 135 140  
Tyr Ala Gly Asp Ile Trp Ser Phe Gly Leu Met Met Leu Glu Leu Leu  
145 150 155 160  
Val Gly His Phe Pro Leu Leu Pro Pro Gly Gln Arg Pro Asp Trp Ala  
165 170 175  
Thr Leu Met Cys Ala Val Cys Phe Gly Glu Pro Pro Arg Ala Pro Glu  
180 185 190  
Gly Cys Ser Glu Glu Phe Arg Ser Phe Val Glu Cys Cys Leu Arg Lys  
195 200 205  
Asp Ser Ser Lys Arg Trp Thr Ala Pro Gln Leu Leu Ala His Pro Phe  
210 215 220  
Leu Arg Glu Asp Leu  
225

(2) INFORMATION FOR SEQ ID NO:1130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..220
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

Met Arg Glu Met Glu Ile Leu Arg Arg Thr Asp Ser Pro Tyr Val Val  
1 5 10 15  
Lys Cys His Gly Ile Phe Glu Lys Pro Val Val Gly Glu Val Ser Ile  
20 25 30  
Leu Met Glu Tyr Met Asp Gly Gly Thr Leu Glu Ser Leu Arg Gly Gly



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 35                                                              | 40  | 45  |
| Val Thr Glu Gln Lys Leu Ala Gly Phe Ala Lys Gln Ile Leu Lys Gly |     |     |
| 50                                                              | 55  | 60  |
| Leu Ser Tyr Leu His Ala Leu Lys Ile Val His Arg Asp Ile Lys Pro |     |     |
| 65                                                              | 70  | 75  |
| Ala Asn Leu Leu Leu Asn Ser Lys Asn Glu Val Lys Ile Ala Asp Phe |     |     |
| 85                                                              | 90  | 95  |
| Gly Val Ser Lys Ile Leu Val Arg Ser Leu Asp Ser Cys Asn Ser Tyr |     |     |
| 100                                                             | 105 | 110 |
| Val Gly Thr Cys Ala Tyr Met Ser Pro Glu Arg Phe Asp Ser Glu Ser |     |     |
| 115                                                             | 120 | 125 |
| Ser Gly Gly Ser Ser Asp Ile Tyr Ala Gly Asp Ile Trp Ser Phe Gly |     |     |
| 130                                                             | 135 | 140 |
| Leu Met Met Leu Glu Leu Leu Val Gly His Phe Pro Leu Leu Pro Pro |     |     |
| 145                                                             | 150 | 155 |
| Gly Gln Arg Pro Asp Trp Ala Thr Leu Met Cys Ala Val Cys Phe Gly |     |     |
| 165                                                             | 170 | 175 |
| Glu Pro Pro Arg Ala Pro Glu Gly Cys Ser Glu Glu Phe Arg Ser Phe |     |     |
| 180                                                             | 185 | 190 |
| Val Glu Cys Cys Leu Arg Lys Asp Ser Ser Lys Arg Trp Thr Ala Pro |     |     |
| 195                                                             | 200 | 205 |
| Gln Leu Leu Ala His Pro Phe Leu Arg Glu Asp Leu                 |     |     |
| 210                                                             | 215 | 220 |

(2) INFORMATION FOR SEQ ID NO:1131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1591
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

|                                                                      |      |
|----------------------------------------------------------------------|------|
| atgcacaatc attccacta atagtttaat aaagtgtata attttttttc aaattaaaaac    | 60   |
| agctaaacac acacaaacc attcaaaaag gggttaaaga ttgaagaata ttctaagaaa     | 120  |
| aattgtttct ctctttcaag aagtaaaagc gtctctctct ctcattaagc atcaaggag     | 180  |
| ttctgttttt ctgtctttgc tgttacattc ttcaggaaaa agcggttacc ttactctct     | 240  |
| ctgcacatca gaggaagcgt gtagaacta aaggagctta atttgagaga tttttttttt     | 300  |
| tgtttctggg ttgtttcaaa gatgcaaat tttagtgtct tTctgtctgt gaaaaggatt     | 360  |
| tgtatggcaa aagaagggtga aaacggagcc atctgtggag atcttttca ctaaggaaat    | 420  |
| tcacgcagca acaaacagtt ttaattacga taacaagctc ggtgaaggca gatttggcag    | 480  |
| tgtgtattgg ggtcagctat gggatggatc tcaaatgca gtcaagagat tgaaggcatc     | 540  |
| gagtagcaga gaagagatag attttgtgtt agaagtcgag attctgtctc gtatcgtca     | 600  |
| caagaatcta ttgagtgtag gaggttactg tgcagaagga caagaacgac tcatgtgata    | 660  |
| tgattacatg ccaaatttga gcttggctct tcatcttcat gggtcaacatt catctgagtc   | 720  |
| gcttcttgat tggactagcc ggaatgaat tctgtgtatc tctgtctacg cgattgccta     | 780  |
| cttgcacatc ttgtcaaac ctagaatagt ccatggagat gtgagagcaa gcaatgtgct     | 840  |
| gctagattct gagtttgaag ctccgggttac agattttcgga tacgataagc tgaatgccaga | 900  |
| tgtatggagct aacaaaggca ccaaggggtaa taacattggg tatctctcac cagaatgtat  | 960  |
| cgaatctgCa aaagaatcag acatgggaga tgtgtatagt tctcgtgttc ttttctggga    | 1020 |
| gcttgttaact ggttaagagac ctacagagag ggtaaaacta acaacaaga ggggtattac   | 1080 |
| cgaatggggt ttacctcttg tttacgaaa aaagtttggg gaaattgtgg atcaaaaggct    | 1140 |
| gaatgggaag tatgtggaag aagagctgaa aaggatagtt ttggttggtc tcatgtgtgc    | 1200 |
| tcagagggag tcagagaaga gaccaacaat gtctgaagtt gtggagatgc taatgattga    | 1260 |
| atcaaaaggag aaaaatggctc agcttgaagc taatccactc ttcaatggaa acaatgatgg  | 1320 |
| tgaagtata gatgaaagct cagagatcat ttctgaagtg agagatcatc aataacaaga     | 1380 |
| acaagaatgt tatccaattt cagcatattc tgtttctctt tctgataatc tggtttttgg    | 1440 |
| ttgtgctgtg ttttagaaga gtgtttgtgc ttgtttttag aatagcgaag ttggctttta    | 1500 |
| aaagtttatt gtgtattttt ttccagctta agattggatt ttgatcattg atatttgagc    | 1560 |

ttgtaagaga gtgtagtgggt acatatattgg t

(2) INFORMATION FOR SEQ ID NO:1132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..235

(D) OTHER INFORMATION: / Ceres Seq. ID 1569066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Asn | Leu | Ser | Leu | Val | Ser | His | Leu | His | Gly | Gln | His | Ser | Ser |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Ser | Leu | Leu | Asp | Trp | Thr | Arg | Arg | Met | Asn | Ile | Ala | Val | Ser | Ser |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Ala | Gln | Ala | Ile | Ala | Tyr | Leu | His | His | Phe | Ala | Thr | Pro | Arg | Ile | Val |
|     |     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |
| His | Gly | Asp | Val | Arg | Ala | Ser | Asn | Val | Leu | Leu | Asp | Ser | Glu | Phe | Glu |
|     |     |     | 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |
| Ala | Arg | Val | Thr | Asp | Phe | Gly | Tyr | Asp | Lys | Leu | Met | Pro | Asp | Asp | Gly |
|     |     |     | 65  |     |     |     |     |     | 70  |     |     |     |     | 75  |     |
| Ala | Asn | Lys | Ser | Thr | Lys | Gly | Asn | Asn | Ile | Gly | Tyr | Leu | Ser | Pro | Glu |
|     |     |     |     |     |     |     |     |     | 85  |     |     |     |     | 90  |     |
| Cys | Ile | Glu | Ser | Gly | Lys | Glu | Ser | Asp | Met | Gly | Asp | Val | Tyr | Ser | Phe |
|     |     |     |     |     |     |     |     |     | 100 |     |     |     |     | 110 |     |
| Gly | Val | Leu | Leu | Leu | Glu | Leu | Val | Thr | Gly | Lys | Arg | Pro | Thr | Glu | Arg |
|     |     |     |     |     |     |     |     |     | 115 |     |     |     |     | 120 |     |
| Val | Asn | Leu | Thr | Thr | Lys | Arg | Gly | Ile | Thr | Glu | Trp | Val | Leu | Pro | Leu |
|     |     |     |     |     |     |     |     |     | 130 |     |     |     |     | 135 |     |
| Val | Tyr | Glu | Arg | Lys | Phe | Gly | Glu | Ile | Val | Asp | Gln | Arg | Leu | Asn | Gly |
|     |     |     |     |     |     |     |     |     | 140 |     |     |     |     | 145 |     |
| Lys | Tyr | Val | Glu | Glu | Glu | Leu | Lys | Arg | Ile | Val | Leu | Val | Gly | Leu | Met |
|     |     |     |     |     |     |     |     |     | 150 |     |     |     |     | 155 |     |
| Cys | Ala | Gln | Arg | Glu | Ser | Glu | Lys | Arg | Pro | Thr | Met | Ser | Glu | Val | Val |
|     |     |     |     |     |     |     |     |     | 160 |     |     |     |     | 165 |     |
| Glu | Met | Leu | Met | Ile | Glu | Ser | Lys | Glu | Lys | Met | Ala | Gln | Leu | Glu | Ala |
|     |     |     |     |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asn | Pro | Leu | Phe | Asn | Gly | Asn | Asn | Asp | Gly | Glu | Val | Ile | Asp | Glu | Ser |
|     |     |     |     |     |     |     |     |     | 180 |     |     |     |     | 185 |     |
| Ser | Glu | Ile | Ile | Ser | Glu | Val | Arg | Asp | His | Gln |     |     |     | 200 |     |
|     |     |     |     |     |     |     |     |     | 210 |     |     |     |     | 215 |     |
| 225 |     |     |     |     |     |     |     |     | 230 |     |     |     |     | 235 |     |

(2) INFORMATION FOR SEQ ID NO:1133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..210

(D) OTHER INFORMATION: / Ceres Seq. ID 1569067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Ile | Ala | Val | Ser | Ser | Ala | Gln | Ala | Ile | Ala | Tyr | Leu | His | His |
| 1   |     |     |     |     |     |     |     |     |     |     |     |     |     | 15  |     |
| Phe | Ala | Thr | Pro | Arg | Ile | Val | His | Gly | Asp | Val | Arg | Ala | Ser | Asn | Val |
|     |     |     |     |     |     |     |     |     | 20  |     |     |     |     | 25  |     |
| Leu | Leu | Asp | Ser | Glu | Phe | Glu | Ala | Arg | Val | Thr | Asp | Phe | Gly | Tyr | Asp |
|     |     |     |     |     |     |     |     |     | 30  |     |     |     |     | 35  |     |
|     |     |     |     |     |     |     |     |     | 40  |     |     |     |     | 45  |     |

Lys Leu Met Pro Asp Asp Gly Ala Asn Lys Ser Thr Lys Gly Asn Asn  
50 55 60  
Ile Gly Tyr Leu Ser Pro Glu Cys Ile Glu Ser Gly Lys Glu Ser Asp  
65 70 75 80  
Met Gly Asp Val Tyr Ser Phe Gly Val Leu Leu Glu Leu Val Thr  
85 90 95  
Gly Lys Arg Pro Thr Glu Arg Val Asn Leu Thr Thr Lys Arg Gly Ile  
100 105 110  
Thr Glu Trp Val Leu Pro Leu Val Tyr Glu Arg Lys Phe Gly Glu Ile  
115 120 125  
Val Asp Gln Arg Leu Asn Gly Lys Tyr Val Glu Glu Glu Leu Lys Arg  
130 135 140  
Ile Val Leu Val Gly Leu Met Cys Ala Gln Arg Glu Ser Glu Lys Arg  
145 150 155 160  
Pro Thr Met Ser Glu Val Val Glu Met Leu Met Ile Glu Ser Lys Glu  
165 170 175  
Lys Met Ala Gln Leu Glu Ala Asn Pro Leu Phe Asn Gly Asn Asn Asp  
180 185 190  
Gly Glu Val Ile Asp Glu Ser Ser Glu Ile Ile Ser Glu Val Arg Asp  
195 200 205  
His Gln  
210

(2) INFORMATION FOR SEQ ID NO:1134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

Met Pro Asp Asp Gly Ala Asn Lys Ser Thr Lys Gly Asn Asn Ile Gly  
1 5 10 15  
Tyr Leu Ser Pro Glu Cys Ile Glu Ser Gly Lys Glu Ser Asp Met Gly  
20 25 30  
Asp Val Tyr Ser Phe Gly Val Leu Leu Leu Val Thr Gly Lys  
35 40 45  
Arg Pro Thr Glu Arg Val Asn Leu Thr Thr Lys Arg Gly Ile Thr Glu  
50 55 60  
Trp Val Leu Pro Leu Val Tyr Glu Arg Lys Phe Gly Glu Ile Val Asp  
65 70 75 80  
Gln Arg Leu Asn Gly Lys Tyr Val Glu Glu Leu Lys Arg Ile Val  
85 90 95  
Leu Val Gly Leu Met Cys Ala Gln Arg Glu Ser Glu Lys Arg Pro Thr  
100 105 110  
Met Ser Glu Val Val Glu Met Leu Met Ile Glu Ser Lys Glu Lys Met  
115 120 125  
Ala Gln Leu Glu Ala Asn Pro Leu Phe Asn Gly Asn Asn Asp Gly Glu  
130 135 140  
Val Ile Asp Glu Ser Ser Glu Ile Ile Ser Glu Val Arg Asp His Gln  
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:1135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1227

(D) OTHER INFORMATION: / Ceres Seq. ID 1569097

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

|             |            |            |            |            |             |      |
|-------------|------------|------------|------------|------------|-------------|------|
| atatctcaaa  | atatgaataa | tcaaaaatgg | agtataggtt | tcatatctct | cgctttttctc | 60   |
| ttcatcacct  | cctcttcagc | tgagttcatc | attcaacagg | tcacaaaagg | cagaggaata  | 120  |
| gagtacaaca  | gttcttcacg | tctcgaggag | aattctggag | tgacaagaga | gttgagagaa  | 180  |
| gagcgacat   | cgagtaagat | agtgaaca   | acaagcttct | ctgtgattaa | aggcagagaa  | 240  |
| gaacctctag  | aatcctctgt | ttttgagcc  | tgctggttac | aaatggagat | tggtttttga  | 300  |
| cgtagaatgt  | aataaaaaac | acggtggaaa | tgatcatatt | tccttttacg | caaggatcga  | 360  |
| agagKacaaa  | ctctcttcca | gtaggatggg | aagtgaatgt | tgatctcaaa | ctctttgtcc  | 420  |
| ataatgggaa  | gctacacaaa | tatttgactg | ttacagatgg | cttagtgaag | cgatataaca  | 480  |
| atgcgaaaaa  | agaatggggg | ttcggacaat | tgattttctg | atcaacattc | tacacgcgca  | 540  |
| acgaaggtta  | ccttgaccag | gacactgggt | cttttggtgc | tgagatcttt | attgtttaaac | 600  |
| cggtcacaac  | acaagagaaa | gttacattca | tatcaaaacc | tcaaaaacat | gttttcacct  | 660  |
| ggaagatact  | tcgtytctct | acottggaag | ataaattcta | ttactccgat | gattttctcg  | 720  |
| ttgaagaccg  | atactggaga | ctaggattta | accggaagg  | ggatggagga | ggaagaccac  | 780  |
| atgcacttcc  | aatcttccca | tttgctcaag | gccataaagg | aaacgcagtt | gttacaacaa  | 840  |
| cttggggagc  | ggtttaactc | cggttaaaga | atcaacgaag | tactaaccat | agacaaatat  | 900  |
| attctgcagc  | ttggtaccgc | attggaagcg | gttatggtgt | gggagtgaac | aatatcatac  | 960  |
| tgttagctga  | tttaaacgat | gcatacaaa  | gatatttggt | gaatgatgcc | attatctttg  | 1020 |
| aaagctgaaat | ggttaaagtc | tctataacca | acatcgcttc | cgcttaaaat | ttctgcacttc | 1080 |
| tttgtctaac  | atcaatcaac | cttatgaata | aagagatat  | tgatgaattt | gtaataagaa  | 1140 |
| aacgcttaag  | tttgtgaatt | gtgaaattat | ttctgttctt | ctgagttttt | tattttcaatg | 1200 |
| aaaataaaac  | tcttaccggt | ttaaaatt   |            |            |             |      |

- (2) INFORMATION FOR SEQ ID NO:1136:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..253

(D) OTHER INFORMATION: / Ceres Seq. ID 1569098

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ile | Lys | Thr | Thr | Val | Glu | Met | Ile | Ile | Phe | Pro | Phe | Thr | Gln |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ser | Lys | Xaa | Thr | Asn | Ser | Leu | Pro | Val | Gly | Trp | Glu | Val | Asn | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Leu | Lys | Leu | Phe | Val | His | Asn | Gly | Lys | Leu | His | Lys | Tyr | Leu | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Val | Thr | Asp | Gly | Leu | Val | Lys | Arg | Tyr | Asn | Asn | Ala | Lys | Lys | Glu | Trp |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Phe | Gly | Gln | Leu | Ile | Ser | Arg | Ser | Thr | Phe | Tyr | Asn | Ala | Asn | Glu |
| 65  |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Tyr | Leu | Asp | Gln | Asp | Thr | Gly | Ser | Phe | Gly | Ala | Glu | Ile | Phe | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Val | Lys | Pro | Ala | Gln | Gln | Gln | Glu | Lys | Val | Thr | Phe | Ile | Ser | Asn | Pro |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Pro | Asn | Asn | Val | Phe | Thr | Trp | Lys | Ile | Leu | Arg | Xaa | Ser | Thr | Leu | Glu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Lys | Phe | Tyr | Tyr | Ser | Asp | Asp | Phe | Leu | Val | Glu | Asp | Arg | Tyr | Trp |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Leu | Gly | Phe | Asn | Pro | Lys | Gly | Asp | Gly | Gly | Gly | Arg | Pro | His | Ala |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Pro | Ile | Phe | Leu | Phe | Ala | Gln | Gly | His | Lys | Ala | Asn | Ala | Val | Val |

(2) INFORMATION FOR SEQ ID NO:1137:

(A) LENGTH: 245 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..245

(D) OTHER INFORMATION: / Ceres Seq. ID 1569099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

(2) INFORMATION FOR SEQ ID NO:1138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1481 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1481

(D) OTHER INFORMATION: / Ceres Seq. ID 1569112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

```

cactgtgtctc tcttcttcaa tggaaacaaca attaacctta gtattgcttg atagcccaaaa 60
aggcgccaaaa tatgtagaaa cctttgaaga agccgttctt tcttcttctt ctctctcttc 120
ttctctctgtt cctctcctga ctgatcaccg ccatcgaaac ttctgcaaat tcttctcttta 180
cttctctcttc gtctgtcttg ctactatttt catcatctcc agtctcgccg tctctccaat 240
tcccccaaca tccgcaatct tctcccgtaa acgtttcatc agcaaatgtg gatcttttca 300
cgggagattg gataccagat ccaacaggtc ctctgtagac aaatgtcact tctctgcaca 360
ttcaagattt tcagaactgc ctattgaatg gacgaccaga tgtgaattat ctcttctgga 420
gatggaagcc tctgtattgt gatcttctta gggttagtcc atcgagttt ctgtcttcag 480
tgaagaacaa atgtgtgggt tttatcgggt attccattgc tctgaatcat gtccagcttc 540
tcattctgat tcttctctag gtggaagaag tggaggaaat ctatcacgat aaggagttca 600
gatccaagat atggagattc ccttctcaca acttcacact atcagtcatt tggctctctt 660
tcttctctcaa atccgaaaac tctagcaact cggatattca gctttaccct gaccagcttg 720
accacaaatg gactgtccaa taccgaaat tctactacgt tgttatctct ggaggcaaat 780
ggtttcttaa aacaacaatt ttccatgaaa acaacgtagt caccggctgt cattactgcc 840
aagggaagaaa caactcaact gatctcggtc atgattactc ctaccgcaaa accctaaacc 900
ttctctgtca ctctgtctta aactcaaccc acaaacgcgt ggttctgttt cgaacaacaa 960
cgcttgacca ttctgaaac ggagagtggg acactgggtg gtattgcac agaacgatgc 1020
cgtttaaaga aggcacaaac aatatgaaaa ctgtagatga tgtgatgcgt gatgttgagc 1080
ttagaggtgt tcagaaattt gggaaaggtt ttggcttagg ttccaacatc aggtatttag 1140
acacagctgg aatgtctctt ctccgtccag acgggcaccc gggaccatac cggcatccaa 1200
atcttcttgc tggagttaag aataagagca atgttcagaa tgattgtctg cattggtgtc 1260
tacctgttcc aattgattca tggaaatgat tgatgggtga aaccacgctt aaccgggaac 1320
gggaactata cgatttaacc ggtaaatgta ccacgatatt gcttgtagct agttacagtc 1380
aatagccatt ccaactgtca atgtctcgta tatgatagtt ctatatatta attttgtaat 1440
ggttctaaac aagaataaac gatgcaaat ttgcagtggt g
```

(2) INFORMATION FOR SEQ ID NO:1139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1569113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

```

Met Ser Ser Leu Ser Ser Ala Phe Ser Leu Arg Trp Lys Lys Trp Arg
1 5 10 15
Lys Ser Ile Thr Ile Arg Ser Ser Asp Pro Arg Tyr Gly Asp Ser Leu
20 25 30
Leu Thr Thr Ser His Tyr Gln Ser Phe Gly Leu Leu Ser Phe Ser Asn
35 40 45
Pro Lys His Leu Ala Thr Arg Ile Phe Ser Phe Thr Ser Thr Ser Leu
50 55 60
Thr Thr Asn Gly Leu Ser Asn Thr Arg Asn Ser Thr Thr Leu Leu Ser
65 70 75 80
Leu Glu Ala Asn Gly Phe Leu Lys Gln Gln Phe Ser Met Lys Thr Thr
85 90 95
```

(2) INFORMATION FOR SEQ ID NO:1140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..109  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569114  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:  
Met Pro Phe Lys Glu Gly Gln Ala Asn Met Lys Thr Val Asp Asp Val  
1 5 10 15  
Met Arg Asp Val Glu Leu Glu Val Phe Gln Lys Phe Gly Lys Gly Phe  
20 25 30  
Gly Leu Gly Ser Asn Ile Arg Leu Leu Asp Thr Thr Gly Met Ser Leu  
35 40 45  
Leu Arg Pro Asp Gly His Pro Gly Pro Tyr Arg His Pro Asn Pro Phe  
50 55 60  
Ala Gly Val Lys Asn Lys Ser Asn Val Gln Asn Asp Cys Leu His Trp  
65 70 75 80  
Cys Leu Pro Gly Pro Ile Asp Ser Trp Asn Asp Val Met Val Glu Thr  
85 90 95  
Thr Leu Asn Arg Glu Arg Glu Leu Tyr Asp Leu Thr Gly  
100 105  
(2) INFORMATION FOR SEQ ID NO:1141:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 100 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..100  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569115  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:  
Met Lys Thr Val Asp Asp Val Met Arg Asp Val Glu Leu Glu Val Phe  
1 5 10 15  
Gln Lys Phe Gly Lys Gly Phe Gly Leu Gly Ser Asn Ile Arg Leu Leu  
20 25 30  
Asp Thr Thr Gly Met Ser Leu Leu Arg Pro Asp Gly His Pro Gly Pro  
35 40 45  
Tyr Arg His Pro Asn Pro Phe Ala Gly Val Lys Asn Lys Ser Asn Val  
50 55 60  
Gln Asn Asp Cys Leu His Trp Cys Leu Pro Gly Pro Ile Asp Ser Trp  
65 70 75 80  
Asn Asp Val Met Val Glu Thr Thr Leu Asn Arg Glu Arg Glu Leu Tyr  
85 90 95  
Asp Leu Thr Gly  
100  
(2) INFORMATION FOR SEQ ID NO:1142:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1794 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1794  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569116  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:  
attcttgctc cgacaatact ctcagaatac gatcttgaag agcaaagatt gttcctttat

(2) INFORMATION FOR SEQ ID NO:1143:

(A) LENGTH: 532 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1...532

(D) OTHER INFORMATION: / Ceres Seq. ID 1569117

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:
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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Leu | Ser | Arg | Gln | Tyr | Ser | Gln | Asn | Thr | Ile | Leu | Lys | Ser | Lys | Asp |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Ser | Phe | Ile | Asp | Glu | Leu | Ser | Ala | Lys | Glu | Cys | Tyr | Ile | Met | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ala | Ala | Val | Ile | Gly | Leu | Asn | Thr | Gly | Lys | Arg | Leu | Leu | Ser | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Phe | Tyr | His | Ser | Asp | Val | Thr | Glu | Lys | Phe | Leu | Ser | Val | Asn | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| His | Cys | Ser | Ser | Gln | Tyr | His | Ile | Ala | Ser | Thr | Lys | Ser | Gly | Ile | Thr |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Lys | Lys | Ala | Ser | Asn | Tyr | Ser | Pro | Ser | Phe | Pro | Ser | Ser | Asn | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| His | Thr | Gln | Ser | Ala | Lys | Ala | Leu | Lys | Glu | Asn | Val | Asp | Val | Ala | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Glu | Lys | Pro | Trp | Leu | Pro | Asn | Gly | Thr | Asp | Lys | Glu | Leu | Glu | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Cys | Tyr | Asp | Asp | Asp | Asp | Leu | Ile | Ser | His | Ser | Val | Glu | Ala | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Leu | Leu | Leu | Gln | Lys | Ser | Met | Leu | Glu | Lys | Ser | Trp | Asn | Leu | Ser | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |



Glu Lys Ala Val Ser Ser Glu Tyr Pro Gly Lys Gly Thr Ile Arg Lys  
165 170 175  
Lys Lys Ile Pro Val Ile Thr Cys Ser Gly Ile Ser Ala Arg Gln Arg  
180 185 190  
Arg Ile Gly Ala Lys Lys Lys Thr Asn Met Thr His Val Lys Ala Val  
195 200 205  
Ser Asp Val Ser Ser Gly Lys Gln Val Arg Gly Tyr Val Lys Gly Val  
210 215 220  
Ile Ser Glu Asp Val Leu Ser His Ala Glu Val Val Arg Leu Ser Lys  
225 230 235 240  
Lys Ile Lys Ser Gly Leu Arg Leu Asp Asp His Lys Ser Arg Leu Gln  
245 250 255  
Asp Arg Leu Gly Cys Glu Pro Ser Asp Glu Gln Leu Ala Val Ser Leu  
260 265 270  
Lys Ile Ser Arg Ala Glu Leu Gln Ala Trp Leu Met Glu Cys His Leu  
275 280 285  
Ala Arg Glu Lys Leu Ala Met Ser Asn Val Arg Leu Val Met Ser Ile  
290 295 300  
Ala Gln Arg Tyr Asp Asn Leu Gly Ala Glu Met Ser Asp Leu Val Gln  
305 310 315 320  
Gly Gly Leu Ile Gly Leu Leu Arg Gly Ile Glu Lys Phe Asp Ser Ser  
325 330 335  
Lys Gly Phe Arg Ile Ser Thr Tyr Val Tyr Trp Trp Ile Arg Gln Gly  
340 345 350  
Val Ser Arg Ala Leu Val Asp Asn Ser Arg Thr Leu Arg Leu Pro Thr  
355 360 365  
His Leu His Glu Arg Leu Gly Leu Ile Arg Asn Ala Lys Leu Arg Leu  
370 375 380  
Gln Glu Lys Gly Ile Thr Pro Ser Ile Asp Arg Ile Ala Glu Ser Leu  
385 390 395 400  
Asn Met Ser Gln Lys Lys Val Arg Asn Ala Thr Glu Ala Val Ser Lys  
405 410 415  
Val Phe Ser Leu Asp Arg Asp Ala Phe Pro Ser Leu Asn Gly Leu Pro  
420 425 430  
Gly Glu Thr His His Ser Tyr Ile Ala Asp Thr Arg Leu Glu Asn Asn  
435 440 445  
Pro Trp His Gly Tyr Asp Asp Leu Ala Leu Lys Glu Glu Val Ser Lys  
450 455 460  
Leu Ile Ser Ala Thr Leu Gly Glu Arg Glu Lys Glu Ile Ile Arg Leu  
465 470 475 480  
Tyr Tyr Gly Leu Asp Lys Glu Cys Leu Thr Trp Glu Asp Ile Ser Lys  
485 490 495  
Arg Ile Gly Leu Ser Arg Glu Arg Val Arg Gln Val Gly Leu Val Ala  
500 505 510  
Leu Glu Lys Leu Lys His Ala Ala Arg Lys Arg Lys Met Glu Ala Met  
515 520 525  
Ile Leu Lys Asn  
530

(2) INFORMATION FOR SEQ ID NO:1144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..502

(D) OTHER INFORMATION: / Ceres Seq. ID 1569118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

Met Ala Thr Ala Ala Val Ile Gly Leu Asn Thr Gly Lys Arg Leu Leu

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Ser Ser Ser Phe Tyr His Ser Asp Val Thr Glu Lys Phe Leu Ser Val | 20  | 25  | 30  |
| Asn Asp His Cys Ser Ser Gln Tyr His Ile Ala Ser Thr Lys Ser Gly | 35  | 40  | 45  |
| Ile Thr Ala Lys Lys Ala Ser Asn Tyr Ser Pro Ser Phe Pro Ser Ser | 50  | 55  | 60  |
| Asn Arg His Thr Gln Ser Ala Lys Ala Leu Lys Glu Asn Val Asp Val | 65  | 70  | 75  |
| Ala Ser Thr Glu Lys Pro Trp Leu Pro Asn Gly Thr Asp Lys Glu Leu | 85  | 90  | 95  |
| Glu Glu Glu Cys Tyr Asp Asp Asp Asp Leu Ile Ser His Ser Val Glu | 100 | 105 | 110 |
| Ala Ile Leu Leu Leu Gln Lys Ser Met Leu Glu Lys Ser Trp Asn Leu | 115 | 120 | 125 |
| Ser Phe Glu Lys Ala Val Ser Ser Glu Tyr Pro Gly Lys Gly Thr Ile | 130 | 135 | 140 |
| Arg Lys Lys Lys Ile Pro Val Ile Thr Cys Ser Gly Ile Ser Ala Arg | 145 | 150 | 155 |
| Gln Arg Arg Ile Gly Ala Lys Lys Lys Thr Asn Met Thr His Val Lys | 165 | 170 | 175 |
| Ala Val Ser Asp Val Ser Ser Gly Lys Gln Val Arg Gly Tyr Val Lys | 180 | 185 | 190 |
| Gly Val Ile Ser Glu Asp Val Leu Ser His Ala Glu Val Val Arg Leu | 195 | 200 | 205 |
| Ser Lys Lys Ile Lys Ser Gly Leu Arg Leu Asp Asp His Lys Ser Arg | 210 | 215 | 220 |
| Leu Gln Asp Arg Leu Gly Cys Glu Pro Ser Asp Glu Gln Leu Ala Val | 225 | 230 | 235 |
| Ser Leu Lys Ile Ser Arg Ala Glu Leu Gln Ala Trp Leu Met Glu Cys | 245 | 250 | 255 |
| His Leu Ala Arg Glu Lys Leu Ala Met Ser Asn Val Arg Leu Val Met | 260 | 265 | 270 |
| Ser Ile Ala Gln Arg Tyr Asp Asn Leu Gly Ala Glu Met Ser Asp Leu | 275 | 280 | 285 |
| Val Gln Gly Gly Leu Ile Gly Leu Leu Arg Gly Ile Glu Lys Phe Asp | 290 | 295 | 300 |
| Ser Ser Lys Gly Phe Arg Ile Ser Thr Tyr Val Tyr Trp Trp Ile Arg | 305 | 310 | 315 |
| Gln Gly Val Ser Arg Ala Leu Val Asp Asn Ser Arg Thr Leu Arg Leu | 325 | 330 | 335 |
| Pro Thr His Leu His Glu Arg Leu Gly Leu Ile Arg Asn Ala Lys Leu | 340 | 345 | 350 |
| Arg Leu Gln Glu Lys Gly Ile Thr Pro Ser Ile Asp Arg Ile Ala Glu | 355 | 360 | 365 |
| Ser Leu Asn Met Ser Gln Lys Lys Val Arg Asn Ala Thr Glu Ala Val | 370 | 375 | 380 |
| Ser Lys Val Phe Ser Leu Asp Arg Asp Ala Phe Pro Ser Leu Asn Gly | 385 | 390 | 395 |
| Leu Pro Gly Glu Thr His His Ser Tyr Ile Ala Asp Thr Arg Leu Glu | 405 | 410 | 415 |
| Asn Asn Pro Trp His Gly Tyr Asp Asp Leu Ala Leu Lys Glu Glu Val | 420 | 425 | 430 |
| Ser Lys Leu Ile Ser Ala Thr Leu Gly Glu Arg Glu Lys Glu Ile Ile | 435 | 440 | 445 |
| Arg Leu Tyr Tyr Gly Leu Asp Lys Glu Cys Leu Thr Trp Glu Asp Ile | 450 | 455 | 460 |
| Ser Lys Arg Ile Gly Leu Ser Arg Glu Arg Val Arg Gln Val Gly Leu | 465 | 470 | 475 |
| Val Ala Leu Glu Lys Leu Lys His Ala Ala Arg Lys Arg Lys Met Glu | 485 | 490 | 495 |

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Ala Met Ile Leu Lys Asn  
500

(2) INFORMATION FOR SEQ ID NO:1145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..382

(D) OTHER INFORMATION: / Ceres Seq. ID 1569119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Glu | Lys | Ser | Trp | Asn | Leu | Ser | Phe | Glu | Lys | Ala | Val | Ser | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     | 15  |     |     |     |     |
| Glu | Tyr | Pro | Gly | Lys | Gly | Thr | Ile | Arg | Lys | Lys | Lys | Ile | Pro | Val | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Cys | Ser | Gly | Ile | Ser | Ala | Arg | Gln | Arg | Arg | Ile | Gly | Ala | Lys | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Lys | Thr | Asn | Met | Thr | His | Val | Lys | Ala | Val | Ser | Asp | Val | Ser | Ser | Gly |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Lys | Gln | Val | Arg | Gly | Tyr | Val | Lys | Gly | Val | Ile | Ser | Glu | Asp | Val | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | His | Ala | Glu | Val | Arg | Leu | Ser | Lys | Lys | Ile | Lys | Ser | Gly | Leu |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Arg | Leu | Asp | Asp | His | Lys | Ser | Arg | Leu | Gln | Asp | Arg | Leu | Gly | Cys | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Ser | Asp | Glu | Gln | Leu | Ala | Val | Ser | Leu | Lys | Ile | Ser | Arg | Ala | Glu |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Leu | Gln | Ala | Trp | Leu | Met | Glu | Cys | His | Leu | Ala | Arg | Glu | Lys | Leu | Ala |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Met | Ser | Asn | Val | Arg | Leu | Val | Met | Ser | Ile | Ala | Gln | Arg | Tyr | Asp | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Gly | Ala | Glu | Met | Ser | Asp | Leu | Val | Gln | Gly | Gly | Leu | Ile | Gly | Leu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Arg | Gly | Ile | Glu | Lys | Phe | Asp | Ser | Ser | Lys | Gly | Phe | Arg | Ile | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Tyr | Val | Tyr | Trp | Trp | Ile | Arg | Gln | Gly | Val | Ser | Arg | Ala | Leu | Val |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Asp | Asn | Ser | Arg | Thr | Leu | Arg | Gly | Pro | Thr | His | Leu | His | Glu | Arg | Leu |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Gly | Leu | Ile | Arg | Asn | Ala | Lys | Leu | Arg | Leu | Gln | Glu | Lys | Gly | Ile | Thr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Pro | Ser | Ile | Asp | Arg | Ile | Ala | Glu | Ser | Leu | Asn | Met | Ser | Gln | Lys | Lys |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Arg | Asn | Ala | Thr | Glu | Ala | Val | Ser | Lys | Val | Phe | Ser | Leu | Asp | Arg |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | Ala | Phe | Pro | Ser | Leu | Asn | Gly | Leu | Pro | Gly | Glu | Thr | His | His | Ser |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Tyr | Ile | Ala | Asp | Thr | Arg | Leu | Glu | Asn | Asn | Pro | Trp | His | Gly | Tyr | Asp |
|     |     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |
| Asp | Leu | Ala | Leu | Lys | Glu | Glu | Val | Ser | Lys | Leu | Ile | Ser | Ala | Thr | Leu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Gly | Glu | Arg | Glu | Lys | Glu | Ile | Ile | Arg | Leu | Tyr | Tyr | Gly | Leu | Asp | Lys |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Glu | Cys | Leu | Thr | Trp | Glu | Asp | Ile | Ser | Lys | Arg | Ile | Gly | Leu | Ser | Arg |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Glu | Arg | Val | Arg | Gln | Val | Gly | Leu | Val | Ala | Leu | Glu | Lys | Leu | Lys | His |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ala | Ala | Arg | Lys | Arg | Lys | Met | Glu | Ala | Met | Ile | Leu | Lys | Asn |     |     |

370 375 380

(2) INFORMATION FOR SEQ ID NO:1146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1352 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1352

(D) OTHER INFORMATION: / Ceres Seq. ID 1569144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| aaaaRoccc   | tctctcttca  | gtctctctct  | ctctagacga  | tctctatctt  | gaataaaaa   | 60   |
| ccgataatga  | cctcaaccaa  | tccgggtggtc | gcggaagtaa  | taccggcgga  | aaactctaca  | 120  |
| gatgctacag  | agacgaagat  | tgcaacgaag  | gaagctgggtg | aagcaccgga  | gaagaagggtg | 180  |
| aggaagagc   | atacaatcac  | caagctctaga | gagagttgga  | ctgaaggaga  | acacgacaa   | 240  |
| tttctggaag  | ctcttcaatt  | gtttgatcgt  | gactggaaaa  | agatagaaga  | ttttgtgtgtg | 300  |
| tcaaagacag  | ttattcagat  | cagtagccat  | gccccaaaa   | actttctaaa  | gggtccaaaa  | 360  |
| aatgggactt  | tagcacatgt  | tccacccctc  | aggcctaagc  | gcaaagctgc  | tcattccatat | 420  |
| cctcaaaaag  | catcgaaaaa  | tgctcaaatg  | tcgcttcacg  | tttccatgtc  | ctttctact   | 480  |
| caataaaaa   | acctgctcgg  | atatactcca  | tggggatgatg | atacatctgc  | attgtttaa   | 540  |
| attgctgtta  | gtgggggttat | tccaccagaa  | gatgaacttg  | atactctttg  | tgagacagaa  | 600  |
| gttgatgttg  | gatcaaatga  | catgataagt  | gaaactagtc  | cttcagcatc  | tggtatcgga  | 660  |
| agctcaagca  | gaacactatc  | agattctaa   | ggttttgagac | tgccgaaaca  | agctccotca  | 720  |
| atgcattggtc | ttctgtattt  | tgctgaggtt  | tataacttca  | ttgggaggtg  | gttcgatcct  | 780  |
| gacagcaaa   | gcgcgatgaa  | aaagctcaag  | gaaatggatc  | ctataaaatt  | cgaaactgtt  | 840  |
| ttgtctgtga  | tgagaaacct  | cacagtgaa   | ttgtcaaac   | ctgactttga  | acctacttct  | 900  |
| gaatatgttg  | atgctgcaga  | ggaaggtcat  | gaacacttaa  | gctcttagct  | gtttgtgcac  | 960  |
| tcaacaagtt  | atatacttc   | ttgacgactt  | cttgctcgca  | acaactctct  | accagctatc  | 1020 |
| aaatgcacatg | taagggtgtt  | gtctgaggag  | aacataactg  | agtcgtctgc  | acaaacaaga  | 1080 |
| ggaactcatg  | cagtttcggt  | cagaaccagt  | cgtgtgaatg  | gtagatatat  | gtatgtgtgt  | 1140 |
| gtagaaaatg  | gtttaccaat  | gtatcttctt  | tttgataatt  | atttttccat  | gcottttgtg  | 1200 |
| atatgtaatg  | ttctttacct  | cgttctctga  | ttggttattt  | cttcgtttatc | tgtttaacca  | 1260 |
| aaagctatgt  | aaacacagtag | caaattgtta  | cttaactcgg  | aagttagata  | cataactctg  | 1320 |
| ttgtattgca  | cttgatcaaa  | gcgttaaagct | cc          |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..293

(D) OTHER INFORMATION: / Ceres Seq. ID 1569145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Ser | Thr | Asn | Pro | Val | Val | Ala | Glu | Val | Ile | Pro | Ala | Glu | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Thr | Asp | Ala | Thr | Glu | Thr | Thr | Ile | Ala | Thr | Thr | Glu | Ala | Gly | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Pro | Glu | Lys | Lys | Val | Arg | Lys | Ala | Tyr | Thr | Ile | Thr | Lys | Ser | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Glu | Ser | Trp | Thr | Glu | Gly | Glu | His | Asp | Lys | Phe | Leu | Glu | Ala | Leu | Gln |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Phe | Asp | Arg | Asp | Trp | Lys | Lys | Ile | Glu | Asp | Phe | Val | Gly | Ser | Lys |
|     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |     |
| Thr | Val | Ile | Gln | Ile | Ser | Ser | His | Ala | Gln | Lys | Tyr | Phe | Leu | Lys | Val |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Gln | Lys | Asn | Gly | Thr | Leu | Ala | His | Val | Pro | Pro | Arg | Pro | Lys | Arg |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ala | Ala | His | Pro | Tyr | Pro | Gln | Lys | Ala | Ser | Lys | Asn | Ala | Gln | Met |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Leu | His | Val | Ser | Met | Ser | Phe | Pro | Thr | Gln | Ile | Asn | Asn | Leu | Pro |
|     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Gly | Tyr | Thr | Pro | Trp | Asp | Asp | Asp | Thr | Ser | Ala | Leu | Leu | Asn | Ile | Ala |
|     | 145 |     |     |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |
| Val | Ser | Gly | Val | Ile | Pro | Pro | Glu | Asp | Glu | Leu | Asp | Thr | Leu | Cys | Gly |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Glu | Val | Asp | Val | Gly | Ser | Asn | Asp | Met | Ile | Ser | Glu | Thr | Ser | Pro |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |
| Ser | Ala | Ser | Gly | Ile | Gly | Ser | Ser | Ser | Arg | Thr | Leu | Ser | Asp | Ser | Lys |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Gly | Leu | Arg | Leu | Ala | Lys | Gln | Ala | Pro | Ser | Met | His | Gly | Leu | Pro | Asp |
|     |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Ala | Glu | Val | Tyr | Asn | Phe | Ile | Gly | Ser | Val | Phe | Asp | Pro | Asp | Ser |
|     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Lys | Gly | Arg | Met | Lys | Lys | Leu | Lys | Glu | Met | Asp | Pro | Ile | Asn | Phe | Glu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Val | Leu | Leu | Leu | Met | Arg | Asn | Leu | Thr | Val | Asn | Leu | Ser | Asn | Pro |
|     |     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |
| Asp | Phe | Glu | Pro | Thr | Ser | Glu | Tyr | Val | Asp | Ala | Ala | Glu | Glu | Gly | His |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     |     |     | 285 |     |
| Glu | His | Leu | Ser | Ser |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 290 |

(2) INFORMATION FOR SEQ ID NO:1148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1569146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | His | Val | Ser | Met | Ser | Phe | Pro | Thr | Gln | Ile | Asn | Asn | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Gly | Tyr | Thr | Pro | Trp | Asp | Asp | Asp | Thr | Ser | Ala | Leu | Leu | Asn | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Val | Ser | Gly | Val | Ile | Pro | Pro | Glu | Asp | Glu | Leu | Asp | Thr | Leu | Cys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Ala | Glu | Val | Asp | Val | Gly | Ser | Asn | Asp | Met | Ile | Ser | Glu | Thr | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Ser | Ala | Ser | Gly | Ile | Gly | Ser | Ser | Ser | Arg | Thr | Leu | Ser | Asp | Ser |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Gly | Leu | Arg | Leu | Ala | Lys | Gln | Ala | Pro | Ser | Met | His | Gly | Leu | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Phe | Ala | Glu | Val | Tyr | Asn | Phe | Ile | Gly | Ser | Val | Phe | Asp | Pro | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Lys | Gly | Arg | Met | Lys | Lys | Leu | Lys | Glu | Met | Asp | Pro | Ile | Asn | Phe |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Glu | Thr | Val | Leu | Leu | Met | Arg | Asn | Leu | Thr | Val | Asn | Leu | Ser | Asn |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Asp | Phe | Glu | Pro | Thr | Ser | Glu | Tyr | Val | Asp | Ala | Ala | Glu | Glu | Gly |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| His | Glu | His | Leu | Ser | Ser |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 165 |

(2) INFORMATION FOR SEQ ID NO:1149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..160  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569147  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:  
Met Ser Phe Pro Thr Gln Ile Asn Asn Leu Pro Gly Tyr Thr Pro Trp  
1 5 10 15  
Asp Asp Asp Thr Ser Ala Leu Leu Asn Ile Ala Val Ser Gly Val Ile  
20 25 30  
Pro Pro Glu Asp Glu Leu Asp Thr Leu Cys Gly Ala Glu Val Asp Val  
35 40 45  
Gly Ser Asn Asp Met Ile Ser Glu Thr Ser Pro Ser Ala Ser Gly Ile  
50 55 60  
Gly Ser Ser Ser Arg Thr Leu Ser Asp Ser Lys Gly Leu Arg Leu Ala  
65 70 75 80  
Lys Gln Ala Pro Ser Met His Gly Leu Pro Asp Phe Ala Glu Val Tyr  
85 90 95  
Asn Phe Ile Gly Ser Val Phe Asp Pro Asp Ser Lys Gly Arg Met Lys  
100 105 110  
Lys Leu Lys Glu Met Asp Pro Ile Asn Phe Glu Thr Val Leu Leu Leu  
115 120 125  
Met Arg Asn Leu Thr Val Asn Leu Ser Asn Pro Asp Phe Glu Pro Thr  
130 135 140  
Ser Glu Tyr Val Asp Ala Ala Glu Glu Gly His Glu His Leu Ser Ser  
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:1150:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1198

(D) OTHER INFORMATION: / Ceres Seq. ID 1569148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

|             |            |             |            |            |             |      |
|-------------|------------|-------------|------------|------------|-------------|------|
| aaaaacccac  | aaatggggat | gagtgtccaa  | agactgcact | ctctctctct | ccctctggctc | 60   |
| cggcgaaaaa  | cccccttttg | atttcattga  | taaaacgcga | atcgatctct | cggtgtggaag | 120  |
| aagaagaaga  | acacgatggg | aacaatgggt  | aaagcattct | acagcgtagg | attctggatc  | 180  |
| cgtagaaactg | gtcaaagca  | tgatcggctc  | ggttgtcgcc | tccaagggaa | aaatcatttc  | 240  |
| cgagaaacagc | tatcaaggca | ccgcacactc  | atgaatgttt | ttgacaaaac | ccctaagtgtg | 300  |
| gataaaggggg | cttttggggc | gtcctaacgct | tctctctctg | gtgatgttca | tgtgggaaga  | 360  |
| ggttcttccca | tttggtatgg | atgtgtctttg | agaggagatg | ctaacagcat | tagtgtttga  | 420  |
| gctgggacga  | atattcagga | caacgctctt  | gtccacgttg | ctaagaccac | cttaagtggg  | 480  |
| aagggtcttac | ctactgtcat | tggagacaat  | gtcaccattg | gtcatagtgc | tgttttaccat | 540  |
| ggctgcactg  | tcgaggatga | ggcctatat   | ggtacaaagt | caactgtctt | ggatggagct  | 600  |
| catgttgaaa  | aacatgccat | ggttgcttct  | ggagactctt | ttaggcagaa | cactagaatt  | 660  |
| Ccctctggcg  | aggtttgggg | agggcaaccga | gctaattttc | tgagggaagt | gacagaaga   | 720  |
| gaagaagtct  | tcttctccag | tctggctgtg  | gagtaactca | acttagctca | agctcacgcc  | 780  |
| acagagaacg  | caaaagaact | ggacgaggtg  | gagttcaaga | agcttctaaa | caagaagaa   | 840  |
| gctcgagata  | cagaatatga | ttcagtaact  | gatgatctga | cgctccctga | gaatgtacca  | 900  |
| aaagcagctt  | gaggcgttta | acctgtgcgc  | ccttgogaat | cttgatttgt | ttggtattga  | 960  |
| aaagtaaaaa  | caaaGAAct  | gatttccctg  | ttctccaata | aagttttctt | gggcgtaaaa  | 1020 |

tccattggcc agtgcctact gggaaagttt tcggcttaaa ggcatcatt tctctgttaa 1080  
agattgtgag gggttttgtt ctcttgtaac ttgagaaaga aaagttgtaa ccttttcttc 1140  
ctttttatgt cgtctaataa attgttgatc agacagacat ttagggtgac ctttgccc

(2) INFORMATION FOR SEQ ID NO:1151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..258

(D) OTHER INFORMATION: / Ceres Seq. ID 1569149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Thr | Met | Gly | Lys | Ala | Phe | Tyr | Ser | Val | Gly | Phe | Trp | Ile | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Thr | Gly | Gln | Ala | Leu | Asp | Arg | Leu | Gly | Cys | Arg | Leu | Gln | Gly | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | His | Phe | Arg | Glu | Gln | Leu | Ser | Arg | His | Arg | Thr | Leu | Met | Asn | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Asp | Lys | Thr | Pro | Asn | Val | Asp | Lys | Gly | Ala | Phe | Val | Ala | Pro | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Ser | Leu | Ser | Gly | Asp | Val | His | Val | Gly | Arg | Gly | Ser | Ser | Ile | Trp |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Tyr | Gly | Cys | Val | Leu | Arg | Gly | Asp | Ala | Asn | Ser | Ile | Ser | Val | Gly | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Thr | Asn | Ile | Gln | Asp | Asn | Ala | Leu | Val | His | Val | Ala | Lys | Thr | Asn |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Ser | Gly | Lys | Val | Leu | Pro | Thr | Val | Ile | Gly | Asp | Asn | Val | Thr | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | His | Ser | Ala | Val | Leu | His | Gly | Cys | Thr | Val | Glu | Asp | Glu | Ala | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Gly | Thr | Ser | Ala | Thr | Val | Leu | Asp | Gly | Ala | His | Val | Glu | Lys | His |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ala | Met | Val | Ala | Ser | Gly | Ala | Leu | Val | Arg | Gln | Asn | Thr | Arg | Ile | Pro |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ser | Gly | Glu | Val | Trp | Gly | Gly | Asn | Pro | Ala | Lys | Phe | Leu | Arg | Lys | Val |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Thr | Glu | Glu | Glu | Arg | Val | Phe | Phe | Ser | Ser | Ser | Ala | Val | Glu | Tyr | Ser |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | Leu | Ala | Gln | Ala | His | Ala | Thr | Glu | Asn | Ala | Lys | Asn | Leu | Asp | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Ala | Glu | Phe | Lys | Lys | Leu | Leu | Asn | Lys | Lys | Asn | Ala | Arg | Asp | Thr | Glu |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Tyr | Asp | Ser | Val | Leu | Asp | Asp | Leu | Thr | Leu | Pro | Glu | Asn | Val | Pro | Lys |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..255

(D) OTHER INFORMATION: / Ceres Seq. ID 1569150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

Met Gly Lys Ala Phe Tyr Ser Val Gly Phe Trp Ile Arg Glu Thr Gly  
1 5 10 15  
Gln Ala Leu Asp Arg Leu Gly Cys Arg Leu Gln Gly Lys Asn His Phe  
20 25 30  
Arg Glu Gln Leu Ser Arg His Arg Thr Leu Met Asn Val Phe Asp Lys  
35 40 45  
Thr Pro Asn Val Asp Lys Gly Ala Phe Val Ala Pro Asn Ala Ser Leu  
50 55 60  
Ser Gly Asp Val His Val Gly Arg Gly Ser Ser Ile Trp Tyr Gly Cys  
65 70 75 80  
Val Leu Arg Gly Asp Ala Asn Ser Ile Ser Val Gly Ala Gly Thr Asn  
85 90 95  
Ile Gln Asp Asn Ala Leu Val His Val Ala Lys Thr Asn Leu Ser Gly  
100 105 110  
Lys Val Leu Pro Thr Val Ile Gly Asp Asn Val Thr Ile Gly His Ser  
115 120 125  
Ala Val Leu His Gly Cys Thr Val Glu Asp Glu Ala Tyr Ile Gly Thr  
130 135 140  
Ser Ala Thr Val Leu Asp Gly Ala His Val Glu Lys His Ala Met Val  
145 150 155 160  
Ala Ser Gly Ala Leu Val Arg Gln Asn Thr Arg Ile Pro Ser Gly Glu  
165 170 175  
Val Trp Gly Gly Asn Pro Ala Lys Phe Leu Arg Lys Val Thr Glu Glu  
180 185 190  
Glu Arg Val Phe Phe Ser Ser Ser Ala Val Glu Tyr Ser Asn Leu Ala  
195 200 205  
Gln Ala His Ala Thr Glu Asn Ala Lys Asn Leu Asp Glu Ala Glu Phe  
210 215 220  
Lys Lys Leu Leu Asn Lys Lys Asn Ala Arg Asp Thr Glu Tyr Asp Ser  
225 230 235 240  
Val Leu Asp Asp Leu Thr Leu Pro Glu Asn Val Pro Lys Ala Ala  
245 250 255

(2) INFORMATION FOR SEQ ID NO:1153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213

(D) OTHER INFORMATION: / Ceres Seq. ID 1569151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:

Met Asn Val Phe Asp Lys Thr Pro Asn Val Asp Lys Gly Ala Phe Val  
1 5 10 15  
Ala Pro Asn Ala Ser Leu Ser Gly Asp Val His Val Gly Arg Gly Ser  
20 25 30  
Ser Ile Trp Tyr Gly Cys Val Leu Arg Gly Asp Ala Asn Ser Ile Ser  
35 40 45  
Val Gly Ala Gly Thr Asn Ile Gln Asp Asn Ala Leu Val His Val Ala  
50 55 60  
Lys Thr Asn Leu Ser Gly Lys Val Leu Pro Thr Val Ile Gly Asp Asn  
65 70 75 80  
Val Thr Ile Gly His Ser Ala Val Leu His Gly Cys Thr Val Glu Asp  
85 90 95  
Glu Ala Tyr Ile Gly Thr Ser Ala Thr Val Leu Asp Gly Ala His Val  
100 105 110  
Glu Lys His Ala Met Val Ala Ser Gly Ala Leu Val Arg Gln Asn Thr  
115 120 125  
Arg Ile Pro Ser Gly Glu Val Trp Gly Gly Asn Pro Ala Lys Phe Leu



```

 130 135 140
Arg Lys Val Thr Glu Glu Arg Val Phe Phe Ser Ser Ser Ala Val
145 150 155 160
Glu Tyr Ser Asn Leu Ala Gln Ala His Ala Thr Glu Asn Ala Lys Asn
 165 170 175
Leu Asp Glu Ala Glu Phe Lys Lys Leu Leu Asn Lys Lys Asn Ala Arg
 180 185 190
Asp Thr Glu Tyr Asp Ser Val Leu Asp Asp Leu Thr Leu Pro Glu Asn
 195 200 205
Val Pro Lys Ala Ala
210

```

(2) INFORMATION FOR SEQ ID NO:1154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1537
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:

```

atcgaaatta ttgtggtggt ttgtgaacag aaaccaagca ggattaaaga tggttcaatc 60
tgtgttaatt tctcgtaaca agggttttgc ggaGcaagat ctaactaagc ttgatgtaac 120
aaagttacat cctctgtctc ctgaagtcac ttctgcgcaa gcaaccataa atatcggaac 180
cattggtcat gtgcgtcacg gtaaatcgac tatagtgaag gctatctctg gtgttcacag 240
tgtgcgtttt aagaatgaat tagagcgtaa cattaccatt aagcttgggt agtcaaatgc 300
aaagatttac aagtggtgag atgacaagtg ccttagacca atgtgtcata agtcatatgg 360
gagtggaaaa gaagacaacc caacttgtga tgtcccggga ttgacaatt gcaagatgac 420
actactgaga catgtctcat gtgtcgattg tccaggacac gatattctta tggcgacaat 480
gtcctaagga gcagcaatcg tggatggtgc ttactctcta attgctgcta acgggagtgt 540
tccacaacca caaacccgtg aacatcttgc ttctgtgat atgatgogcc ttaagcatat 600
cataatcctt cagaacaaga ttgatctcat taatgagaaa gccgccactg aacagcacga 660
ggctattccg aaatttataa cgaacacgaa tgctgaggat gcacctatag ttctgtctc 720
agcacaaact aaatacaaca ttgatgttgt gagtgaatac gatgattgtg attcgttcct tcatgtc 780
cctgtgaga gactttgtgt caccaccaaa gatgattgtg attcgttcct tcatgtc 840
taaacctggc tcggcgggtc atgaaatgaa aggtgtgtgt gctggtggaa gtaacctcca 900
gtgaacccaa tgattgaaat tagaccttgt atcaactggca aagatgagca tggaaactca 960
aaatgcactc caatttactc gcgtataact tcaactacac cggaacagaa cgaagcttcag 1020
tttgtgttac cgggaggtct atactcgaagt ggaacaacca ttgacctac gtctaccggt 1080
gtgatgaagt ttgttgggtc agtccttggt gaaatgggta ctctccctga cgtcttgggt 1140
gagcttgtag taagttaaca gctttctgac gctctcattg gagtggagac aaagga 1200
gagaagcata tgaagtgttc aaagctaacc aaagaagaga tattgatggt gaacactcgg 1260
tctatgtcta cgggagctaa ggtttattgga gtcaagaaa atatggtgaa actccaactg 1320
acgtctccgg ttgtaccac cataggagag aaggttgctt taagccgacg ttgtcagagg 1380
cattggcgctc taattggtaa gggtcagatt atggctggaa ccaccatcga gttctcctc 1440
cctcctttct aatgaagtag tgatgagttt ttatatgtt ttgcattcaa aaataattaa 1500
catgtgcctt tgtatgttta atcactttct ttcgact

```

(2) INFORMATION FOR SEQ ID NO:1155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..300
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:

```

Ser Lys Leu Leu Trp Cys Phe Val Asn Arg Asn Gln Ala Gly Leu Lys
1 5 10
Met Val Gln Ser Val Leu Ile Ser Arg Asn Lys Gly Leu Ala Glu Gln
20 25 30
Asp Leu Thr Lys Leu Asp Val Thr Lys Leu His Pro Leu Ser Pro Glu
35 40 45
Val Ile Ser Arg Gln Ala Thr Ile Asn Ile Gly Thr Ile Gly His Val
50 55 60
Ala His Gly Lys Ser Thr Ile Val Lys Ala Ile Ser Gly Val Gln Thr
65 70 75 80
Val Arg Phe Lys Asn Glu Leu Glu Arg Asn Ile Thr Ile Lys Leu Gly
85 90 95
Tyr Ala Asn Ala Lys Ile Tyr Lys Cys Glu Asp Asp Lys Cys Pro Arg
100 105 110
Pro Met Cys Tyr Lys Ser Tyr Gly Ser Gly Lys Glu Asp Asn Pro Thr
115 120 125
Cys Asp Val Pro Gly Phe Asp Asn Cys Lys Met Thr Leu Leu Arg His
130 135 140
Val Ser Cys Val Asp Cys Pro Gly His Asp Ile Leu Met Ala Thr Met
145 150 155 160
Leu Asn Gly Ala Ala Ile Val Asp Gly Ala Leu Leu Ile Ala Ala
165 170 175
Asn Gly Ser Cys Pro Gln Pro Gln Thr Ala Glu His Leu Ala Ser Val
180 185 190
Asp Met Met Arg Leu Lys His Ile Ile Ile Leu Gln Asn Lys Ile Asp
195 200 205
Leu Ile Asn Glu Lys Ala Ala Thr Glu Gln His Glu Ala Ile Gln Lys
210 215 220
Phe Ile Thr Asn Thr Asn Ala Glu Asp Ala Pro Ile Val Pro Val Ser
225 230 235 240
Ala Gln Leu Lys Tyr Asn Ile Asp Val Val Ser Glu Tyr Ile Val Lys
245 250 255
Lys Ile Pro Ile Pro Val Arg Asp Phe Val Ser Pro Pro Lys Met Ile
260 265 270
Val Ile Arg Ser Phe Asp Val Asn Lys Pro Gly Ser Ala Gly His Glu
275 280 285
Met Lys Gly Gly Val Ala Gly Gly Ser Ile Leu Gln
290 295 300

```

(2) INFORMATION FOR SEQ ID NO:1156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..284

(D) OTHER INFORMATION: / Ceres Seq. ID 1569158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:

```

Met Val Gln Ser Val Leu Ile Ser Arg Asn Lys Gly Leu Ala Glu Gln
1 5 10
Asp Leu Thr Lys Leu Asp Val Thr Lys Leu His Pro Leu Ser Pro Glu
20 25 30
Val Ile Ser Arg Gln Ala Thr Ile Asn Ile Gly Thr Ile Gly His Val
35 40 45
Ala His Gly Lys Ser Thr Ile Val Lys Ala Ile Ser Gly Val Gln Thr
50 55 60
Val Arg Phe Lys Asn Glu Leu Glu Arg Asn Ile Thr Ile Lys Leu Gly
65 70 75 80
Tyr Ala Asn Ala Lys Ile Tyr Lys Cys Glu Asp Asp Lys Cys Pro Arg

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Tyr | Lys | Ser | Thr | Gly | Ser | Gly | Lys | Glu | Asp | Asn | Pro | Thr | Cys |
| 1   | Asp | Val | Pro | Gly | Phe | Asp | Asn | Cys | Lys | Met | Thr | Leu | Leu | Arg | His |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Ser | Cys | Val | Asp | Cys | Pro | Gly | His | Asp | Ile | Leu | Met | Ala | Thr | Met | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Asn | Gly | Ala | Ala | Ile | Val | Asp | Gly | Ala | Leu | Leu | Leu | Ile | Ala | Ala | Asn |
|     |     | 50  |     |     |     | 55  |     |     |     |     |     |     |     |     |     |
| Gly | Ser | Cys | Pro | Gln | Pro | Gln | Thr | Ala | Glu | His | Leu | Ala | Ser | Val | Asp |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Met | Met | Arg | Leu | Lys | His | Ile | Ile | Ile | Leu | Gln | Asn | Lys | Ile | Asp | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Asn | Glu | Lys | Ala | Ala | Thr | Glu | Gln | His | Glu | Ala | Ile | Gln | Lys | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Thr | Asn | Thr | Asn | Ala | Glu | Asp | Ala | Pro | Ile | Val | Pro | Val | Ser | Ala |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Leu | Lys | Tyr | Asn | Ile | Asp | Val | Val | Ser | Glu | Tyr | Ile | Val | Lys | Lys |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Pro | Ile | Pro | Val | Arg | Asp | Phe | Val | Ser | Pro | Pro | Lys | Met | Ile | Val |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Ile | Arg | Ser | Phe | Asp | Val | Asn | Lys | Pro | Gly | Ser | Ala | Gly | His | Glu | Met |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Gly | Gly | Val | Ala | Gly | Gly | Ser | Ile | Leu | Gln |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..1311

- (D) OTHER INFORMATION: / Ceres Seq. ID 1569164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:

```
aaggcgtgag ataataaaac cotttggcctt totcatagag atttgtccgg tctcttgttc 60
ctctttctcc ttcttctact gttagaattcc tcgaccaaac aactagctcc aatggcataa 120
tgagcattgt agtttgcatt ttcttctctc gtgaagaaga agaagatggc ttgggagaaa 180
gagggaagaag cgtcacaaaa cgggtgcgtt ttgtgtcctg atggggctcta ttgcgaggaa 240
gaaacgcgggt ttgtggagga cgaatcttga gacgatggag atttagattt tctcgagaaa 300
tctgatgaga gtgtgtgaaa gtttcagttt ttacctcttt tggatattgt cttatgggat 360
gacgatgaga ttctgagttt gatttcaaa gaaaacgaaa cgaatccatg ttttggggaa 420
caaatcttag atggcctttt gggttcttgt aggaagaggc ctttagattg gggtcttagg 480
gttaaatctc attatggggt tacttcattg acggctatac ttgctgtgaa ctacttcgat 540
aggtttatga caagtataaa gcttcagact gataagccat ggaatgtctc gcttgtgtgt 600
gtggctctct tgtcttttagc tgcataaagt gaagagattc aagttccatt gctcttagac 660
ctccaagtgg aagaagcaag atatctcttt gaagctaaga cgattcaaa aatggagcgt 720
ttgattcttt ctactcttca atggagaatg caccctgtga tagactctg taggaagtgt 780
cacattatcc ggcgatttgg ctctaaatgg caccagcaat tcgaactctg taggaagtgt 840
gagcgtcttc tgactcttgt tattgtgatg acgaggttta tgaggtactt cctctctctc 900
ttagctactg caataatgat ccttgccttc gaggaaatga agccatgtga tgaagtgtga 960
taccaatctc aaataacgac tctactcaaa gtcaatcagg agaaaagtaa tgaatgtcat 1020
gaactgttgt tggagcacaa tccaagcaag aagaggatga tgaatttgtt tgatcaggac 1080
agtcacaagt gtgtattaga cttttagtgc agtcacaata gctcctggaa tgtctccact 1140
actgtctcag tgcctctcac atcttctgtt ccagagcctc tgcgtcaag aagaagagtt 1200
caggagcagc aaatgagatt gccctcaata aaccgtatgt tctcgtatgt gcttagtagt 1260
cctcgctagt acctttcttt gatcaaatgt gtcaaaacat aaattcGat c
```

(2) INFORMATION FOR SEQ ID NO:1159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..367

- (D) OTHER INFORMATION: / Ceres Seq. ID 1569165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:

```
Met Ala Leu Glu Lys Glu Glu Glu Ala Ser Gln Asn Gly Ala Phe Cys
1 5 10 15
Val Leu Asp Gly Leu Tyr Cys Glu Glu Glu Thr Gly Phe Val Glu Asp
20 25 30
Asp Leu Asp Asp Asp Gly Asp Leu Asp Phe Leu Glu Lys Ser Asp Glu
35 40 45
Ser Val Val Lys Phe Gln Phe Leu Pro Leu Leu Asp Met Phe Leu Trp
50 55 60
Asp Asp Asp Glu Ile Leu Ser Leu Ile Ser Lys Glu Asn Glu Thr Asn
65 70 75 80
Pro Cys Phe Gly Glu Gln Ile Leu Asp Gly Phe Leu Val Ser Cys Arg
85 90 95
Lys Glu Ala Leu Asp Trp Val Leu Arg Val Lys Ser His Tyr Gly Phe
100 105 110
Thr Ser Leu Thr Ala Ile Leu Ala Val Asn Tyr Phe Asp Arg Phe Met
```

| (X1) SEQUENCE DESCRIPTION: SEQ INFORMATION |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|--------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met                                        | Phe | Leu | Trp | Asp | Asp | Asp | Glu | Ile | Leu | Ser | Leu | Ile | Ser | Lys | Glu |  |
| 1                                          |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asn                                        | Glu | Thr | Asn | Pro | Cys | Phe | Gly | Glu | Gln | Ile | Leu | Asp | Gly | Phe | Leu |  |
|                                            |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val                                        | Ser | Cys | Arg | Lys | Glu | Ala | Leu | Asp | Trp | Val | Leu | Arg | Val | Lys | Ser |  |
|                                            |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| His                                        | Tyr | Gly | Phe | Thr | Ser | Leu | Thr | Ala | Ile | Leu | Ala | Val | Asn | Tyr | Phe |  |
|                                            |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Asp                                        | Arg | Phe | Met | Thr | Ser | Ile | Lys | Leu | Gln | Thr | Asp | Lys | Pro | Trp | Met |  |
| 65                                         |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Ser                                        | Gln | Leu | Val | Ala | Val | Ala | Ser | Leu | Ser | Leu | Ala | Ala | Lys | Val | Glu |  |
|                                            |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Glu                                        | Ile | Gln | Val | Pro | Leu | Leu | Leu | Asp | Leu | Gln | Val | Glu | Glu | Ala | Arg |  |
|                                            |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Tyr                                        | Leu | Phe | Glu | Ala | Lys | Thr | Ile | Gln | Arg | Met | Glu | Leu | Leu | Ile | Leu |  |
|                                            |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ser                                        | Thr | Leu | Gln | Trp | Arg | Met | His | Pro | Val | Thr | Pro | Ile | Ser | Phe | Phe |  |
|                                            |     |     | 130 |     |     | 135 |     |     |     |     |     | 140 |     |     |     |  |

Asp His Ile Ile Arg Arg Phe Gly Ser Lys Trp His Gln Gln Leu Asp  
145 150 155 160  
Phe Cys Arg Lys Cys Glu Arg Leu Leu Ile Ser Val Ile Ala Asp Thr  
165 170 175  
Arg Phe Met Arg Tyr Phe Pro Ser Val Leu Ala Thr Ala Ile Met Ile  
180 185 190  
Leu Val Phe Glu Glu Leu Lys Pro Cys Asp Glu Val Glu Tyr Gln Ser  
195 200 205  
Gln Ile Thr Thr Leu Leu Lys Val Asn Gln Glu Lys Val Asn Glu Cys  
210 215 220  
Tyr Glu Leu Leu Leu Glu His Asn Pro Ser Lys Lys Arg Met Met Asn  
225 230 235 240  
Leu Val Asp Gln Asp Ser Pro Ser Gly Val Leu Asp Phe Asp Asp Ser  
245 250 255  
Ser Asn Ser Ser Trp Asn Val Ser Thr Thr Ala Ser Val Ser Ser Ser  
260 265 270  
Ser Ser Ser Pro Glu Pro Leu Leu Lys Arg Arg Arg Val Gln Glu Gln  
275 280 285  
Gln Met Arg Leu Pro Ser Ile Asn Arg Met Phe Leu Asp Val Leu Ser  
290 295 300  
Ser Pro Arg  
305

(2) INFORMATION FOR SEQ ID NO:1161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..240
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:

Met Thr Ser Ile Lys Leu Gln Thr Asp Lys Pro Trp Met Ser Gln Leu  
1 5 10 15  
Val Ala Val Ala Ser Leu Ser Leu Ala Ala Lys Val Glu Glu Ile Gln  
20 25 30  
Val Pro Leu Leu Leu Asp Leu Gln Val Glu Glu Ala Arg Tyr Leu Phe  
35 40 45  
Glu Ala Lys Thr Ile Gln Arg Met Glu Leu Leu Ile Leu Ser Thr Leu  
50 55 60  
Gln Trp Arg Met His Pro Val Thr Pro Ile Ser Phe Phe Asp His Ile  
65 70 75 80  
Ile Arg Arg Phe Gly Ser Lys Trp His Gln Gln Leu Asp Phe Cys Arg  
85 90 95  
Lys Cys Glu Arg Leu Leu Ile Ser Val Ile Ala Asp Thr Arg Phe Met  
100 105 110  
Arg Tyr Phe Pro Ser Val Leu Ala Thr Ala Ile Met Ile Leu Val Phe  
115 120 125  
Glu Glu Leu Lys Pro Cys Asp Glu Val Glu Tyr Gln Ser Gln Ile Thr  
130 135 140  
Thr Leu Leu Lys Val Asn Gln Glu Lys Val Asn Glu Cys Tyr Glu Leu  
145 150 155 160  
Leu Leu Glu His Asn Pro Ser Lys Lys Arg Met Met Asn Leu Val Asp  
165 170 175  
Gln Asp Ser Pro Ser Gly Val Leu Asp Phe Asp Asp Ser Ser Asn Ser  
180 185 190  
Ser Trp Asn Val Ser Thr Thr Ala Ser Val Ser Ser Ser Ser Ser Ser  
195 200 205  
Pro Glu Pro Leu Leu Lys Arg Arg Val Gln Glu Gln Met Arg

|                         |                     |                     |
|-------------------------|---------------------|---------------------|
| 210                     | 215                 | 220                 |
| Leu Pro Ser Ile Asn Arg | Met Phe Leu Asp Val | Leu Ser Ser Pro Arg |
| 225                     | 230                 | 235                 |
|                         |                     | 240                 |

(2) INFORMATION FOR SEQ ID NO:1162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1386

(D) OTHER INFORMATION: / Ceres Seq. ID 1569168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| attttctcta  | cttgtccact  | tttctcacgc  | cgcacatccc  | ttctcccttg  | tgcgataatc  | 60   |
| tttgcgtgag  | atttgtctga  | aaagttagcta | accatgggta  | aagagaagtt  | tcacatcaac  | 120  |
| atttgcgtca  | ttggccacgt  | cgattctgga  | aagtcgacaa  | ccactggaca  | cttgatctac  | 180  |
| aagttgggtg  | gtattgacaa  | cggtgtgac   | gagaggttcg  | agaaggaggg  | tgctgagatg  | 240  |
| aacaagaggt  | ccttcaagta  | cgcattgggtg | ttggacaaac  | tttaaggctga | gcgtgagcgt  | 300  |
| ggtatcacca  | ttgacattgc  | ttcttggaa   | ttcggagacca | ccaagtacta  | ctgcactgtc  | 360  |
| attgatgctc  | ctgtgtcatc  | tgatttcaatc | aagaacatga  | tcactgtgtac | ctcccaggct  | 420  |
| gattgtgctc  | tccttatcat  | cgactccacc  | actgggtgGtt | ttgaggctgg  | tatctccaag  | 480  |
| gatggtcaga  | cccgtagaga  | cgcttcctct  | gctttcacc   | ttgggtgcaa  | gcagatgatc  | 540  |
| tgctgtgtga  | acaagatgga  | tgccactacc  | cccaagtact  | ccaaggccag  | gtacgatgaa  | 600  |
| atcatcaagg  | agggtgtctc  | ctacttgaag  | aagggtgggt  | acaaccccca  | caaaatccca  | 660  |
| tttgcgcca   | ttcttggtat  | tgagggtgac  | aacatgattg  | agaggtccac  | caactctgac  | 720  |
| tggtacaagg  | gaccaactct  | ccttgaggct  | cttgaccaga  | tcaacgagcc  | caagaggccg  | 780  |
| tcagacaagg  | cccttcgtct  | cccacttcag  | gatgtctaca  | agattgtggg  | tattggaacg  | 840  |
| gtgcatttgg  | gacgtgttga  | gactgggtatg | atcaagcctg  | gtatggttgt  | gacottttgt  | 900  |
| cccacaggat  | tgaccaactga | ggtcaagctc  | gttgagatgc  | accacgagtc  | tccttttgag  | 960  |
| gcacttccag  | gtgacaacgt  | tggtttcaat  | gttaagaatg  | ttgccgtgaa  | ggatcttaag  | 1020 |
| agagggtacg  | tgcatccaa   | ctccaaggat  | gacctgccca  | agggtgtgac  | taacttcaac  | 1080 |
| tcacagggtca | tcactcatgaa | ccaccctgg   | cagattggta  | acgggttaacg | ccagctttgt  | 1140 |
| gattgcccaca | ctctccact   | tgacgtcaag  | ttctctgaga  | tcctgacca   | gattgacagg  | 1200 |
| cgttcttgta  | aggagattga  | gaaggagccc  | aaattcttga  | agaatgggtga | tgctgggtatg | 1260 |
| gtgaagatga  | ctccaaccaa  | gcccatgggt  | gtggagacct  | ttcttgagta  | cccaccactt  | 1320 |
| ggacgttttcg | ctgttaggga  | catgaggcag  | actgttgcag  | tcggtgttat  | caagagtgtt  | 1380 |
| gacaag      |             |             |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..431

(D) OTHER INFORMATION: / Ceres Seq. ID 1569169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Lys | Glu | Lys | Phe | His | Ile | Asn | Ile | Val | Val | Ile | Gly | His | Val |
| 1   |     |     |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |
| Asp | Ser | Gly | Lys | Ser | Thr | Thr | Thr | Gly | His | Leu | Ile | Tyr | Lys | Leu | Gly |
|     |     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |
| Gly | Ile | Asp | Lys | Arg | Val | Ile | Glu | Arg | Phe | Glu | Lys | Glu | Ala | Ala | Glu |
|     |     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |
| Met | Asn | Lys | Arg | Ser | Phe | Lys | Tyr | Ala | Trp | Val | Leu | Asp | Lys | Leu | Lys |
|     |     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ala | Glu | Arg | Glu | Arg | Gly | Ile | Thr | Ile | Asp | Ile | Ala | Leu | Trp | Lys | Phe |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Glu | Thr | Thr | Lys | Tyr | Tyr | Cys | Thr | Val | Ile | Asp | Ala | Pro | Gly | His | Arg |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Asp | Phe | Ile | Lys | Asn | Met | Ile | Thr | Gly | Thr | Ser | Gln | Ala | Asp | Cys | Ala |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |
| Val | Leu | Ile | Ile | Asp | Ser | Thr | Thr | Gly | Gly | Phe | Glu | Ala | Gly | Ile | Ser |  |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |  |
| Lys | Asp | Gly | Gln | Thr | Arg | Glu | His | Ala | Leu | Leu | Ala | Phe | Thr | Leu | Gly |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |  |
| Val | Lys | Gln | Met | Ile | Cys | Cys | Cys | Asn | Lys | Met | Asp | Ala | Thr | Thr | Pro |  |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |  |
| Lys | Tyr | Ser | Lys | Ala | Arg | Tyr | Asp | Glu | Ile | Ile | Lys | Glu | Val | Ser | Ser |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Tyr | Leu | Lys | Lys | Val | Gly | Tyr | Asn | Pro | Asp | Lys | Ile | Pro | Phe | Val | Pro |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |  |
| Ile | Ser | Gly | Phe | Glu | Gly | Asp | Asn | Met | Ile | Glu | Arg | Ser | Thr | Asn | Leu |  |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     | 205 |     |     |     |  |
| Asp | Trp | Tyr | Lys | Gly | Pro | Thr | Leu | Leu | Glu | Ala | Leu | Asp | Gln | Ile | Asn |  |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |  |
| Glu | Pro | Lys | Arg | Pro | Ser | Asp | Lys | Pro | Leu | Arg | Leu | Pro | Leu | Gln | Asp |  |
|     |     |     | 225 |     |     |     | 230 |     |     |     | 235 |     |     |     | 240 |  |
| Val | Tyr | Lys | Ile | Gly | Gly | Ile | Gly | Thr | Val | Pro | Leu | Gly | Arg | Val | Glu |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |  |
| Thr | Gly | Met | Ile | Lys | Pro | Gly | Met | Val | Val | Thr | Phe | Ala | Pro | Thr | Gly |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |  |
| Leu | Thr | Thr | Glu | Val | Lys | Ser | Val | Glu | Met | His | His | Glu | Ser | Leu | Leu |  |
|     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |  |
| Glu | Ala | Leu | Pro | Gly | Asp | Asn | Val | Gly | Phe | Asn | Val | Lys | Asn | Val | Ala |  |
|     |     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |  |
| Val | Lys | Asp | Leu | Lys | Arg | Gly | Tyr | Val | Ala | Ser | Asn | Ser | Lys | Asp | Asp |  |
|     |     |     | 305 |     |     |     | 310 |     |     |     | 315 |     |     |     | 320 |  |
| Pro | Ala | Lys | Gly | Ala | Ala | Asn | Phe | Thr | Ser | Gln | Val | Ile | Ile | Met | Asn |  |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |  |
| His | Pro | Gly | Gln | Ile | Gly | Asn | Gly | Tyr | Ala | Pro | Val | Leu | Asp | Cys | His |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |  |
| Thr | Ser | His | Ile | Ala | Val | Lys | Phe | Ser | Glu | Ile | Leu | Thr | Lys | Ile | Asp |  |
|     |     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |  |
| Arg | Arg | Ser | Gly | Lys | Glu | Ile | Glu | Lys | Glu | Pro | Lys | Phe | Leu | Lys | Asn |  |
|     |     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |  |
| Gly | Asp | Ala | Gly | Met | Val | Lys | Met | Thr | Pro | Thr | Lys | Pro | Met | Val | Val |  |
|     |     |     | 385 |     |     |     | 390 |     |     |     | 395 |     |     |     | 400 |  |
| Glu | Thr | Phe | Ser | Glu | Tyr | Pro | Pro | Leu | Gly | Arg | Phe | Ala | Val | Arg | Asp |  |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     |     | 415 |     |  |
| Met | Arg | Gln | Thr | Val | Ala | Val | Gly | Val | Ile | Lys | Ser | Val | Asp | Lys |     |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     |     | 430 |     |  |

(2) INFORMATION FOR SEQ ID NO:1164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 383 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..383

(D) OTHER INFORMATION: / Ceres Seq. ID 1569170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asn | Lys | Arg | Ser | Phe | Lys | Tyr | Ala | Trp | Val | Leu | Asp | Lys | Leu | Lys |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Ala | Glu | Arg | Glu | Arg | Gly | Ile | Thr | Ile | Asp | Ile | Ala | Leu | Trp | Lys | Phe |  |



Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala Val Leu Ile Ile Asp  
1 5 10 15  
Ser Thr Thr Gly Phe Glu Ala Gly Ile Ser Lys Asp Gly Gln Thr  
20 25 30

(2) INFORMATION FOR SEQ ID NO:1166:

```

SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

```

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1227  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569179

|            |           |            |            |            |            |     |
|------------|-----------|------------|------------|------------|------------|-----|
| tctgaagact | attaaagga | tctcgcaaa  | gaagaaaaa  | aaaactttt  | tttggtaag  | 60  |
| gactaaagt  | tttgttttg | tctggcatc  | ctaaccttc  | gtatgtgtg  | tttgttttg  | 120 |
| agcgaatacc | tagaatcgt | cttaacccat | ttagcagag  | atgctcgag  | tagcaggaag | 180 |
| gagctctttt | tctgtctgc | agagatctc  | gaacgtgac  | tctctcgct  | tttcccgta  | 240 |
| ctataaccct | tccgattgg | gcaactctc  | tctcgcttc  | agatctgtc  | cctctcgag  | 300 |
| tctctcatct | tccaattct | accacccgg  | cggtataag  | ggttttgtct | ctcaagttt  | 360 |
| ctacacggga | aatgagtag | gttttgtgtc | ggaagctcc  | ccacagctg  | aagctgtca  | 420 |
| aacacctaac | tcaaaattg | tctatgaca  | ccataacct  | gacggttac  | cactcggtg  | 480 |
| ccctagacga | cggcgattg | ctcttttgt  | cttgtgggt  | ggaagtttg  | AtHWWQc    | 540 |
| ctgttctcgc | cctcctgtg | ctggaactg  | tgtgagcat  | gctgcgaag  | aaagatgtc  | 600 |
| tttccctctc | atccctcgt | gttgacacta | ggagcataga | accggaact  | accgtgacg  | 660 |

|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| tcaagtggcg | tggaagagccc | gtcttcatca  | ggcgaagaac  | agaagatgac  | atcaagctgg  | 720  |
| ccaatagtgt | ggatgttga   | tccttgaggg  | accacacaaga | agactcgggt  | agagtcaaga  | 780  |
| atccagaatg | gttgatcggt  | gttgagatg   | gcactcattt  | gggtgcatc   | cccttgcccta | 840  |
| atgctggtga | ttaatgggtg  | tggtttttgt  | cgtgtcacgg  | atcaccattac | gatatactgt  | 900  |
| gaagaattag | gaaaggtcct  | gcaccataca  | acctggaagt  | accgacctac  | agctttcttgg | 960  |
| aagagaataa | attactcaat  | ggttaaatgaa | taaaagcaca  | cagtccgagt  | gtcatgggtct | 1020 |
| ggatgatctt | aaatctgttt  | ttgtttttat  | attttccggc  | atttttagctg | gcaagttcgc  | 1080 |
| tttctcaaca | ctttgggctc  | agcaaaaatt  | ggcttggttt  | gctgaataat  | acaaacttgt  | 1140 |
| catgtgatga | cttagtatct  | gtctcatctg  | gtgaaaaatac | attgttcata  | cttcatagtc  | 1200 |
| tctgtttatt | attgaaaag   | agttttg     |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1569180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Leu | Arg | Val | Ala | Gly | Arg | Arg | Leu | Phe | Ser | Val | Ser | Gln | Arg | Ser |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Ser | Thr | Val | Thr | Ser | Phe | Val | Leu | Ser | Arg | Asp | His | Thr | Leu | Ser | Asp |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gly | Gly | Asn | Ser | Ser | Ser | Ala | Ser | Arg | Ser | Val | Pro | Ser | Ala | Asp | Leu |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Ser | Ser | Phe | Asn | Ser | Tyr | His | Arg | Ser | Val | Ile | Arg | Gly | Phe | Ala | Ser |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |  |
| Gln | Val | Ile | Thr | Gln | Gly | Asn | Glu | Ile | Gly | Phe | Gly | Ser | Glu | Val | Pro |  |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     |     | 80  |     |  |
| Ala | Thr | Val | Glu | Ala | Val | Lys | Thr | Pro | Asn | Ser | Lys | Ile | Val | Tyr | Asp |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Asp | His | Asn | His | Glu | Arg | Tyr | Pro | Pro | Gly | Asp | Pro | Ser | Lys | Arg | Ala |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Phe | Ala | Tyr | Phe | Val | Leu | Ser | Gly | Gly | Arg | Phe | Asp | Xaa | Xaa | Leu | Cys |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |
| Ser | Pro | Pro | Ala | Cys | Ser | Glu | Ala | Tyr | Cys | Glu | His | Val | Cys | Lys |     |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1569181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Thr | Thr | Ile | Thr | Met | Ser | Val | Thr | His | Leu | Val | Thr | Leu | Ala | Ser |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Gly | His | Ser | Pro | Ile | Leu | Ser | Cys | Arg | Val | Glu | Gly | Leu | Xaa | Xaa | Ala |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Val | Leu | Arg | Leu | Leu | Val | Leu | Lys | Leu | Ile | Val | Ser | Met | Ser | Ala |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Ser | Lys | Asp | Val | Leu | Ala | Leu | Ala | Ser | Leu | Glu | Val | Asp | Leu | Gly | Ser |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |  |
| Ile | Glu | Pro | Gly | Thr | Thr | Val | Thr | Val | Lys | Trp | Arg | Gly | Lys | Pro | Val |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |
| Phe | Ile | Arg | Arg | Thr | Glu | Asp | Asp | Ile | Lys | Leu | Ala | Asn | Ser |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |
| Asp | Val | Gly | Ser | Leu | Arg | Asp | Pro | Gln | Glu | Asp | Ser | Val | Arg |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |
| Asn | Pro | Glu | Trp | Leu | Ile | Val | Val | Gly | Val | Cys | Thr | His | Leu |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |
| Ile | Pro | Leu | Pro | Asn | Ala | Gly | Asp | Tyr | Gly | Gly | Trp | Phe | Cys |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |
| His | Gly | Ser | His | Tyr | Asp | Ile | Ser | Gly | Arg | Ile | Arg | Lys | Gly |
|     |     |     |     | 145 |     |     |     | 150 |     |     |     |     | 155 |
| Pro | Tyr | Asn | Leu | Glu | Val | Pro | Thr | Tyr | Ser | Phe | Leu | Glu | Glu |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     | 175 |
| Leu | Leu | Ile | Gly |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1569182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Val | Thr | His | Leu | Val | Thr | Leu | Ala | Ser | Gly | His | Ser | Pro | Ile |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Ser | Cys | Arg | Val | Glu | Gly | Leu | Xaa | Xaa | Ala | Ser | Val | Leu | Arg | Leu |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Val | Leu | Lys | Leu | Ile | Val | Ser | Met | Ser | Ala | Ser | Lys | Asp | Val | Leu |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ala | Leu | Ala | Ser | Leu | Glu | Val | Asp | Leu | Gly | Ser | Ile | Glu | Pro | Gly | Thr |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Thr | Val | Thr | Val | Lys | Trp | Arg | Gly | Lys | Pro | Val | Phe | Ile | Arg | Arg | Arg |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     |     | 80  |     |
| Thr | Glu | Asp | Asp | Ile | Lys | Leu | Ala | Asn | Ser | Val | Asp | Val | Gly | Ser | Leu |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | Asp | Pro | Gln | Glu | Asp | Ser | Val | Arg | Val | Lys | Asn | Pro | Glu | Trp | Leu |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Ile | Val | Val | Gly | Val | Cys | Thr | His | Leu | Gly | Cys | Ile | Pro | Leu | Pro | Asn |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Ala | Gly | Asp | Tyr | Gly | Gly | Trp | Phe | Cys | Pro | Cys | His | Gly | Ser | His | Tyr |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |
| Asp | Ile | Ser | Gly | Arg | Ile | Arg | Lys | Gly | Pro | Ala | Pro | Tyr | Asn | Leu | Glu |
|     |     |     |     | 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |
| Val | Pro | Thr | Tyr | Ser | Phe | Leu | Glu | Glu | Asn | Lys | Leu | Leu | Ile | Gly |     |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |

(2) INFORMATION FOR SEQ ID NO:1170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1507 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1507

(D) OTHER INFORMATION: / Ceres Seq. ID 1569183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:

```

acctgaatat tgactacgca ttataagagg tttgtttttt gggttttttc ttcttcacat 60
atcatttttt tgatttctccc acgaagatga accacctcgt tcgtaaaaagc tccgtcggtt 120
actccgcctt gaggtcgcgt ttgtacctcc gtcaactctgc cgttacctct ccacctccga 180
tttttccgcg cgcgcgttca accgttcgcc agttcacttc cgcgcggtat ccttccaaca 240
gttttcaatt gagccgcgcg acgaattggg gaatccggag aggaagcggt 300
ttgtgattga gcgattcgtt aaatacgcta cgacgttgcc gtccggggatt catttctcta 360
ttccgttcgt ggatcgtatt gcttatgttc attctctcaa ggaagaagct atcccgattc 420
cgaatcacag tcgatttact aaagacaacg ttagtatcca catcgatggt gtctctctacg 480
ttaagattgt ggatcctaag ttatgcttctt atggcggtga gagtccctatc tatgtcgttt 540
tacagcttgc tcagaccaca atgcgttagt agcttggtta gatcactctt gataagacct 600
ttgaggaaac agacactctc acgagaaga tagtggaagc catcaatggt gctgcaaaag 660
actggggtct tcagtgcctt cgttatgaga taagggatat tatgccccct catggagtgc 720
gagctgctat ggaaatgcaa gctgaagctg agcgtaaaaa gagagccacg attcttgagt 780
ctgaaggaga aaggcaatcc catatcaaca ttgctgatgg taagaaaaat tctgtaatct 840
tggaactctg agcagcaaac atggaccagg tgaatcgagc acaaggtgag gcagaaacaa 900
tactagtatg agcacaagca actgcgaaa gctcgtgctt gttatctcag tccctcaagg 960
aaactggggg agtagagggc gcgagtttga gagttgcaga gcaataactt acagctctcg 1020
gtaacattgc caaggagggt acgataatgt tgcctccaag ttgtgcttca aatcctgcta 1080
gcatgattgc tcaagcttta acaatgtaca aaagccttgt catcaatggt ccaagcaaaag 1140
atcaccgaag aacacaagca cttgatgaaa cagatttgga agagtttgaa gacatgggtg 1200
agaaacatat atcagaagcg tctaataacc gatcaggctc aatatcattt gacacagaga 1260
aaccagggtc caccgggtga ccacgatttt ctcttcagaa ccgcaacaaag gatccgcagt 1320
agggcagcca accgggggatg agataaaatt ttgtggcttg aaaaaactgg aaacattttt 1380
tcattcttca aatatgagcg agtaaacatc ttttccgttt gaatagctag aatatcatca 1440
ctttgcatat agaaacgaat ctgaacatct gttctccgat aagaattttc ctactggatt 1500
tggttatg

```

(2) INFORMATION FOR SEQ ID NO:1171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..411

(D) OTHER INFORMATION: / Ceres Seq. ID 1569184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:

```

Met Asn His Leu Val Arg Lys Ser Ser Val Gly Tyr Ser Ala Leu Arg
1 5 10 15
Ser Val Ser Tyr Leu Arg Gln Ser Ala Val Thr Ser Pro Pro Pro Ile
20 25 30
Phe Ser Ala Ala Ala Ser Thr Val Arg Gln Phe Thr Ser Ala Gly Tyr
35 40 45
Pro Ser Asn Ser Phe Gln Leu Thr Pro Pro Thr Asn Trp Gly Ile Arg
50 55 60
Ile Val Pro Glu Arg Lys Ala Phe Val Ile Glu Arg Phe Gly Lys Tyr
65 70 75 80
Ala Thr Thr Leu Pro Ser Gly Ile His Phe Leu Ile Pro Phe Val Asp
85 90 95
Arg Ile Ala Tyr Val His Ser Leu Lys Glu Glu Ala Ile Pro Ile Pro
100 105 110
Asn Gln Thr Ala Ile Thr Lys Asp Asn Val Ser Ile His Ile Asp Gly
115 120 125
Val Leu Tyr Val Lys Ile Val Asp Pro Lys Leu Ala Ser Tyr Gly Val
130 135 140
Glu Ser Pro Ile Tyr Ala Val Val Gln Leu Ala Gln Thr Thr Met Arg
145 150 155 160
Ser Glu Leu Gly Lys Ile Thr Leu Asp Lys Thr Phe Glu Glu Arg Asp
165 170 175
Thr Leu Asn Glu Lys Ile Val Glu Ala Ile Asn Val Ala Ala Lys Asp

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Gly | Leu | Gln | Cys | Leu | Arg | Tyr | Glu | Ile | Arg | Asp | Ile | Met | Pro | Pro |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| His | Gly | Val | Arg | Ala | Ala | Met | Glu | Met | Gln | Ala | Glu | Ala | Glu | Arg | Lys |
|     |     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Lys | Arg | Ala | Gln | Ile | Leu | Glu | Ser | Glu | Gly | Glu | Arg | Gln | Ser | His | Ile |
|     |     | 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     | 240 |
| Asn | Ile | Ala | Asp | Gly | Lys | Lys | Ser | Ser | Val | Ile | Leu | Ala | Ser | Glu | Ala |
|     |     |     |     |     |     |     | 245 |     |     |     | 250 |     |     |     | 255 |
| Ala | Lys | Met | Asp | Gln | Val | Asn | Arg | Ala | Gln | Gly | Glu | Ala | Glu | Ala | Ile |
|     |     |     |     |     |     |     | 260 |     |     |     | 265 |     |     |     | 270 |
| Leu | Ala | Arg | Ala | Gln | Ala | Thr | Ala | Lys | Gly | Leu | Val | Leu | Leu | Ser | Gln |
|     |     |     |     |     |     |     | 275 |     |     |     |     |     |     |     | 285 |
| Ser | Leu | Lys | Glu | Thr | Gly | Gly | Val | Glu | Ala | Ala | Ser | Leu | Arg | Val | Ala |
|     |     |     |     |     |     |     | 280 |     |     |     |     |     |     |     | 290 |
| Glu | Gln | Tyr | Ile | Thr | Ala | Phe | Gly | Asn | Ile | Ala | Lys | Glu | Gly | Thr | Ile |
|     |     |     |     |     |     |     | 295 |     |     |     | 300 |     |     |     | 305 |
| Met | Leu | Leu | Pro | Ser | Gly | Ala | Ser | Asn | Pro | Ala | Ser | Met | Ile | Ala | Gln |
|     |     |     |     |     |     |     | 310 |     |     |     | 315 |     |     |     | 320 |
|     |     |     |     |     |     |     | 325 |     |     |     | 330 |     |     |     | 335 |
| Ala | Leu | Thr | Met | Tyr | Lys | Ser | Leu | Val | Ile | Asn | Gly | Pro | Ser | Lys | Asp |
|     |     |     |     |     |     |     | 340 |     |     |     | 345 |     |     |     | 350 |
| His | Gln | Glu | Thr | Gln | Ala | Leu | Asp | Glu | Thr | Asp | Leu | Glu | Glu | Leu | Glu |
|     |     |     |     |     |     |     | 355 |     |     |     | 360 |     |     |     | 365 |
| Asp | Met | Gly | Glu | Lys | His | Ile | Ser | Glu | Gly | Ser | Asn | Asn | Arg | Ser | Gly |
|     |     |     |     |     |     |     | 370 |     |     |     | 375 |     |     |     | 380 |
| Ser | Ile | Ser | Phe | Asp | Thr | Glu | Lys | Pro | Gly | His | Thr | Gly | Glu | Pro | Arg |
|     |     |     |     |     |     |     | 385 |     |     |     | 390 |     |     |     | 400 |
| Phe | Ser | Leu | Gln | Asn | Arg | Asn | Lys | Asp | Pro | Gln |     |     |     |     |     |
|     |     |     |     |     |     |     | 405 |     |     |     | 410 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..253

(D) OTHER INFORMATION: / Ceres Seq. ID 1569185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ser | Glu | Leu | Gly | Lys | Ile | Thr | Leu | Asp | Lys | Thr | Phe | Glu | Glu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Asp | Thr | Leu | Asn | Glu | Lys | Ile | Val | Glu | Ala | Ile | Asn | Val | Ala | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Asp | Trp | Gly | Leu | Gln | Cys | Leu | Arg | Tyr | Glu | Ile | Arg | Asp | Ile | Met |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Pro | Pro | His | Gly | Val | Arg | Ala | Ala | Met | Glu | Met | Gln | Ala | Glu | Ala | Glu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Arg | Lys | Lys | Arg | Ala | Gln | Ile | Leu | Glu | Ser | Glu | Gly | Glu | Arg | Gln | Ser |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| His | Ile | Asn | Ile | Ala | Asp | Gly | Lys | Lys | Ser | Ser | Val | Ile | Leu | Ala | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Ala | Ala | Lys | Met | Asp | Gln | Val | Asn | Arg | Ala | Gln | Gly | Glu | Ala | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Ile | Leu | Ala | Arg | Ala | Gln | Ala | Thr | Ala | Lys | Gly | Leu | Val | Leu | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Gln | Ser | Leu | Lys | Glu | Thr | Gly | Gly | Val | Glu | Ala | Ala | Ser | Leu | Arg |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Val | Ala | Glu | Gln | Tyr | Ile | Thr | Ala | Phe | Gly | Asn | Ile | Ala | Lys | Glu | Gly |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     | 160 |     |

Thr Ile Met Leu Leu Pro Ser Gly Ala Ser Asn Pro Ala Ser Met Ile  
165 170 175  
Ala Gln Ala Leu Thr Met Tyr Lys Ser Leu Val Ile Asn Gly Pro Ser  
180 185 190  
Lys Asp His Gln Glu Thr Gln Ala Leu Asp Glu Thr Asp Leu Glu Glu  
195 200 205  
Leu Glu Asp Met Gly Glu Lys His Ile Ser Glu Gly Ser Asn Asn Arg  
210 215 220  
Ser Gly Ser Ile Ser Phe Asp Thr Glu Lys Pro Gly His Thr Gly Glu  
225 230 235 240  
Pro Arg Phe Ser Leu Gln Asn Arg Asn Lys Asp Pro Gln  
245 250

(2) INFORMATION FOR SEQ ID NO:1173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..206
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:

Met Pro Pro His Gly Val Arg Ala Ala Met Glu Met Gln Ala Glu Ala  
1 5 10 15  
Glu Arg Lys Lys Arg Ala Gln Ile Leu Glu Ser Glu Gly Glu Arg Gln  
20 25 30  
Ser His Ile Asn Ile Ala Asp Gly Lys Lys Ser Ser Val Ile Leu Ala  
35 40 45  
Ser Glu Ala Ala Lys Met Asp Gln Val Asn Arg Ala Gln Gly Glu Ala  
50 55 60  
Glu Ala Ile Leu Ala Arg Ala Gln Ala Thr Ala Lys Gly Leu Val Leu  
65 70 75 80  
Leu Ser Gln Ser Leu Lys Glu Thr Gly Gly Val Glu Ala Ala Ser Leu  
85 90 95  
Arg Val Ala Glu Gln Tyr Ile Thr Ala Phe Gly Asn Ile Ala Lys Glu  
100 105 110  
Gly Thr Ile Met Leu Leu Pro Ser Gly Ala Ser Asn Pro Ala Ser Met  
115 120 125  
Ile Ala Gln Ala Leu Thr Met Tyr Lys Ser Leu Val Ile Asn Gly Pro  
130 135 140  
Ser Lys Asp His Gln Glu Thr Gln Ala Leu Asp Glu Thr Asp Leu Glu  
145 150 155 160  
Glu Leu Glu Asp Met Gly Glu Lys His Ile Ser Glu Gly Ser Asn Asn  
165 170 175  
Arg Ser Gly Ser Ile Ser Phe Asp Thr Glu Lys Pro Gly His Thr Gly  
180 185 190  
Glu Pro Arg Phe Ser Leu Gln Asn Arg Asn Lys Asp Pro Gln  
195 200 205

(2) INFORMATION FOR SEQ ID NO:1174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1646 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1646
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:

|            |             |             |            |             |             |      |
|------------|-------------|-------------|------------|-------------|-------------|------|
| atcaactcaa | tctgtttgtc  | tattttctct  | cccttgta   | gttttttgtt  | ttttaccaa   | 60   |
| gcgaacacgt | tcacaaaca   | gatcgcgga   | cggatctggc | gaagccacgc  | gtttctcgc   | 120  |
| ccatcagct  | cgctcatgt   | tgtctctccg  | cgtttccggg | tacccggagta | tctttctcag  | 180  |
| tctgtctctc | ctccggcgct  | gcgcccattc  | tttgttcacc | ctcccacttt  | gatgaaatgg  | 240  |
| ggtggagaaa | gtagaagctg  | gttttcgaac  | gaagccatgg | ccactgattc  | aaattcaggg  | 300  |
| tttaattgtg | tgccactagc  | tcaaaactgg  | gaaggtattg | ctgaatgtga  | gcttctcaag  | 360  |
| tgtgtttgtc | aagaggagga  | tctgtgtgaa  | gagtttcagc | cactctgtga  | agttcagagc  | 420  |
| gataaagcaa | ctatagagat  | cacaagctgt  | tttaaaagga | aagtggctct  | gatttcacat  | 480  |
| tctcaggtgt | acattattaa  | ggttggagag  | actctgtgta | ggttgccggt  | tgaagactcg  | 540  |
| caggattcgc | tcttaaccac  | tgatagtcca  | gaaattgtaa | ctctggggag  | tccaaagcag  | 600  |
| ggaacagaaa | atcttcttgg  | agctctctca  | acgcccgcgg | tctgtaacct  | tgcaaaagac  | 660  |
| cttggcatag | atatcaatgt  | tataactgga  | actggtaaa  | atggtagagt  | tttgaagaag  | 720  |
| gatgttctcc | ggttttagtg  | ccagaaaagga | tttgaacag  | atccagtttc  | tctctgacat  | 780  |
| gctgttatag | gaggagactc  | ggtttccact  | aaagctagta | gtaactttga  | agataaaaaca | 840  |
| gttctctcaa | ggggattcag  | ccgagcaatg  | gtcaagacaa | tgactatggc  | tacaagtgtga | 900  |
| ccgcattttc | attttgttga  | agagataaac  | tgcgactcac | ttgtggagct  | caagcagttc  | 960  |
| ttcaagagaa | acaatacaga  | tcccaccact  | aaacacactt | ttcttctact  | tttaatacaag | 1020 |
| tctctgtcaa | tggctctaac  | caaatatccc  | ttctggaata | gttgcttcaa  | cgcggaaattc | 1080 |
| ctcgagatca | tcttcaagg   | ttcacataat  | attggagttg | caatggccac  | tgaacatggc  | 1140 |
| cttctcgttc | caaatataaa  | gaatgttcag  | tcatattctc | tgctagagat  | aaccaaaagag | 1200 |
| ctgtcccggt | tacaacattt  | ggcagcaaac  | aacaaactta | accccgagga  | tgtgactggg  | 1260 |
| ggaaccatga | ctctgagtga  | cattggagca  | attggtggta | aattcggatc  | ccctcttttta | 1320 |
| aacttaccgg | caagttgcaat | catcgctctt  | ggaagaatcg | agaaagtctc  | aaaattctcca | 1380 |
| aaagaagaaa | tcgtctatcc  | tgcatcgata  | atgatgggta | acattgctcg  | ggaatcataga | 1440 |
| gttctagatg | gggcaaccgt  | agctcggttt  | tgctgccagt | ggaagaagta  | tgtcgagaaa  | 1500 |
| ccggagctgc | tgatgcttca  | aatgagataa  | gaaggaaggg | ttcatgttta  | tttgtgaact  | 1560 |
| attatgtatg | aaacctctat  | gttcgaataa  | gatcaagaac | tgagctagca  | gttgtaaaact | 1620 |
| aaacaaSvaa | agtaaaagtc  | atatct      |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..509
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Asn | Ser | Ile | Cys | Leu | Ser | Ile | Ser | Ser | Pro | Leu | Tyr | Cys | Phe | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Phe | Phe | Thr | Lys | Asp | Gln | Pro | Phe | Thr | Thr | Met | Ile | Ala | Arg | Arg | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp | Arg | Ser | His | Arg | Phe | Leu | Arg | Pro | Phe | Ser | Ser | Ser | Ser | Val | Cys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Pro | Pro | Phe | Arg | Val | Pro | Glu | Tyr | Leu | Ser | Gln | Ser | Ser | Ser | Ser |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Pro | Ala | Ser | Arg | Pro | Phe | Phe | Val | His | Pro | Pro | Thr | Leu | Met | Lys | Trp |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     | 80  |     |     |
| Gly | Gly | Gly | Ser | Arg | Ser | Trp | Phe | Ser | Asn | Glu | Ala | Met | Ala | Thr | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Asn | Ser | Gly | Leu | Ile | Asp | Val | Pro | Leu | Ala | Gln | Thr | Gly | Gly | Gly |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ile | Ala | Glu | Cys | Glu | Leu | Leu | Lys | Trp | Phe | Val | Lys | Glu | Gly | Asp | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Val | Glu | Glu | Phe | Gln | Pro | Leu | Cys | Glu | Val | Gln | Ser | Asp | Lys | Ala | Thr |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Ile | Glu | Ile | Thr | Ser | Arg | Phe | Lys | Gly | Lys | Val | Ala | Leu | Ile | Ser | His |
|     |     |     | 145 |     |     |     | 150 |     |     | 155 |     |     |     |     | 160 |

SEQUENCE DESCRIPTION



Ser Pro Gly Asp Ile Ile Lys Val Gly Glu Thr Leu Val Arg Leu Ala  
165 170 175  
Val Glu Asp Ser Gln Asp Ser Leu Leu Thr Thr Asp Ser Ser Glu Ile  
180 185 190  
Val Thr Leu Gly Gly Ser Lys Gln Gly Thr Glu Asn Leu Leu Gly Ala  
195 200 205  
Leu Ser Thr Pro Ala Val Arg Asn Leu Ala Lys Asp Leu Gly Ile Asp  
210 215 220  
Ile Asn Val Ile Thr Gly Thr Gly Lys Asp Gly Arg Val Leu Lys Glu  
225 230 235  
Asp Val Leu Arg Phe Ser Asp Gln Lys Gly Phe Val Thr Asp Ser Val  
245 250 255  
Ser Ser Glu His Ala Val Ile Gly Gly Asp Ser Val Ser Thr Lys Ala  
260 265 270  
Ser Ser Asn Phe Glu Asp Lys Thr Val Pro Leu Arg Gly Phe Ser Arg  
275 280 285  
Ala Met Val Lys Thr Met Thr Met Ala Thr Ser Val Pro His Phe His  
290 295 300  
Phe Val Glu Glu Ile Asn Cys Asp Ser Leu Val Glu Leu Lys Gln Phe  
305 310 315  
Phe Lys Glu Asn Asn Thr Asp Ser Thr Ile Lys His Thr Phe Leu Pro  
325 330 335  
Thr Leu Ile Lys Ser Leu Ser Met Ala Leu Thr Lys Tyr Pro Phe Val  
340 345 350  
Asn Ser Cys Phe Asn Ala Glu Ser Leu Glu Ile Ile Leu Lys Gly Ser  
355 360 365  
His Asn Ile Gly Val Ala Met Ala Thr Glu His Gly Leu Val Val Pro  
370 375 380  
Asn Ile Lys Asn Val Gln Ser Leu Ser Leu Leu Glu Ile Thr Lys Glu  
385 390 395  
Leu Ser Arg Leu Gln His Leu Ala Ala Asn Asn Lys Leu Asn Pro Glu  
405 410 415  
Asp Val Thr Gly Gly Thr Ile Thr Leu Ser Asn Ile Gly Ala Ile Gly  
420 425 430  
Gly Lys Phe Gly Ser Pro Leu Leu Asn Leu Pro Glu Val Ala Ile Ile  
435 440 445  
Ala Leu Gly Arg Ile Glu Lys Val Pro Lys Phe Ser Lys Glu Gly Thr  
450 455 460  
Val Tyr Pro Ala Ser Ile Met Met Val Asn Ile Ala Ala Asp His Arg  
465 470 475  
Val Leu Asp Gly Ala Thr Val Ala Arg Phe Cys Cys Gln Trp Lys Glu  
485 490 495  
Tyr Val Glu Lys Pro Glu Leu Leu Met Leu Gln Met Arg  
500 505

(2) INFORMATION FOR SEQ ID NO:1176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..483
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

Met Ile Ala Arg Arg Ile Trp Arg Ser His Arg Phe Leu Arg Pro Phe  
1 5 10 15  
Ser Ser Ser Ser Val Cys Ser Pro Pro Phe Arg Val Pro Glu Tyr Leu  
20 25 30  
Ser Gln Ser Ser Ser Ser Pro Ala Ser Arg Pro Phe Phe Val His Pro

(2) INFORMATION FOR SEQ ID NO:1177:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 432 amino acids  
 (B) TYPE: amino acid



420

425

430

(2) INFORMATION FOR SEQ ID NO:1178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1211

(D) OTHER INFORMATION: / Ceres Seq. ID 1569230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| attcatattt  | gctcacotca  | aactctctct  | ttctctctct  | ctctgggtcc  | ctagaatttg  | 60   |
| agcaaaattt  | ctaccataat  | tgctaattat  | taaaaggaaa  | cataagtaat  | cggtgcttcg  | 120  |
| atccctttgt  | acatggatgg  | atccctgaaca | ggaatctcca  | aacgagactt  | tggaacctat  | 180  |
| attggtaagt  | tcaacaaaaa  | gaagcaataa  | taacAaataa  | gaaaatggaa  | gaagaaatga  | 240  |
| agaagaaagt  | atcaagagga  | gaattaggag  | gtgaagctca  | aaattgtcca  | agatgtgaat  | 300  |
| ctccaacac   | aaagttttgt  | tactacaaca  | actatagtct  | ctcacaacct  | cgttacttct  | 360  |
| gcaaatcttg  | toggagatat  | tggaactaaa  | gcggtactct  | tcgtaacggt  | cccgctcggtg | 420  |
| gtgggtgccc  | togaacacaaa | cgatcctctt  | cctcagcttt  | ctccaagaac  | aacaacaata  | 480  |
| agtcatttaa  | ttctcatact  | gatccacttc  | agaacccctt  | aattacggga  | atgccaccat  | 540  |
| catctttttg  | ttatgatcac  | tccattgato  | tcaacctctgc | tttcgctact  | ctccaaaagc  | 600  |
| atcattttat  | ctctcaagct  | actactcctt  | cttttgggtt  | tggaagtgat  | ctttctattt  | 660  |
| atggaaacct  | aacgaatgat  | gtagggatct  | tcggagggca  | aaacggtact  | tataacaata  | 720  |
| gtttgtgtta  | tggttttgtg  | tccggaaaatg | gtaataataa  | tcaaaaatgaa | atcaagatgg  | 780  |
| ctcttcacatt | ggggatgtct  | ttggaaggaa  | acgagagaaa  | gcaagagaa   | gtgaacaata  | 840  |
| acaataataa  | ctcagagaat  | cctagcaagg  | tgttctgggg  | gtttccatgg  | cagatgaccg  | 900  |
| gagattccgc  | cggagtgtga  | ccggagattg  | atcccggaa   | ggaaagctgg  | aatgggatgg  | 960  |
| tttcattctg  | gaataatgtg  | ttaactcaaca | ctccttttgt  | ctagcagatc  | atataataat  | 1020 |
| aaatatataa  | tatattacta  | tatatataag  | Kttatgtcat  | cacatgtttg  | tacaccactt  | 1080 |
| tcactataat  | gggggatggt  | tggtttttat  | aattcttagg  | gtttctatct  | ttttttagtt  | 1140 |
| tcaccaattt  | tctgtttgag  | acgaagactt  | ataagagttc  | ttctatgaaa  | actatagaaa  | 1200 |
| aaagtttctc  | c           |             |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..259

(D) OTHER INFORMATION: / Ceres Seq. ID 1569231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Glu | Glu | Met | Lys | Lys | Lys | Val | Ser | Arg | Gly | Glu | Leu | Gly | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Ala | Gln | Asn | Cys | Pro | Arg | Cys | Glu | Ser | Pro | Asn | Thr | Lys | Phe | Cys |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Tyr | Asn | Asn | Tyr | Ser | Leu | Ser | Gln | Pro | Arg | Tyr | Phe | Cys | Lys | Ser |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Cys | Arg | Arg | Tyr | Trp | Thr | Lys | Gly | Gly | Thr | Leu | Arg | Asn | Val | Pro | Val |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Gly | Gly | Gly | Cys | Arg | Arg | Asn | Lys | Arg | Ser | Ser | Ser | Ala | Phe | Ser |     |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |
| Lys | Asn | Asn | Asn | Asn | Lys | Ser | Ile | Asn | Phe | His | Thr | Asp | Pro | Leu | Gln |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asn | Pro | Leu | Ile | Thr | Gly | Met | Pro | Pro | Ser | Ser | Phe | Gly | Tyr | Asp | His |

|             |         |         |         |         |                     |
|-------------|---------|---------|---------|---------|---------------------|
|             | 100     |         | 105     |         | 110                 |
| Ser Ile Asp | Leu Asn | Leu Ala | Phe Ala | Thr Leu | Gln Lys His His Leu |
|             | 115     |         | 120     |         | 125                 |
| Ser Ser Gln | Ala Thr | Thr Pro | Ser Phe | Gly Phe | Gly Gly Asp Leu Ser |
|             | 130     |         | 135     |         | 140                 |
| Ile Tyr Gly | Asn Ser | Thr Asn | Asp Val | Gly Ile | Phe Gly Gly Gln Asn |
|             | 145     |         | 150     |         | 155                 |
| Gly Thr Tyr | Asn Asn | Ser Leu | Cys Tyr | Gly Phe | Val Ser Gly Asn Gly |
|             | 165     |         | 170     |         | 175                 |
| Asn Asn Asn | Gln Asn | Glu Ile | Lys Met | Ala Ser | Thr Leu Gly Met Ser |
|             | 180     |         | 185     |         | 190                 |
| Leu Glu Gly | Asn Glu | Arg Lys | Gln Glu | Asn Val | Asn Asn Asn Asn     |
|             | 195     |         | 200     |         | 205                 |
| Asn Ser Glu | Asn Pro | Ser Lys | Val Phe | Trp Gly | Phe Pro Trp Gln Met |
|             | 210     |         | 215     |         | 220                 |
| Thr Gly Asp | Ser Ala | Gly Val | Val Pro | Glu Ile | Asp Pro Gly Arg Glu |
|             | 225     |         | 230     |         | 235                 |
| Ser Trp Asn | Gly Met | Val Ser | Ser Trp | Asn Asn | Gly Leu Leu Asn Thr |
|             | 245     |         | 250     |         | 255                 |
| Pro Leu Val |         |         |         |         |                     |

(2) INFORMATION FOR SEQ ID NO:1180:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 255 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..255

(D) OTHER INFORMATION: / Ceres Seq. ID 1569232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:

|             |         |         |         |         |         |         |     |
|-------------|---------|---------|---------|---------|---------|---------|-----|
| Met Lys Lys | Lys Val | Ser Arg | Gly Glu | Leu Gly | Gly Glu | Ala Gln | Asn |
| 1           | 5       |         | 10      |         |         | 15      |     |
| Cys Pro Arg | Cys Glu | Ser Pro | Asn Thr | Lys Phe | Cys Tyr | Tyr Asn | Asn |
|             | 20      |         | 25      |         |         | 30      |     |
| Tyr Ser Leu | Ser Gln | Pro Arg | Tyr Phe | Cys Lys | Ser Cys | Arg Arg | Tyr |
|             | 35      |         | 40      |         |         | 45      |     |
| Trp Thr Lys | Gly Gly | Thr Leu | Arg Asn | Val Pro | Val Gly | Gly Gly | Cys |
|             | 50      |         | 55      |         |         | 60      |     |
| Arg Arg Asn | Lys Arg | Ser Ser | Ser Ser | Ala Phe | Ser Lys | Asn Asn | Asn |
| 65          | 70      |         |         | 75      |         | 80      |     |
| Asn Lys Ser | Ile Asn | Phe His | Thr Asp | Pro Leu | Gln Asn | Pro Leu | Ile |
|             | 85      |         | 90      |         |         | 95      |     |
| Thr Gly Met | Pro Pro | Ser Ser | Phe Gly | Tyr Asp | His Ser | Ile Asp | Leu |
|             | 100     |         | 105     |         |         | 110     |     |
| Asn Leu Ala | Phe Ala | Thr Leu | Gln Lys | His His | Leu Ser | Ser Gln | Ala |
|             | 115     |         | 120     |         |         | 125     |     |
| Thr Thr Pro | Ser Phe | Gly Phe | Gly Gly | Asp Leu | Ser Ile | Tyr Gly | Asn |
|             | 130     |         | 135     |         |         | 140     |     |
| Ser Thr Asn | Asp Val | Gly Ile | Phe Gly | Gly Gln | Asn Gly | Thr Tyr | Asn |
|             | 145     |         | 150     |         |         | 155     |     |
| Asn Ser Leu | Cys Tyr | Gly Phe | Val Ser | Gly Asn | Gly Asn | Asn Asn | Gln |
|             | 165     |         | 170     |         |         | 175     |     |
| Asn Glu Ile | Lys Met | Ala Ser | Thr Leu | Gly Met | Ser Leu | Glu Gly | Asn |
|             | 180     |         | 185     |         |         | 190     |     |
| Glu Arg Lys | Gln Glu | Asn Val | Asn Asn | Asn Asn | Asn Asn | Ser Glu | Asn |
|             | 195     |         | 200     |         |         | 205     |     |
| Pro Ser Lys | Val Phe | Trp Gly | Phe Pro | Trp Gln | Met Thr | Gly Asp | Ser |
|             | 210     |         | 215     |         |         | 220     |     |

Ala Gly Val Val Pro Glu Ile Asp Pro Gly Arg Glu Ser Trp Asn Gly  
225 230 235 240  
Met Val Ser Ser Trp Asn Asn Gly Leu Leu Asn Thr Pro Leu Val  
245 250 255

(2) INFORMATION FOR SEQ ID NO:1181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1569233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Pro | Ser | Ser | Phe | Gly | Tyr | Asp | His | Ser | Ile | Asp | Leu | Asn | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Phe | Ala | Thr | Leu | Gln | Lys | His | His | Leu | Ser | Ser | Gln | Ala | Thr | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ser | Phe | Gly | Phe | Gly | Gly | Asp | Leu | Ser | Ile | Tyr | Gly | Asn | Ser | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Asp | Val | Gly | Ile | Phe | Gly | Gly | Gln | Asn | Gly | Thr | Tyr | Asn | Asn | Ser |
|     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |
| Leu | Cys | Tyr | Gly | Phe | Val | Ser | Gly | Asn | Gly | Asn | Asn | Gln | Asn | Glu |     |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Lys | Met | Ala | Ser | Thr | Leu | Gly | Met | Ser | Leu | Glu | Gly | Asn | Glu | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Gln | Glu | Asn | Val | Asn | Asn | Asn | Asn | Asn | Ser | Glu | Asn | Pro | Ser |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Val | Phe | Trp | Gly | Phe | Pro | Trp | Gln | Met | Thr | Gly | Asp | Ser | Ala | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Val | Pro | Glu | Ile | Asp | Pro | Gly | Arg | Glu | Ser | Trp | Asn | Gly | Met | Val |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Ser | Ser | Trp | Asn | Asn | Gly | Leu | Leu | Asn | Thr | Pro | Leu | Val |     |     |     |
|     |     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1125

(D) OTHER INFORMATION: / Ceres Seq. ID 1569234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182:

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| gactccatta  | ttatccctct | ctctacaaaa | aaaaacagta | gagagagata  | tagagagcat  | 60  |
| caatggcgctc | gtcgtaaga  | ctttgcgatt | cgtgcaaatc | gacggcgacga | actctattct  | 120 |
| gcgcgcgaga  | cgccgcgttt | ctctgcggca | actgcgcagg | taagatccac  | acagctaaca  | 180 |
| aactgcagtc  | acgtcacgaa | cgagtttgcc | tatgtgaagt | atgcgaacaa  | gcaccagcac  | 240 |
| acgtcacgtc  | caaagctgac | gcgcgtcgct | tatgcgtcac | gtgcgacgtg  | gatattccact | 300 |
| cagctaatcc  | actctctcgc | cgccacgagc | gcgtaccaat | cactctcttc  | tacgacgctg  | 360 |
| ttggtccagc  | aaaatccgct | tctctctccg | tcaatttcgt | agatgaagat  | ggcggtagacg | 420 |
| tcactgcctc  | gtgggtttta | gctaaagaag | gaatcgaaat | cactaatttg  | ttttccgattc | 480 |
| ttgattatcc  | gaagattgag | gtcacgtcgg | aggagaatag | ctccggtaac  | gacggagttg  | 540 |
| ttctctgtga  | gaataagttg | ttctccaagt | aagattactt | caatttcgat  | ctctctgctt  | 600 |
| ccaaaatttc  | tcaacaagga | ttcaatttca | tcaaccaaac | tggttcgacg  | agaacgatag  | 660 |
| atgtaccggt  | ggtgcctgaa | agtgaggagg | tgcagcgagg | gatgacgaac  | acgggagacg  | 720 |
| cagctgtgca  | gttatccacg | gcggagaggg | aagcaagggt | tttgagggtat | agagagaaga  | 780 |

ggaagaatcg gaaatttgag aagacgatta ggtatgcgtc gcgtaaaagCt tacgctgaga 840  
tgaggccgag aatcaaaagga cgttttgcta agagaacaga ttcgagagag aatgatgggtg 900  
gagacgtcgg agtttatggc ggattcgggtg ttgttcggag tttctgatat ttcccggtta 960  
aagaacaatg gtagtagtat atcgggttaat agcagattaa ggataattaa aactaaaaatg 1020  
tttcttgatt taatcagggg ctaagttatt gttagaagat tgttgttttt tgaattaatt 1080  
ctcacaaattg tatectaaat tatatatgtt acttaagtgtt gaact

(2) INFORMATION FOR SEQ ID NO:1183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..294

(D) OTHER INFORMATION: / Ceres Seq. ID 1569235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183:

Met Ala Ser Ser Arg Leu Cys Asp Ser Cys Lys Ser Thr Ala Ala  
1 5 10 15  
Thr Leu Phe Cys Arg Ala Asp Ala Ala Phe Leu Cys Gly Asn Cys Asp  
20 25 30  
Gly Lys Ile His Thr Ala Asn Lys Leu Ala Ser Arg His Glu Arg Val  
35 40 45  
Trp Leu Cys Glu Val Cys Glu Gln Ala Pro Ala His Val Thr Cys Lys  
50 55 60  
Ala Asp Ala Ala Ala Leu Cys Val Thr Cys Asp Arg Ile His Ser  
65 70 75 80  
Ala Asn Pro Leu Ser Arg Arg His Glu Arg Val Pro Ile Thr Pro Phe  
85 90 95  
Tyr Asp Ala Val Gly Pro Ala Lys Ser Ala Ser Ser Val Asn Phe  
100 105 110  
Val Asp Glu Asp Gly Gly Asp Val Thr Ala Ser Trp Leu Leu Ala Lys  
115 120 125  
Glu Gly Ile Glu Ile Thr Asn Leu Phe Ser Asp Leu Asp Tyr Pro Lys  
130 135 140  
Ile Glu Val Thr Ser Glu Glu Asn Ser Ser Gly Asn Asp Gly Val Val  
145 150 155 160  
Pro Val Gln Asn Lys Leu Phe Leu Asn Glu Asp Tyr Phe Asn Phe Asp  
165 170 175  
Leu Ser Ala Ser Lys Ile Ser Gln Gln Gly Phe Asn Phe Ile Asn Gln  
180 185 190  
Thr Val Ser Thr Arg Thr Ile Asp Val Pro Leu Val Pro Glu Ser Gly  
195 200 205  
Gly Val Thr Ala Glu Met Thr Asn Thr Glu Thr Pro Ala Val Gln Leu  
210 215 220  
Ser Pro Ala Glu Arg Glu Ala Arg Val Leu Arg Tyr Arg Glu Lys Arg  
225 230 235 240  
Lys Asn Arg Lys Phe Glu Lys Thr Ile Arg Tyr Ala Ser Arg Lys Ala  
245 250 255  
Tyr Ala Glu Met Arg Pro Arg Ile Lys Gly Arg Phe Ala Lys Arg Thr  
260 265 270  
Asp Ser Arg Glu Asn Asp Gly Gly Asp Val Gly Val Tyr Cys Gly Phe  
275 280 285  
Gly Val Val Pro Ser Phe  
290

(2) INFORMATION FOR SEQ ID NO:1184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..1515  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184:

|            |             |             |            |            |            |      |
|------------|-------------|-------------|------------|------------|------------|------|
| aagttcagct | tcgtacctga  | gccaaagagt  | gtttcaggat | ggagctaagg | tcgagaatgc | 60   |
| tcaaagactg | tctcttggaa  | gattccaact  | catgttcctc | aaacgggttc | aaatcgattc | 120  |
| ccagacggca | tcctctcaac  | cctttcccaa  | tgataccaaa | gaggaacaaa | tccaatgcac | 180  |
| tcgacgctgt | gattaacgac  | atcaagaacc  | tccattccaa | caccatccaa | tcgcgtccat | 240  |
| cggggatctt | accaaggagc  | ctttctcgcc  | ggttagcaac | caagaacaaa | gcagaaaacc | 300  |
| aagcaagcat | caccgttatt  | cgggtcaaa   | acatcgtgcg | atggcactcg | tctaaggacc | 360  |
| tgcattgagg | catatcacat  | tttgaacctc  | atcagtcac  | aaaccaagac | acgacaacaa | 420  |
| ccacaggatc | ctccaccaMc  | agcggcacat  | cctgcagcag | ttggtctgac | ttggatttta | 480  |
| catcgagatt | tttaccatca  | tcatggggaa  | gtaacgttga | ggagtgcggt | gaaaaacaga | 540  |
| gtgttaaaaa | caacttacac  | tgcgtcgccg  | aagattcttg | cacagcagta | atactagccg | 600  |
| acactgaagt | gggacctgag  | gagaacttac  | agtgtagaaa | ggagcacaac | agccctgtct | 660  |
| cagtgattga | gattcaacat  | gaggaatatg  | acgaacatc  | agactcttct | ttcagtcaat | 720  |
| gccttgacaa | tgtgaaagaa  | accaaacaac  | agctcatgca | aacgattcag | cggtttgagt | 780  |
| ctttgtccaa | cattagtccct | ttcaatttgg  | atgaatgggg | ctcaatggat | gaagcatcct | 840  |
| gcattggaag | aggacaagag  | acagatacca  | agtatgatga | tgatgagaa  | tgtgatactg | 900  |
| ttgatagaga | aagtgaagat  | gaatacaatg  | atgaggttga | agagaaggca | gcacagctat | 960  |
| ggaaccgagt | caaagaaaga  | cacgccattt  | ggatccacga | agaacatctg | ataatggact | 1020 |
| atttcagaga | tgaattgatg  | caaaaggacaa | actcattcca | cgaactcAa  | acactttgac | 1080 |
| aaccatttgg | tatgcgaggg  | aaaaggatgg  | ttgcaggaaa | agagagaatc | agagcttgaa | 1140 |
| cgcggaacaa | gtgagcagag  | gagacaagca  | tgtgctagag | aaatcgaaag | acgagactgg | 1200 |
| aatgagaaac | agatagagga  | ggagcacgaa  | gtgggtggta | ccagatttga | ggaagaactc | 1260 |
| ttcagcctgt | tattggacga  | aactttaaca  | acgctctcta | ccaaaactga | ttccagtcca | 1320 |
| cctgaacatc | acaaaacagt  | aacatcaatg  | cttaagcttt | agaatttaga | aagcaaaaac | 1380 |
| atttttgaat | aaggctttga  | cttaaaagot  | caggtttttt | tagctctact | tttgtaagaa | 1440 |
| tgaagcaaac | gaataataca  | atgtatatgt  | acctctaaaa | ccatatatat | atatatgcct | 1500 |
| aattcatatt | tcctgc      |             |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:1185:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 346 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..346  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Leu | Arg | Ser | Arg | Met | Leu | Lys | Asp | Cys | Leu | Leu | Glu | Asp | Ser |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asn | Ser | Cys | Ser | Ser | Asn | Gly | Phe | Lys | Ser | Ile | Pro | Arg | Arg | His | Pro |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Leu | Asn | Pro | Phe | Pro | Met | Ile | Pro | Lys | Arg | Lys | Gln | Ser | Asn | Ala | Leu |  |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Gln | Ala | Val | Ile | Asn | Ala | Ile | Lys | Asn | Leu | His | Ser | Asn | Thr | Ile | Lys |  |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Ser | Ala | Pro | Ser | Gly | Ile | Leu | Pro | Arg | Ser | Leu | Ser | Arg | Arg | Leu | Ala |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Thr | Lys | Asn | Lys | Ala | Glu | Asn | Gln | Ala | Ser | Ile | Thr | Val | Ile | Arg | Val |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Lys | Asp | Ile | Val | Arg | Trp | His | Ser | Ser | Lys | Asp | Leu | His | Glu | Asp | Ile |  |
|     |     |     |     | 100 |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Ser | His | Phe | Glu | Pro | His | Gln | Tyr | Thr | Thr | Lys | Asn | Thr | Thr | Thr | Thr |  |
|     |     |     |     | 115 |     |     | 120 |     |     |     |     |     | 125 |     |     |  |



Thr Gly Ser Ser Thr Xaa Ser Gly Thr Ser Cys Ser Ser Trp Ser Asp  
130 135 140  
Leu Asp Phe Thr Ser Glu Phe Leu Pro Ser Ser Trp Gly Ser Asn Val  
145 150 155 160  
Glu Glu Cys Gly Glu Lys Gln Ser Val Lys Asn Asn Leu His Cys Val  
165 170 175  
Gly Glu Asp Ser Cys Thr Ala Val Ile Leu Ala Asp Thr Glu Val Gly  
180 185 190  
Pro Glu Glu Asn Leu Gln Cys Glu Lys Glu His Asn Ser Pro Val Ser  
195 200 205  
Val Phe Glu Ile Gln His Glu Glu Tyr Asp Glu Thr Ser Asp Ser Ser  
210 215 220  
Phe Ser Gln Cys Leu Asp Asn Val Glu Arg Thr Lys Gln Lys Leu Met  
225 230 235 240  
Gln Thr Ile Gln Arg Phe Glu Ser Leu Ala Asn Ile Ser Pro Phe Asn  
245 250 255  
Leu Asp Glu Trp Gly Ser Met Asp Glu Ala Ser Cys Met Glu Gly Gly  
260 265 270  
Gln Glu Thr Asp Thr Lys Tyr Asp Asp Asp Glu Asn Cys Asp Thr Val  
275 280 285  
Asp Arg Glu Ser Glu Asp Glu Tyr Asn Asp Glu Val Glu Glu Lys Ala  
290 295 300  
Ala Gln Leu Trp Asn Arg Val Lys Glu Arg His Ala Ile Trp Ile His  
305 310 315 320  
Glu Glu His Leu Ile Met Asp Tyr Phe Arg Asp Glu Leu Met Gln Arg  
325 330 335  
Thr Asn Ser Phe His Glu Thr Gln Thr Leu  
340 345

(2) INFORMATION FOR SEQ ID NO:1186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..340
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:

Met Leu Lys Asp Cys Leu Leu Glu Asp Ser Asn Ser Cys Ser Ser Asn  
1 5 10 15  
Gly Phe Lys Ser Ile Pro Arg Arg His Pro Leu Asn Pro Phe Pro Met  
20 25 30  
Ile Pro Lys Arg Lys Gln Ser Asn Ala Leu Gln Ala Val Ile Asn Ala  
35 40 45  
Ile Lys Asn Leu His Ser Asn Thr Ile Lys Ser Ala Pro Ser Gly Ile  
50 55 60  
Leu Pro Arg Ser Leu Ser Arg Arg Leu Ala Thr Lys Asn Lys Ala Glu  
65 70 75 80  
Asn Gln Ala Ser Ile Thr Val Ile Arg Val Lys Asp Ile Val Arg Trp  
85 90 95  
His Ser Ser Lys Asp Leu His Glu Asp Ile Ser His Phe Glu Pro His  
100 105 110  
Gln Tyr Thr Thr Lys Asn Thr Thr Thr Thr Gly Ser Ser Thr Xaa  
115 120 125  
Ser Gly Thr Ser Cys Ser Ser Trp Ser Asp Leu Asp Phe Thr Ser Glu  
130 135 140  
Phe Leu Pro Ser Ser Trp Gly Ser Asn Val Glu Glu Cys Gly Glu Lys  
145 150 155 160  
Gln Ser Val Lys Asn Asn Leu His Cys Val Gly Glu Asp Ser Cys Thr

165 170 175  
Ala Val Ile Leu Ala Asp Thr Glu Val Gly Pro Glu Glu Asn Leu Gln  
180 185 190  
Cys Glu Lys Glu His Asn Ser Pro Val Ser Val Phe Glu Ile Gln His  
195 200 205  
Glu Glu Tyr Asp Glu Thr Ser Asp Ser Ser Phe Ser Gln Cys Leu Asp  
210 215 220  
Asn Val Glu Arg Thr Lys Gln Lys Leu Met Gln Thr Ile Gln Arg Phe  
225 230 235 240  
Glu Ser Leu Ala Asn Ile Ser Pro Phe Asn Leu Asp Glu Trp Gly Ser  
245 250 255  
Met Asp Glu Ala Ser Cys Met Glu Gly Gly Gln Glu Thr Asp Thr Lys  
260 265 270  
Tyr Asp Asp Asp Glu Asn Cys Asp Thr Val Asp Arg Glu Ser Glu Asp  
275 280 285  
Glu Tyr Asn Asp Glu Val Glu Glu Lys Ala Ala Gln Leu Trp Asn Arg  
290 295 300  
Val Lys Glu Arg His Ala Ile Trp Ile His Glu Glu His Leu Ile Met  
305 310 315 320  
Asp Tyr Phe Arg Asp Glu Leu Met Gln Arg Thr Asn Ser Phe His Glu  
325 330 335  
Thr Gln Thr Leu  
340

(2) INFORMATION FOR SEQ ID NO:1187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..309
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:

Met Ile Pro Lys Arg Lys Gln Ser Asn Ala Leu Gln Ala Val Ile Asn  
1 5 10 15  
Ala Ile Lys Asn Leu His Ser Asn Thr Ile Lys Ser Ala Pro Ser Gly  
20 25 30  
Ile Leu Pro Arg Ser Leu Ser Arg Arg Leu Ala Thr Lys Asn Lys Ala  
35 40 45  
Glu Asn Gln Ala Ser Ile Thr Val Ile Arg Val Lys Asp Ile Val Arg  
50 55 60  
Trp His Ser Ser Lys Asp Leu His Glu Asp Ile Ser His Phe Glu Pro  
65 70 75 80  
His Gln Tyr Thr Thr Lys Asn Thr Thr Thr Thr Gly Ser Ser Thr  
85 90 95  
Xaa Ser Gly Thr Ser Cys Ser Ser Trp Ser Asp Leu Asp Phe Thr Ser  
100 105 110  
Glu Phe Leu Pro Ser Ser Trp Gly Ser Asn Val Glu Glu Cys Gly Glu  
115 120 125  
Lys Gln Ser Val Lys Asn Asn Leu His Cys Val Gly Glu Asp Ser Cys  
130 135 140  
Thr Ala Val Ile Leu Ala Asp Thr Glu Val Gly Pro Glu Glu Asn Leu  
145 150 155 160  
Gln Cys Glu Lys Glu His Asn Ser Pro Val Ser Val Phe Glu Ile Gln  
165 170 175  
His Glu Glu Tyr Asp Glu Thr Ser Asp Ser Ser Phe Ser Gln Cys Leu  
180 185 190  
Asp Asn Val Glu Arg Thr Lys Gln Lys Leu Met Gln Thr Ile Gln Arg  
195 200 205

Phe Glu Ser Leu Ala Asn Ile Ser Pro Phe Asn Leu Asp Glu Trp Gly  
210 215 220  
Ser Met Asp Glu Ala Ser Cys Met Glu Gly Glu Glu Thr Asp Thr  
225 230 235 240  
Lys Tyr Asp Asp Asp Glu Asn Cys Asp Thr Val Asp Arg Glu Ser Glu  
245 250 255  
Asp Glu Tyr Asn Asp Glu Val Glu Glu Lys Ala Ala Gln Leu Trp Asn  
260 265 270  
Arg Val Lys Glu Arg His Ala Ile Trp Ile His Glu Glu His Leu Ile  
275 280 285  
Met Asp Tyr Phe Arg Asp Glu Leu Met Gln Arg Thr Asn Ser Phe His  
290 295 300  
Glu Thr Gln Thr Leu  
305

(2) INFORMATION FOR SEQ ID NO:1188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1198

(D) OTHER INFORMATION: / Ceres Seq. ID 1569277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:

|             |             |             |            |             |            |      |
|-------------|-------------|-------------|------------|-------------|------------|------|
| actccctatt  | cttcagtaatt | gactaatatt  | agaactctct | atactactag  | ctaaaactaa | 60   |
| aaattgaaga  | aaaaacatga  | gtctcaccac  | cgacgaaatc | gaagtgaag   | atttcgtggt | 120  |
| gaaccaaaag  | aatggagatga | aaggactcgt  | cgactttcta | acctaaca    | cactctcttc | 180  |
| tcatacatt   | caactctctc  | aagaacgctt  | cacttcogac | aagatcctcc  | tcggatcacc | 240  |
| tgctccgggtc | attgacgtgt  | ccaattggaa  | tgaaccgcac | gtggctagag  | agatctgcc  | 300  |
| tgacgcgtca  | aagctcgggt  | tgtttcagat  | agtgaaccac | gggatagctc  | cggtcgatgt | 360  |
| caagggtgtg  | attgctgcgg  | cgctgggttt  | tttcgagttg | ccggcgagg   | agagaagaag | 420  |
| gtattggaga  | gggagttcac  | tgctggagac  | ggcgtggttg | accacaagtt  | tcaatccttg | 480  |
| catagaaagt  | gttttgaat   | ggagagattt  | cctcaagttt | gagtatcttc  | ctcaacgaca | 540  |
| tgacttcgct  | gccacgtggc  | cttctgtctg  | caaggaaaca | gtgatagacc  | atttcaaaag | 600  |
| gatcaaacca  | atcacagaga  | ggatcttaaa  | catactctac | aacaatctaa  | acacaatcat | 660  |
| cgatgagtc   | aataaaagaa  | cctaattggg  | aacaatgaga | atgaacttca  | actactatcc | 720  |
| gaaatgtctc  | gagccaagcc  | tggccatagg  | aactggtcgc | cactcagaca  | tcaacactct | 780  |
| cactctctc   | ctacaagaag  | atggtgtatt  | aagcagtcct | tacgcccag   | ccactgagga | 840  |
| tgagacaaa   | tggtattcatg | tcctccaat   | tccgggagct | attgtctga   | atatcggaag | 900  |
| tgattacag   | atattgagca  | atgatatgta  | taggagcgtg | gagcattgtg  | tggtggtcaa | 960  |
| taagtattgt  | agccgggttt  | cattccggt   | ttctgcgga  | ccggttcaatg | attcggttat | 1020 |
| tgagccgtta  | ccggaggtgt  | tagataagaa  | caatgagatg | gctcgtgata  | gaagaattgt | 1080 |
| gtattcggac  | tacttgaagt  | tttttttttg  | aagacctcat | gatggaaaga  | agactattga | 1140 |
| gtcgataaaa  | ttaccatgat  | atgattttacg | aagcttaaat | catcattatc  | tacggscc   |      |

(2) INFORMATION FOR SEQ ID NO:1189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..360

(D) OTHER INFORMATION: / Ceres Seq. ID 1569278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ser Leu Thr Thr Asp Glu Ile Glu Val Arg Asp Phe Val Val Asn |  |
| 1 5 10 15                                                       |  |
| Gln Lys Asn Gly Val Lys Gly Leu Val Asp Phe Leu Thr Leu Thr Thr |  |

20 25 30  
Leu Pro Ser Pro Tyr Ile Gln Pro Pro Gln Glu Arg Phe Thr Ser Asp  
35 40 45  
Lys Ile Leu Leu Gly Ser Pro Val Pro Val Ile Asp Val Ser Asn Trp  
50 55 60  
Asn Glu Pro His Val Ala Arg Glu Ile Cys His Ala Ala Ser Lys Leu  
65 70 75 80  
Gly Leu Phe Gln Ile Val Asn His Gly Ile Ala Pro Ala Glu Phe Lys  
85 90 95  
Gly Val Ile Ala Ala Ala Arg Gly Phe Phe Glu Leu Pro Ala Glu Glu  
100 105 110  
Arg Arg Arg Tyr Trp Arg Gly Ser Ser Val Ser Glu Thr Ala Trp Leu  
115 120 125  
Thr Thr Ser Phe Asn Pro Cys Ile Glu Ser Val Leu Glu Trp Arg Asp  
130 135 140  
Phe Leu Lys Phe Glu Tyr Leu Pro Gln Arg His Asp Phe Ala Ala Thr  
145 150 155 160  
Trp Pro Ser Val Cys Lys Glu Gln Val Ile Asp His Phe Lys Arg Ile  
165 170 175  
Lys Pro Ile Thr Glu Arg Ile Leu Asn Ile Leu Ile Asn Asn Leu Asn  
180 185 190  
Thr Ile Ile Asp Glu Ser Asn Lys Glu Thr Leu Met Gly Thr Met Arg  
195 200 205  
Met Asn Phe Asn Tyr Tyr Pro Lys Cys Pro Glu Pro Ser Leu Ala Ile  
210 215 220  
Gly Thr Gly Arg His Ser Asp Ile Asn Thr Leu Thr Leu Leu Gln  
225 230 235 240  
Glu Asp Gly Val Leu Ser Ser Leu Tyr Ala Arg Ala Thr Glu Asp Gly  
245 250 255  
Asp Lys Trp Ile His Val Pro Pro Ile Pro Gly Ala Ile Val Val Asn  
260 265 270  
Ile Gly Asp Val Leu Gln Ile Leu Ser Asn Asp Arg Tyr Arg Ser Val  
275 280 285  
Glu His Cys Val Val Val Asn Lys Tyr Cys Ser Arg Val Ser Ile Pro  
290 295 300  
Val Phe Cys Gly Pro Val His Asp Ser Val Ile Glu Pro Leu Pro Glu  
305 310 315 320  
Val Leu Asp Lys Asn Asn Glu Met Ala Arg Tyr Arg Lys Ile Val Tyr  
325 330 335  
Ser Asp Tyr Leu Lys Phe Phe Phe Gly Arg Pro His Asp Gly Lys Lys  
340 345 350  
Thr Ile Glu Ser Ile Lys Leu Pro  
355 360

(2) INFORMATION FOR SEQ ID NO:1190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1308
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:

|             |            |             |            |             |            |     |
|-------------|------------|-------------|------------|-------------|------------|-----|
| attattatttc | cactctctct | ctctagactc  | tgaattagct | cattcttgcc  | tccaaacaaa | 60  |
| tattctcgac  | agaccagacc | actcgtgaaga | cagaccacaa | cctaaactaa  | aagcatccac | 120 |
| gttcttttgt  | ttgtatttga | tggctgtgatc | tcatatccat | ggagatggag  | aatcaccgcc | 180 |
| cggcgagttt  | caactacatg | ggccgcgaat  | tcagcgattt | aagctctcaac | gatgactcct | 240 |
| ctgctttcag  | cgattgtaac | agcgacagat  | cggcggaatt | ccccactgct  | tcctcccgag | 300 |
| gcgcgtgctc  | ctctctctct | tcgcctcttg  | agaattccga | tgatctcatt  | aatcatctct | 360 |

(2) INFORMATION FOR SEQ ID NO:1191:

(17) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..355  
(D) OTHER INFORMATION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Met | Glu | Asn | His | Arg | Pro | Gly | Ser | Phe | Thr | Tyr | Met | Gly | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Lys | Phe | Ser | Asp | Leu | Ser | Leu | Asn | Asp | Asp | Ser | Ser | Ala | Phe | Ser | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Asn | Ser | Asp | Arg | Ser | Gly | Glu | Phe | Pro | Thr | Ala | Ser | Ser | Glu | Ser |
|     |     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Arg | Arg | Leu | Leu | Leu | Ser | Cys | Ala | Ser | Glu | Asn | Ser | Asp | Asp | Leu | Ile |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | His | Leu | Val | Ser | His | Leu | Asp | Ser | Ser | Tyr | Ser | Ile | Asp | Glu | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Gln | Ala | Ala | Met | Glu | Ile | Arg | Leu | Leu | Ser | Lys | Asn | Lys | Pro | Glu |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asn | Arg | Ile | Lys | Ile | Ala | Lys | Ala | Gly | Ala | Ile | Lys | Pro | Leu | Ile | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Ile | Ser | Ser | Ser | Asp | Leu | Gln | Leu | Gln | Glu | Tyr | Gly | Val | Thr | Xaa |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Leu | Asn | Leu | Ser | Leu | Cys | Asp | Glu | Asn | Lys | Gly | Ser | Ile | Ala | Ser |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Gly | Ala | Ile | Lys | Pro | Leu | Val | Arg | Ala | Leu | Lys | Met | Gly | Thr | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Thr | Ala | Lys | Asp | Asn | Ala | Ala | Cys | Ala | Leu | Leu | Arg | Leu | Ser | Gln | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Glu | Asn | Lys | Val | Ala | Ile | Gly | Arg | Ser | Gly | Ala | Ile | Pro | Leu | Leu |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Asn | Leu | Leu | Glu | Thr | Gly | Gly | Phe | Arg | Ala | Lys | Lys | Asp | Ala | Ser |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Ala | Leu | Tyr | Ser | Leu | Cys | Ser | Ala | Lys | Glu | Asn | Lys | Ile | Arg | Ala |
|     |     |     |     | 210 |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Gln | Ser | Gly | Ile | Met | Lys | Pro | Leu | Val | Glu | Leu | Met | Ala | Asp | Phe |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Gly | Ser | Asn | Met | Val | Asp | Lys | Ser | Ala | Phe | Val | Met | Ser | Leu | Leu | Met |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ser | Val | Pro | Glu | Ser | Lys | Pro | Ala | Ile | Val | Glu | Glu | Gly | Gly | Val | Pro |

260 265 270  
Val Leu Val Glu Ile Val Glu Val Gly Thr Gln Arg Gln Lys Glu Met  
275 280 285  
Ala Val Ser Ile Leu Leu Gln Leu Cys Glu Glu Ser Val Val Tyr Arg  
290 295 300  
Thr Met Val Ala Arg Glu Gly Ala Ile Pro Pro Leu Val Ala Leu Ser  
305 310 315 320  
Gln Ala Gly Thr Ser Arg Ala Lys Gln Lys Ala Glu Ala Leu Ile Glu  
325 330 335  
Leu Leu Arg Gln Pro Arg Ser Ile Ser Asn Gly Gly Ala Arg Ser Ser  
340 345 350  
Ser Gln Leu  
355

(2) INFORMATION FOR SEQ ID NO:1192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..353

(D) OTHER INFORMATION: / Ceres Seq. ID 1569288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:

Met Glu Asn His Arg Pro Gly Ser Phe Thr Tyr Met Gly Arg Lys Phe  
1 5 10 15  
Ser Asp Leu Ser Leu Asn Asp Asp Ser Ser Ala Phe Ser Asp Cys Asn  
20 25 30  
Ser Asp Arg Ser Gly Glu Phe Pro Thr Ala Ser Ser Glu Ser Arg Arg  
35 40 45  
Leu Leu Leu Ser Cys Ala Ser Glu Asn Ser Asp Asp Leu Ile Asn His  
50 55 60  
Leu Val Ser His Leu Asp Ser Ser Tyr Ser Ile Asp Glu Gln Lys Gln  
65 70 75 80  
Ala Ala Met Glu Ile Arg Leu Leu Ser Lys Asn Lys Pro Glu Asn Arg  
85 90 95  
Ile Lys Ile Ala Lys Ala Gly Ala Ile Lys Pro Leu Ile Ser Leu Ile  
100 105 110  
Ser Ser Ser Asp Leu Gln Leu Glu Tyr Gly Val Thr Xaa Ile Leu  
115 120 125  
Asn Leu Ser Leu Cys Asp Glu Asn Lys Glu Ser Ile Ala Ser Ser Gly  
130 135 140  
Ala Ile Lys Pro Leu Val Arg Ala Leu Lys Met Gly Thr Pro Thr Ala  
145 150 155 160  
Lys Asp Asn Ala Ala Cys Ala Leu Leu Arg Leu Ser Gln Ile Glu Glu  
165 170 175  
Asn Lys Val Ala Ile Gly Arg Ser Gly Ala Ile Pro Leu Leu Val Asn  
180 185 190  
Leu Leu Glu Thr Gly Gly Phe Arg Ala Lys Lys Asp Ala Ser Thr Ala  
195 200 205  
Leu Tyr Ser Leu Cys Ser Ala Lys Glu Asn Lys Ile Arg Ala Val Gln  
210 215 220  
Ser Gly Ile Met Lys Pro Leu Val Glu Leu Met Ala Asp Phe Gly Ser  
225 230 235 240  
Asn Met Val Asp Lys Ser Ala Phe Val Met Ser Leu Leu Met Ser Val  
245 250 255  
Pro Glu Ser Lys Pro Ala Ile Val Glu Glu Gly Gly Val Pro Val Leu  
260 265 270  
Val Glu Ile Val Glu Val Gly Thr Gln Arg Gln Lys Glu Met Ala Val  
275 280 285

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Ser Ile Leu Leu Gln Leu Cys Glu Glu Ser Val Val Tyr Arg Thr Met  
290 295 300  
Val Ala Arg Glu Gly Ala Ile Pro Pro Leu Val Ala Leu Ser Gln Ala  
305 310 315 320  
Gly Thr Ser Arg Ala Lys Gln Lys Ala Glu Ala Leu Ile Glu Leu Leu  
325 330 335  
Arg Gln Pro Arg Ser Ile Ser Asn Gly Gly Ala Arg Ser Ser Ser Gln  
340 345 350  
Leu

(2) INFORMATION FOR SEQ ID NO:1193:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..342

(D) OTHER INFORMATION: / Ceres Seq. ID 1569289

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:

Met Gly Arg Lys Phe Ser Asp Leu Ser Leu Asn Asp Asp Ser Ser Ala  
1 5 10 15  
Phe Ser Asp Cys Asn Ser Asp Arg Ser Gly Glu Phe Pro Thr Ala Ser  
20 25 30  
Ser Glu Ser Arg Arg Leu Leu Ser Cys Ala Ser Glu Asn Ser Asp  
35 40 45  
Asp Leu Ile Asn His Leu Val Ser His Leu Asp Ser Ser Tyr Ser Ile  
50 55 60  
Asp Glu Gln Lys Gln Ala Ala Met Glu Ile Arg Leu Leu Ser Lys Asn  
65 70 75 80  
Lys Pro Glu Asn Arg Ile Lys Ile Ala Lys Ala Gly Ala Ile Lys Pro  
85 90 95  
Leu Ile Ser Leu Ile Ser Ser Ser Asp Leu Gln Leu Gln Glu Tyr Gly  
100 105 110  
Val Thr Xaa Ile Leu Asn Leu Ser Leu Cys Asp Glu Asn Lys Glu Ser  
115 120 125  
Ile Ala Ser Ser Gly Ala Ile Lys Pro Leu Val Arg Ala Leu Lys Met  
130 135 140  
Gly Thr Pro Thr Ala Lys Asp Asn Ala Ala Cys Ala Leu Leu Arg Leu  
145 150 155 160  
Ser Gln Ile Glu Glu Asn Lys Val Ala Ile Gly Arg Ser Gly Ala Ile  
165 170 175  
Pro Leu Leu Val Asn Leu Leu Glu Thr Gly Phe Arg Ala Lys Lys  
180 185 190  
Asp Ala Ser Thr Ala Leu Tyr Ser Leu Cys Ser Ala Lys Glu Asn Lys  
195 200 205  
Ile Arg Ala Val Gln Ser Gly Ile Met Lys Pro Leu Val Glu Leu Met  
210 215 220  
Ala Asp Phe Gly Ser Asn Met Val Asp Lys Ser Ala Phe Val Met Ser  
225 230 235 240  
Leu Leu Met Ser Val Pro Glu Ser Lys Pro Ala Ile Val Glu Glu Gly  
245 250 255  
Gly Val Pro Val Leu Val Glu Ile Val Glu Val Gly Thr Gln Arg Gln  
260 265 270  
Lys Glu Met Ala Val Ser Ile Leu Leu Gln Leu Cys Glu Glu Ser Val  
275 280 285  
Val Tyr Arg Thr Met Val Ala Arg Glu Gly Ala Ile Pro Pro Leu Val  
290 295 300  
Ala Leu Ser Gln Ala Gly Thr Ser Arg Ala Lys Gln Lys Ala Glu Ala

305 310 315 320  
Leu Ile Glu Leu Leu Arg Gln Pro Arg Ser Ile Ser Asn Gly Gly Ala  
325 330 335  
Arg Ser Ser Ser Gln Leu  
340

(2) INFORMATION FOR SEQ ID NO:1194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1204
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:

|             |             |             |            |            |             |      |
|-------------|-------------|-------------|------------|------------|-------------|------|
| acactagct   | tctctgtatt  | caattcttca  | caaagtttct | aaaagctttt | ctcttgttat  | 60   |
| tcaacaactt  | ggcacccgagc | tctgtaacgc  | cggtgtgtgt | ttctacttga | ttctccGgag  | 120  |
| ctcttgatgc  | tgttgaggat  | gacacaagcg  | taccagtgga | catcaaatgt | ccaattctga  | 180  |
| tagcttttcca | cogtcatata  | tacgatggtg  | actggcattt | ttcatgtggt | acaaaagagt  | 240  |
| ataaactttct | aatggaccaa  | tttcacccatg | ttctgcagc  | ttttctgaaa | cttgaaaaag  | 300  |
| gggtatcaaga | ggctattgaa  | gatataacta  | aaagaatggg | tgcaggaatg | gccaaagtta  | 360  |
| tttgcaaggga | gtgtagaaca  | attgatgact  | atgatgaata | ctgccattat | gctgcaggag  | 420  |
| ttgttggttt  | aggtttgtca  | aaaactctca  | ttgtcttcga | attagaaata | ctgactccag  | 480  |
| attggaagca  | gatttcaaat  | tctacagggt  | tattttctga | gaaaacaac  | attatcaaat  | 540  |
| attatcttga  | agacattaat  | gagagaccac  | agtcgcgcac | gttttggcct | cgtgagattt  | 600  |
| ggggaaaaata | tgttgacaaa  | cttgaggact  | tcaaaaatga | ggagaaagct | acaaaagcag  | 660  |
| tgcagtgttt  | gaatgaaatg  | gtcactaatg  | cattgaaatc | tgttgaagat | tgtttgaaat  | 720  |
| ccttggcNtt  | cActgcgtga  | tcttgcaata  | tttcagtctt | gcgccatccc | tcagatcggt  | 780  |
| gcgattgtgaa | cacttacatt  | atgctataac  | aattgacaag | tgtttagagg | cgtcgtgaga  | 840  |
| atgagacgag  | gtcttaatagc | taaaagtcatt | gatcgcacaa | agacaatgga | tgaatgtctat | 900  |
| gggtgcgttct | atgatttttc  | tgtcatgcta  | caaacaaaag | ttgacataat | cgatccaaat  | 960  |
| gctatgaaaa  | cattaaatcg  | actcgaaaac  | atcaagaaag | ttgcagagga | aaatggagta  | 1020 |
| cttcacaaaa  | gaaaactctta | tgtttaacgat | gaaacacaa  | ccaaggctat | ctttgttgta  | 1080 |
| atgtttgtgc  | ttctactggc  | tatagtcgtt  | gtatatctca | aagcaaacca | acgtaagtga  | 1140 |
| ctctgattgt  | gaagcatcat  | tgaacataat  | ttctagcttt | ttgaaatgt  | ttgatcaaat  | 1200 |

(2) INFORMATION FOR SEQ ID NO:1195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Gln | Phe | His | His | Val | Ser | Ala | Ala | Phe | Leu | Lys | Leu | Glu | Lys |
| 1   |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |     |     |
| Gly | Tyr | Gln | Glu | Ala | Ile | Glu | Asp | Ile | Thr | Lys | Arg | Met | Gly | Ala | Gly |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Met | Ala | Lys | Phe | Ile | Cys | Lys | Glu | Val | Glu | Thr | Ile | Asp | Asp | Tyr | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Tyr | Cys | His | Tyr | Ala | Ala | Gly | Leu | Val | Gly | Leu | Gly | Leu | Ser | Lys |
|     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ile | Phe | Ile | Ala | Ser | Glu | Leu | Glu | Ile | Leu | Thr | Pro | Asp | Trp | Lys | Gln |
| 65  |     |     |     |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Ile | Ser | Asn | Ser | Thr | Gly | Leu | Phe | Leu | Gln | Lys | Thr | Asn | Ile | Ile | Lys |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Phe | Ile | Cys | Lys | Glu | Val | Glu | Thr | Ile | Asp | Asp | Tyr | Asp |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Tyr | Cys | His | Tyr | Ala | Ala | Gly | Leu | Val | Gly | Leu | Gly | Leu | Ser | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Phe | Ile | Ala | Ser | Glu | Leu | Glu | Ile | Leu | Thr | Pro | Asp | Trp | Lys | Gln |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ser | Asn | Ser | Thr | Gly | Leu | Phe | Leu | Gln | Lys | Thr | Asn | Ile | Ile | Lys |
| 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |

Asp Tyr Leu Glu Asp Ile Asn Glu Arg Pro Lys Ser Arg Met Phe Trp  
65 70 75 80  
Pro Arg Glu Ile Trp Gly Lys Tyr Val Asp Lys Leu Glu Asp Phe Lys  
85 90 95  
Asn Glu Glu Lys Ala Thr Lys Ala Val Gln Cys Leu Asn Glu Met Val  
100 105 110  
Thr Asn Ala Leu Asn His Val Glu Asp Cys Leu Lys Ser Leu Xaa Phe  
115 120 125  
Thr Ala  
130

(2) INFORMATION FOR SEQ ID NO:1198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1156

(D) OTHER INFORMATION: / Ceres Seq. ID 1569298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:

|            |            |             |             |             |             |      |
|------------|------------|-------------|-------------|-------------|-------------|------|
| atactctctt | ttttctcgg  | acaagaaggc  | tacagaaaga  | tatgtcgtg   | tcgtctttacc | 60   |
| tcagcccgac | gcgccttcta | taaggctacc  | tcgcgcgttg  | tctcaggcg   | gcaggactga  | 120  |
| cgtcgcagac | gctttccata | gactctgaaa  | caaccatcca  | cttctggggc  | ccaccactc   | 180  |
| tagaccaccg | gagcgacgat | gacagaccgg  | ttatgcttct  | cctccacggc  | ttcgggtccgt | 240  |
| cgtccatgtg | gcagtgggcg | cgacagatgc  | aagccttctc  | tcctcccgct  | ttcagggggtt | 300  |
| attctccgca | ttctgtcttc | ttcggcgact  | ctacctcttc  | ctccaccaat  | cgcaccgaaag | 360  |
| ctctccaggc | ggaatgtatg | gcaaaagctaa | tggcgaaaat  | aggaataggg  | aagtataatg  | 420  |
| tggctggaac | aagctacggg | gggtttgttg  | cgtaaccacat | ggccaaaatg  | tggccggaata | 480  |
| aagtggagaa | agtggtgat  | gcaagctccg  | gcatacaat   | gcgaaagtgt  | gacgggtgaaa | 540  |
| gtttattgca | aagatccaat | tgtgagtgc   | tcgagaagg   | tatgtttacca | tcactgtcaa  | 600  |
| ctgagtttgc | cacacttatg | gctttggcat  | cttcattgctg | gttatgttctg | atgtttctctg | 660  |
| atgctctctg | gaacgacgta | atcaataatt  | tgtataaaaa  | aaatagaaaa  | gagaagatag  | 720  |
| aattgttgaa | gggagtgact | ttcggccgga  | gcgaaaaatt  | aaacatcgat  | tctctttctc  | 780  |
| aggaggtcct | aattgtatgg | ggagacaaa   | atcagatatt  | tctgtgaaag  | atggctttacg | 840  |
| aattaaaaga | gattcttgga | gacaaaacga  | aactagaaat  | cattgacaac  | acttcacatg  | 900  |
| ttctccagat | tgaatgtgct | caagagtcca  | acaatattgt  | tttgagattt  | ttgaagggtt  | 960  |
| cttaagagcc | gtaattttat | tccatgctac  | atgattcttc  | agtttttttt  | aagtgttaaa  | 1020 |
| ctattggtta | cgtaattttt | cgactttact  | tgccatgctt  | tctcattttt  | catgtaagaa  | 1080 |
| ctttatccat | tactgtcatt | gtagagaact  | ctattttatg  | caaaaagtta  | tactaatatg  | 1140 |
| caacttaatt | ttcgtc     |             |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..250

(D) OTHER INFORMATION: / Ceres Seq. ID 1569299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Leu | Leu | His | Gly | Phe | Gly | Pro | Ser | Ser | Met | Trp | Gln | Trp | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Arg | Gln | Met | Gln | Ala | Phe | Ser | Pro | Ser | Ala | Phe | Arg | Val | Tyr | Ser | Pro |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Leu | Val | Phe | Phe | Gly | Asp | Ser | Thr | Ser | Ser | Ser | Thr | Asn | Arg | Thr |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Glu | Val | Phe | Gln | Ala | Glu | Cys | Met | Ala | Lys | Leu | Met | Ala | Lys | Ile | Gly |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 50                                                              | 55  | 60  |
| Ile Gly Lys Tyr Asn Val Ala Gly Thr Ser Tyr Gly Gly Phe Val Ala |     |     |
| 65                                                              | 70  | 75  |
| Tyr His Met Ala Lys Met Trp Pro Glu Lys Val Glu Lys Val Val Ile |     | 80  |
|                                                                 | 85  | 90  |
| Ala Ser Ser Gly Ile Asn Met Arg Lys Cys Asp Gly Glu Ser Leu Leu |     | 95  |
|                                                                 | 100 | 105 |
| Gln Arg Ser Asn Cys Glu Cys Ile Glu Lys Val Met Leu Pro Ser Thr |     | 110 |
|                                                                 | 115 | 120 |
| Ala Thr Glu Phe Arg Thr Leu Met Ala Leu Ala Ser Ser Trp Arg Leu |     | 125 |
|                                                                 | 130 | 135 |
| Val Arg Met Phe Pro Asp Ala Leu Trp Asn Asp Val Ile Asn Asn Leu |     | 140 |
|                                                                 | 145 | 150 |
| Tyr Lys Lys Asn Arg Lys Glu Lys Ile Glu Leu Lys Gly Val Thr     |     | 155 |
|                                                                 | 160 | 165 |
| Phe Gly Arg Ser Glu Asn Leu Asn Ile Asp Ser Leu Ser Gln Glu Val |     | 170 |
|                                                                 | 175 | 180 |
| Leu Ile Val Trp Gly Asp Lys Asp Gln Ile Phe Pro Val Lys Met Ala |     | 185 |
|                                                                 | 190 | 195 |
| Tyr Glu Leu Lys Glu Ile Leu Gly Asp Lys Thr Lys Leu Glu Ile Ile |     | 200 |
|                                                                 | 205 | 210 |
| Asp Asn Thr Ser His Val Pro Gln Ile Glu Cys Ala Gln Glu Phe Asn |     | 215 |
|                                                                 | 220 | 225 |
| Asn Ile Val Leu Arg Phe Leu Lys Gly Ser                         |     | 230 |
|                                                                 | 235 | 240 |
|                                                                 | 245 | 250 |

(2) INFORMATION FOR SEQ ID NO:1200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1569300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Trp Gln Trp Arg Arg Gln Met Gln Ala Phe Ser Pro Ser Ala Phe |     |     |
| 1                                                               | 5   | 10  |
| Arg Val Tyr Ser Pro Asp Leu Val Phe Phe Gly Asp Ser Thr Ser Ser |     | 15  |
|                                                                 | 20  | 25  |
| Ser Thr Asn Arg Thr Glu Val Phe Gln Ala Glu Cys Met Ala Lys Leu |     | 30  |
|                                                                 | 35  | 40  |
| Met Ala Lys Ile Gly Ile Gly Lys Tyr Asn Val Ala Gly Thr Ser Tyr |     | 45  |
|                                                                 | 50  | 55  |
| Gly Gly Phe Val Ala Tyr His Met Ala Lys Met Trp Pro Glu Lys Val |     | 60  |
|                                                                 | 65  | 70  |
| Glu Lys Val Val Ile Ala Ser Ser Gly Ile Asn Met Arg Lys Cys Asp |     | 75  |
|                                                                 | 80  | 85  |
| Gly Glu Ser Leu Gln Arg Ser Asn Cys Glu Cys Ile Glu Lys Val     |     | 90  |
|                                                                 | 95  | 100 |
| Met Leu Pro Ser Thr Ala Thr Glu Phe Arg Thr Leu Met Ala Leu Ala |     | 105 |
|                                                                 | 110 | 115 |
| Ser Ser Trp Arg Leu Val Arg Met Phe Pro Asp Ala Leu Trp Asn Asp |     | 120 |
|                                                                 | 125 | 130 |
| Val Ile Asn Asn Leu Tyr Lys Lys Asn Arg Lys Glu Lys Ile Glu Leu |     | 135 |
|                                                                 | 140 | 145 |
| Leu Lys Gly Val Thr Phe Gly Arg Ser Glu Asn Leu Asn Ile Asp Ser |     | 150 |
|                                                                 | 155 | 160 |
| Leu Ser Gln Glu Val Leu Ile Val Trp Gly Asp Lys Asp Gln Ile Phe |     | 165 |
|                                                                 | 170 | 175 |
|                                                                 | 180 | 185 |
|                                                                 | 190 |     |

Pro Val Lys Met Ala Tyr Glu Leu Lys Glu Ile Leu Gly Asp Lys Thr  
195 200 205  
Lys Leu Glu Ile Ile Asp Asn Thr Ser His Val Pro Gln Ile Glu Cys  
210 215 220  
Ala Gln Glu Phe Asn Asn Ile Val Leu Arg Phe Leu Lys Gly Ser  
225 230 235

(2) INFORMATION FOR SEQ ID NO:1201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..232
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1201:

Met Gln Ala Phe Ser Pro Ser Ala Phe Arg Val Tyr Ser Pro Asp Leu  
1 5 10 15  
Val Phe Phe Gly Asp Ser Thr Ser Ser Thr Thr Asn Arg Thr Glu Val  
20 25 30  
Phe Gln Ala Glu Cys Met Ala Lys Leu Met Ala Lys Ile Gly Ile Gly  
35 40 45  
Lys Tyr Asn Val Ala Gly Thr Ser Tyr Gly Gly Phe Val Ala Tyr His  
50 55 60  
Met Ala Lys Met Trp Pro Glu Lys Val Glu Lys Val Val Ile Ala Ser  
65 70 75 80  
Ser Gly Ile Asn Met Arg Lys Cys Asp Gly Glu Ser Leu Leu Gln Arg  
85 90 95  
Ser Asn Cys Glu Cys Ile Glu Lys Val Met Leu Pro Ser Thr Ala Thr  
100 105 110  
Glu Phe Arg Thr Leu Met Ala Leu Ala Ser Ser Trp Arg Leu Val Arg  
115 120 125  
Met Phe Pro Asp Ala Leu Trp Asn Asp Val Ile Asn Asn Leu Tyr Lys  
130 135 140  
Lys Asn Arg Lys Glu Lys Ile Glu Leu Leu Lys Gly Val Thr Phe Gly  
145 150 155 160  
Arg Ser Glu Asn Leu Asn Ile Asp Ser Leu Ser Gln Glu Val Leu Ile  
165 170 175  
Val Trp Gly Asp Lys Asp Gln Ile Phe Pro Val Lys Met Ala Tyr Glu  
180 185 190  
Leu Lys Glu Ile Leu Gly Asp Lys Thr Lys Leu Glu Ile Ile Asp Asn  
195 200 205  
Thr Ser His Val Pro Gln Ile Glu Cys Ala Gln Glu Phe Asn Asn Ile  
210 215 220  
Val Leu Arg Phe Leu Lys Gly Ser  
225 230

(2) INFORMATION FOR SEQ ID NO:1202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1431
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202:

attttatttt ctggaatctt ctctctcttc ctgattcca ggcagcttaac aacaacaaca

|             |             |             |            |            |            |      |
|-------------|-------------|-------------|------------|------------|------------|------|
| acaacatatt  | ctctgctg    | ggttattg    | gaatttct   | ttttgtgat  | agaaatggat | 120  |
| cgaggtccgg  | tgaccacagg  | accgttggat  | atgccgatta | tgccagcacg | tgatcgatat | 180  |
| gaacttcgtta | aggatatggg  | ttctggtaat  | ttcgggtgtg | ctcgtcttat | gagagataaa | 240  |
| ctcactaaag  | agcttgttgc  | tgccaagtag  | atcgagagag | gagacaagat | tgatgaaaaa | 300  |
| gttccaaagg  | agatcattaa  | ccacagggtca | ctaaggcatc | ctaattattg | cagattttaa | 360  |
| gaggtcattt  | tgacgccgac  | tcactctggt  | atcataatgg | aatatgcttc | tgccggtgaa | 420  |
| ctttacagag  | ggatttgc    | tgccaggacgg | tttagtgaag | atgaggtcgt | gttcttcttt | 480  |
| cagcagcttc  | tatctggagt  | cagttatgtg  | catgcatgac | aaatttgcca | tcgtgacctg | 540  |
| aagctagaga  | atacatttgt  | ggatggaagt  | ccctgctctc | gattaaaaat | ttgtgatttt | 600  |
| ggatatccaa  | agtcctctgt  | ttctcattca  | caaccaaaat | caactgttgg | tactcctgca | 660  |
| tacatctctc  | cagaggttct  | gcttcgtcag  | gaatatgatg | gcaagattgc | agatgtatgg | 720  |
| tcagtgtggg  | tgacccttata | cgctcatgtt  | gttgagcggt | atccgttcga | agatccagaa | 780  |
| gagccaagag  | actatcggaa  | aacaatacag  | agaatcctta | gcgttaaaat | ctcaatccct | 840  |
| gctgacatac  | ggatatccac  | tgaatcgtgt  | catcttattt | caagaatctt | cgtggtgatg | 900  |
| cccgctacca  | gaataagcat  | accagagatc  | aaaacccata | gttggttctt | gaagaatctc | 960  |
| ccctgctgat  | taatgaacga  | gagcaacaca  | ggaagccagt | tcacaggacc | tgacaacca  | 1020 |
| atgcacagcc  | ttgacacaat  | catgcaaatc  | attctctga  | ccacaattcc | cgctgttgca | 1080 |
| aaccgttgcc  | tagacgattt  | catgactgac  | aatcttgatc | ttgacgatga | catggatgac | 1140 |
| tttgactctg  | aatctgaaat  | cgacattgac  | atagcggagg | agatagttta | cgctctctaa | 1200 |
| taaaaagcct  | tttttaacaa  | ccaaaacact  | ttcttatctg | ttctaagacc | agtagtgctc | 1260 |
| tgatctctct  | gtttcaaat   | ctaccaattt  | ttgtattgtc | ttctgtttgt | ttctgttttc | 1320 |
| ttcatgcaca  | catatcatat  | atgtgtaatg  | taaaatatca | ttctgtgtat | tatatccaa  | 1380 |
| gtgcacacaa  | aagcaratta  | gcaGttaaaa  | cagttgaagc | aagttgaggt | c          |      |

(2) INFORMATION FOR SEQ ID NO:1203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..361

(D) OTHER INFORMATION: / Ceres Seq. ID 1569307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Arg | Ala | Pro | Val | Thr | Thr | Gly | Pro | Leu | Asp | Met | Pro | Ile | Met |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| His | Asp | Ser | Asp | Arg | Tyr | Asp | Phe | Val | Lys | Asp | Ile | Gly | Ser | Gly | Asn |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Phe | Gly | Val | Ala | Arg | Leu | Met | Arg | Asp | Lys | Leu | Thr | Lys | Glu | Leu | Val |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Ala | Val | Lys | Tyr | Ile | Glu | Arg | Gly | Asp | Lys | Ile | Asp | Glu | Asn | Val | Gln |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Arg | Glu | Ile | Ile | Asn | His | Arg | Ser | Leu | Arg | His | Pro | Asn | Ile | Val | Arg |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |
| Phe | Lys | Glu | Val | Ile | Leu | Thr | Pro | Thr | His | Leu | Ala | Ile | Ile | Met | Glu |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Tyr | Ala | Ser | Gly | Gly | Glu | Leu | Tyr | Glu | Arg | Ile | Cys | Asn | Ala | Gly | Arg |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Phe | Ser | Glu | Asp | Glu | Ala | Arg | Phe | Phe | Gln | Gln | Leu | Leu | Ser | Gly |     |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Val | Ser | Tyr | Cys | His | Ala | Met | Gln | Ile | Cys | His | Arg | Asp | Leu | Lys | Leu |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |
| Glu | Asn | Thr | Leu | Leu | Asp | Gly | Ser | Pro | Ala | Pro | Arg | Leu | Lys | Ile | Cys |
|     |     |     |     | 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |
| Asp | Phe | Gly | Tyr | Ser | Lys | Ser | Ser | Val | Leu | His | Ser | Gln | Pro | Lys | Ser |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Thr | Val | Gly | Thr | Pro | Ala | Tyr | Ile | Ala | Pro | Glu | Val | Leu | Leu | Arg | Gln |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Glu | Tyr | Asp | Gly | Lys | Ile | Ala | Asp | Val | Trp | Ser | Cys | Gly | Val | Thr | Leu |
|     |     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |

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Tyr Val Met Leu Val Gly Ala Tyr Pro Phe Glu Asp Pro Glu Glu Pro  
210 215 220  
Arg Asp Tyr Arg Lys Thr Ile Gln Arg Ile Leu Ser Val Lys Tyr Ser  
225 230 235 240  
Ile Pro Asp Asp Ile Arg Ile Ser Pro Glu Cys Cys His Leu Ile Ser  
245 250 255  
Arg Ile Phe Val Ala Asp Pro Ala Thr Arg Ile Ser Ile Pro Glu Ile  
260 265 270  
Lys Thr His Ser Trp Phe Leu Lys Asn Leu Pro Ala Asp Leu Met Asn  
275 280 285  
Glu Ser Asn Thr Gly Ser Gln Phe Gln Glu Pro Glu Gln Pro Met Gln  
290 295 300  
Ser Leu Asp Thr Ile Met Gln Ile Ile Ser Glu Ala Thr Ile Pro Ala  
305 310 315 320  
Val Arg Asn Arg Cys Leu Asp Asp Phe Met Thr Asp Asn Leu Asp Leu  
325 330 335  
Asp Asp Asp Met Asp Asp Phe Asp Ser Glu Ser Glu Ile Asp Ile Asp  
340 345 350  
Ser Ser Gly Glu Ile Val Tyr Ala Leu  
355 360

(2) INFORMATION FOR SEQ ID NO:1204:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 349 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..349

(D) OTHER INFORMATION: / Ceres Seq. ID 1569308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:

Met Pro Ile Met His Asp Ser Asp Arg Tyr Asp Phe Val Lys Asp Ile  
1 5 10 15  
Gly Ser Gly Asn Phe Gly Val Ala Arg Leu Met Arg Asp Lys Leu Thr  
20 25 30  
Lys Glu Leu Val Ala Val Lys Tyr Ile Glu Arg Gly Asp Lys Ile Asp  
35 40 45  
Glu Asn Val Gln Arg Glu Ile Ile Asn His Arg Ser Leu Arg His Pro  
50 55 60  
Asn Ile Val Arg Phe Lys Glu Val Ile Leu Thr Pro Thr His Leu Ala  
65 70 75 80  
Ile Ile Met Glu Tyr Ala Ser Gly Gly Glu Leu Tyr Glu Arg Ile Cys  
85 90 95  
Asn Ala Gly Arg Phe Ser Glu Asp Glu Ala Arg Phe Phe Phe Gln Gln  
100 105 110  
Leu Leu Ser Gly Val Ser Tyr Cys His Ala Met Gln Ile Cys His Arg  
115 120 125  
Asp Leu Lys Leu Glu Asn Thr Leu Leu Asp Gly Ser Pro Ala Pro Arg  
130 135 140  
Leu Lys Ile Cys Asp Phe Gly Tyr Ser Lys Ser Ser Val Leu His Ser  
145 150 155 160  
Gln Pro Lys Ser Thr Val Gly Thr Pro Ala Tyr Ile Ala Pro Glu Val  
165 170 175  
Leu Leu Arg Gln Glu Tyr Asp Gly Lys Ile Ala Asp Val Trp Ser Cys  
180 185 190  
Gly Val Thr Leu Tyr Val Met Leu Val Gly Ala Tyr Pro Phe Glu Asp  
195 200 205  
Pro Glu Glu Pro Arg Asp Tyr Arg Lys Thr Ile Gln Arg Ile Leu Ser  
210 215 220  
Val Lys Tyr Ser Ile Pro Asp Asp Ile Arg Ile Ser Pro Glu Cys Cys

225 230 235 240  
His Leu Ile Ser Arg Ile Phe Val Ala Asp Pro Ala Thr Arg Ile Ser  
245 250 255  
Ile Pro Glu Ile Lys Thr His Ser Trp Phe Leu Lys Asn Leu Pro Ala  
260 265 270  
Asp Leu Met Asn Glu Ser Asn Thr Gly Ser Gln Phe Gln Glu Pro Glu  
275 280 285  
Gln Pro Met Gln Ser Leu Asp Thr Ile Met Gln Ile Ile Ser Glu Ala  
290 295 300  
Thr Ile Pro Ala Val Arg Asn Arg Cys Leu Asp Asp Phe Met Thr Asp  
305 310 315 320  
Asn Leu Asp Leu Asp Asp Asp Met Asp Asp Phe Asp Ser Glu Ser Glu  
325 330 335  
Ile Asp Ile Asp Ser Ser Gly Glu Ile Val Tyr Ala Leu  
340 345

(2) INFORMATION FOR SEQ ID NO:1205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..346

(D) OTHER INFORMATION: / Ceres Seq. ID 1569309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:

Met His Asp Ser Asp Arg Tyr Asp Phe Val Lys Asp Ile Gly Ser Gly  
1 5 10 15  
Asn Phe Gly Val Ala Arg Leu Met Arg Asp Lys Leu Thr Lys Glu Leu  
20 25 30  
Val Ala Val Lys Tyr Ile Glu Arg Gly Asp Lys Ile Asp Glu Asn Val  
35 40 45  
Gln Arg Glu Ile Ile Asn His Arg Ser Leu Arg His Pro Asn Ile Val  
50 55 60  
Arg Phe Lys Glu Val Ile Leu Thr Pro Thr His Leu Ala Ile Ile Met  
65 70 75 80  
Glu Tyr Ala Ser Gly Gly Glu Leu Tyr Glu Arg Ile Cys Asn Ala Gly  
85 90 95  
Arg Phe Ser Glu Asp Glu Ala Arg Phe Phe Gln Gln Leu Leu Ser  
100 105 110  
Gly Val Ser Tyr Cys His Ala Met Gln Ile Cys His Arg Asp Leu Lys  
115 120 125  
Leu Glu Asn Thr Leu Leu Asp Gly Ser Pro Ala Pro Arg Leu Lys Ile  
130 135 140  
Cys Asp Phe Gly Tyr Ser Lys Ser Ser Val Leu His Ser Gln Pro Lys  
145 150 155 160  
Ser Thr Val Gly Thr Pro Ala Tyr Ile Ala Pro Glu Val Leu Leu Arg  
165 170 175  
Gln Glu Tyr Asp Gly Lys Ile Ala Asp Val Trp Ser Cys Gly Val Thr  
180 185 190  
Leu Tyr Val Met Leu Val Gly Ala Tyr Pro Phe Glu Asp Pro Glu Glu  
195 200 205  
Pro Arg Asp Tyr Arg Lys Thr Ile Gln Arg Ile Leu Ser Val Lys Tyr  
210 215 220  
Ser Ile Pro Asp Asp Ile Arg Ile Ser Pro Glu Cys Cys His Leu Ile  
225 230 235 240  
Ser Arg Ile Phe Val Ala Asp Pro Ala Thr Arg Ile Ser Ile Pro Glu  
245 250 255  
Ile Lys Thr His Ser Trp Phe Leu Lys Asn Leu Pro Ala Asp Leu Met  
260 265 270

Asn Glu Ser Asn Thr Gly Ser Gln Phe Gln Glu Pro Glu Gln Pro Met  
275 280 285  
Gln Ser Leu Asp Thr Ile Met Gln Ile Ile Ser Glu Ala Thr Ile Pro  
290 295 300  
Ala Val Arg Asn Arg Cys Leu Asp Asp Phe Met Thr Asp Asn Leu Asp  
305 310 315 320  
Leu Asp Asp Asp Met Asp Asp Phe Asp Ser Glu Ser Glu Ile Asp Ile  
325 330 335  
Asp Ser Ser Gly Glu Ile Val Tyr Ala Leu  
340 345

(2) INFORMATION FOR SEQ ID NO:1206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1533
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:

|             |             |             |             |             |            |      |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| ctgatttttt  | gacgttaaga  | gatagaacca  | gggagagata  | gagagataga  | gttatggcct | 60   |
| tggcgatgat  | gatccgaac   | gcagcttcga  | agcgaggaa   | gactccgac   | tccggtgatt | 120  |
| tgggtggttt  | gagatctatg  | tcttcatggt  | ggaagagcgt  | tgagcctgct  | cttaagaatc | 180  |
| cgatccctcgg | agttaccgaa  | gcttttctcg  | ctgatctctag | tcttgaaaaa  | gttaattgtt | 240  |
| gtgtgggagc  | atatactgat  | gataatggga  | agcctgttgt  | cttggaatgt  | gtcagagaa  | 300  |
| ctgagaaaag  | gcttgcgtgg  | agcaactttca | tgagtagcct  | tccatgggga  | ggaagtgcga | 360  |
| aaatggtgga  | cctaaccatca | agcttgccta  | cggggacaat  | agtgaattta  | tcaagataa  | 420  |
| aagaattgct  | gcagttcaga  | ctctgtctgg  | cactggagcc  | tgccggctct  | ttgcagactt | 480  |
| ccagaaacgt  | ttttctctcg  | gttcacagat  | ctacattcct  | gttccaacct  | ggtccaacca | 540  |
| ccacaacatc  | tggaaaagatg | cacaagtcct  | tcaaaagaca  | tatcattact  | atcatccaga | 600  |
| aaccaagggc  | tggattttct  | cagcattgat  | ggatgatgtg  | aagaatgctc  | cggaagggtc | 660  |
| attcttcctt  | cttcatgctt  | gtgctcataa  | tctactgcca  | gtagacccta  | cagaggaaca | 720  |
| atggagagag  | atatcacagc  | tattcaaggc  | taaaagcat   | ttcgctattc  | tcatatggc  | 780  |
| ttaccaaggt  | tttgctagtg  | gagatccagc  | gagagatgcc  | aagtccatca  | ggatctttct | 840  |
| tgaagatggt  | catcatattg  | gaatttctca  | gtcttatgca  | aaaaacatgg  | gactctacgg | 900  |
| ccagaggggt  | ggatgtctca  | gtgtgcttgg  | tgaagatccg  | aagcaagccg  | tggctgtgaa | 960  |
| aagtcaattg  | cagcagctag  | ctagaccaat  | gtacagcaac  | ccacctttgc  | attggtgtca | 1020 |
| gctggtctca  | accattcttg  | aagaccaga   | gttaaagagt  | ctgtggctta  | aagaagttaa | 1080 |
| ggtcatggct  | gataggatca  | tccgcatgag  | aactactttg  | cgagaaagcc  | ctgagaagtt | 1140 |
| aggaatgcct  | ttgtcatggg  | agcacgttac  | caaacagatt  | ggaatgtctc  | gtcacagtgg | 1200 |
| gttaataaga  | gaacaggttg  | accgcttaac  | aagcgaatat  | acacatctata | tgacccgtaa | 1260 |
| cggcgcgtatc | agtatggctg  | gtgttaCaac  | aggaaacctg  | ggataccttg  | cgaatgctat | 1320 |
| acatgaagtc  | accaagtcac  | cttaaatcat  | ttacttacat  | gtttcagcca  | aacatacaaa | 1380 |
| ttttgtttga  | agagtcaata  | agacaggagg  | ctagatttgt  | acttctgcga  | ttggtttttg | 1440 |
| gagaactgaa  | agtttaacca  | taaacagtaa  | ttttattagc  | catttttttc  | ttagctgggc | 1500 |
| aataaaaagca | aagcctaacc  | gatggatttt  | tgg         |             |            |      |

(2) INFORMATION FOR SEQ ID NO:1207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..191
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:

Met Ala Leu Ala Met Met Ile Arg Asn Ala Ala Ser Lys Arg Gly Met



1 5 10 15  
Thr Pro Ile Ser Gly Asp Phe Gly Gly Leu Arg Ser Met Ser Ser Trp  
20 25 30  
Trp Lys Ser Val Glu Pro Ala Pro Lys Asp Pro Ile Leu Gly Val Thr  
35 40 45  
Glu Ala Phe Leu Ala Asp Pro Ser Pro Glu Lys Val Asn Val Gly Val  
50 55 60  
Gly Ala Tyr Arg Asp Asp Asn Gly Lys Pro Val Val Leu Glu Cys Val  
65 70 75 80  
Arg Glu Ala Glu Lys Arg Leu Ala Gly Ser Thr Phe Met Glu Tyr Leu  
85 90 95  
Pro Met Gly Gly Ser Ala Lys Met Val Asp Leu Thr Leu Ser Leu Pro  
100 105 110  
Thr Gly Thr Ile Val Asn Leu Ser Lys Ile Lys Glu Leu Leu Gln Phe  
115 120 125  
Arg Leu Cys Leu Ala Leu Glu Pro Ala Gly Ser Leu Gln Thr Ser Arg  
130 135 140  
Asn Val Phe Leu Leu Val His Arg Ser Thr Phe Leu Phe Gln Pro Gly  
145 150 155 160  
Pro Thr Thr Thr Thr Ser Gly Lys Met His Lys Ser Leu Lys Arg His  
165 170 175  
Ile Ile Thr Ile Ile Gln Lys Pro Arg Ala Trp Ile Ser Gln His  
180 185 190

(2) INFORMATION FOR SEQ ID NO:1208:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 238 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..238  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569312  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:  
Met Asp Asp Val Lys Asn Ala Pro Glu Gly Ser Phe Phe Leu Leu His  
1 5 10 15  
Ala Cys Ala His Asn Pro Thr Gly Val Asp Pro Thr Glu Gln Trp  
20 25 30  
Arg Glu Ile Ser Gln Leu Phe Lys Ala Lys Lys His Phe Ala Phe Phe  
35 40 45  
Asp Met Ala Tyr Gln Gly Phe Ala Ser Gly Asp Pro Ala Arg Asp Ala  
50 55 60  
Lys Ser Ile Arg Ile Phe Leu Glu Asp Gly His His Ile Gly Ile Ser  
65 70 75 80  
Gln Ser Tyr Ala Lys Asn Met Gly Leu Tyr Gly Gln Arg Val Gly Cys  
85 90 95  
Leu Ser Val Leu Cys Glu Asp Pro Lys Gln Ala Val Ala Val Lys Ser  
100 105 110  
Gln Leu Gln Gln Leu Ala Arg Pro Met Tyr Ser Asn Pro Pro Leu His  
115 120 125  
Gly Ala Gln Leu Val Ser Thr Ile Leu Glu Asp Pro Glu Leu Lys Ser  
130 135 140  
Leu Trp Leu Lys Glu Val Lys Val Met Ala Asp Arg Ile Ile Gly Met  
145 150 155 160  
Arg Thr Thr Leu Arg Glu Ser Leu Glu Lys Leu Gly Ser Pro Leu Ser  
165 170 175  
Trp Glu His Val Thr Lys Gln Ile Gly Met Phe Cys Tyr Ser Gly Leu  
180 185 190  
Thr Pro Glu Gln Val Asp Arg Leu Thr Ser Glu Tyr His Ile Tyr Met  
195 200 205

Thr Arg Asn Gly Arg Ile Ser Met Ala Gly Val Thr Thr Gly Asn Val  
210 215 220  
Gly Tyr Leu Ala Asn Ala Ile His Glu Val Thr Lys Ser Ser  
225 230 235

(2) INFORMATION FOR SEQ ID NO:1209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..189
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:

Met Ala Tyr Gln Gly Phe Ala Ser Gly Asp Pro Ala Arg Asp Ala Lys  
1 5 10 15  
Ser Ile Arg Ile Phe Leu Glu Asp Gly His His Ile Gly Ile Ser Gln  
20 25 30  
Ser Tyr Ala Lys Asn Met Gly Leu Tyr Gly Gln Arg Val Gly Cys Leu  
35 40 45  
Ser Val Leu Cys Glu Asp Pro Lys Gln Ala Val Ala Lys Ser Gln  
50 55 60  
Leu Gln Gln Leu Ala Arg Pro Met Tyr Ser Asn Pro Pro Leu His Gly  
65 70 75 80  
Ala Gln Leu Val Ser Thr Ile Leu Glu Asp Pro Glu Leu Lys Ser Leu  
85 90 95  
Trp Leu Lys Glu Val Lys Val Met Ala Asp Arg Ile Ile Gly Met Arg  
100 105 110  
Thr Thr Leu Arg Glu Ser Leu Glu Lys Leu Gly Ser Pro Leu Ser Trp  
115 120 125  
Glu His Val Thr Lys Gln Ile Gly Met Phe Cys Tyr Ser Gly Leu Thr  
130 135 140  
Pro Glu Gln Val Asp Arg Leu Thr Ser Glu Tyr His Ile Tyr Met Thr  
145 150 155 160  
Arg Asn Gly Arg Ile Ser Met Ala Gly Val Thr Thr Gly Asn Val Gly  
165 170 175  
Tyr Leu Ala Asn Ala Ile His Glu Val Thr Lys Ser Ser  
180 185

(2) INFORMATION FOR SEQ ID NO:1210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

cttctcgcat cttatatgaa acacattcac tctccaaaat aatctatact ttctctacat 60  
attctccttga cgatcatgag actcatttcg tgaaaaatc gtcattatat caaattagaa 120  
gttgatggaa aacatggggg attcgagcat agggccgggc catccgcac tcctcccg 180  
gtttcggttt caccgcagct atgaggaact agtagttcat tactcaaga agaaagcagc 240  
ttctgttcca cttccagttc caatcatcgc agagattgat ctttacaagt ttgatccttg 300  
ggagcttcca agcaaggcga gttttggaga gcacgagtggt tacttttcta gtccctcgga 360  
tcggaagtat ccaaatgggg ttaggcctaa cgggcagca acttcgggtt attggaaagc 420  
aacgggaacc gataaaccca tatttactgt caatagtcac aagggttggt tcaagaaagc 480  
gcttgttttt tacggtggaa agcctcctaa agggataaaa acagattgga tcatgcata 540

|             |             |             |             |             |            |      |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| atatacgcctc | actgatggta  | accttagcac  | tgccggctaag | cgcgcctgact | taaccacgac | 600  |
| aaggaaaaaac | tcactacgac  | tagacgattg  | ggttctatgt  | aggatctata  | agaagaatag | 660  |
| ttccacaagS  | accaCacaat  | ggagagagta  | ttagagagga  | tctaattggaa | ggcatgctct | 720  |
| caaaatcatc  | tgctaatctt  | tcttctacat  | cagtactaga  | caacaacgac  | aacaataatr | 780  |
| acaataacaa  | agaacacttt  | ttcgacggta  | tggtcgtttc  | ttcagacaaa  | cggtccctgt | 840  |
| gtggtcaata  | ccgaatgggc  | gacgaggcct  | caggatcatc  | ttcattcgga  | tctttcttat | 900  |
| cgagcaagag  | gtttcatcat  | acagggtgatc | tcaacaatga  | taactacaat  | gtctcttttg | 960  |
| tttcgatgct  | tagtgagatt  | cctcagagtt  | cggggtttca  | tgcaaatggt  | ggtatggata | 1020 |
| cgagctgctc  | tctagctgat  | catgggggttt | taagacaggc  | gtttcagctt  | cctaacatga | 1080 |
| actggcactc  | ataatctata  | tagatatata  | tgtatgtatc  | atatatgtat  | ctatgcaggc | 1140 |
| ctaataatag  | ttacacataa  | atcatctggg  | aatatatata  | tacaagtacg  | cggtcttaca | 1200 |
| aatgtatacg  | tattctgttta | attacgtcaa  | gaaaaagtgt  | atacgtttct  | ttttactcaa | 1260 |
| tggtctcгаа  | gatgtgtact  | aataacagaa  | gctgattaat  | aaaaataata  | aaagtatatt | 1320 |
| ttttcc      |             |             |             |             |            |      |

(2) INFORMATION FOR SEQ ID NO:1211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..189
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asn | Met | Gly | Asp | Ser | Ser | Ile | Gly | Pro | Gly | His | Pro | His | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Pro | Gly | Phe | Arg | Phe | His | Pro | Thr | Asp | Glu | Glu | Leu | Val | Val | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Leu | Lys | Lys | Lys | Ala | Ala | Ser | Val | Pro | Leu | Pro | Val | Ser | Ile | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Glu | Ile | Asp | Leu | Tyr | Lys | Phe | Asp | Pro | Trp | Glu | Leu | Pro | Ser | Lys |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Ser | Phe | Gly | Glu | His | Glu | Trp | Tyr | Phe | Phe | Ser | Pro | Arg | Asp | Arg |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Tyr | Pro | Asn | Gly | Val | Arg | Pro | Asn | Arg | Ala | Ala | Thr | Ser | Gly | Tyr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Trp | Lys | Ala | Thr | Gly | Thr | Asp | Lys | Pro | Ile | Phe | Thr | Cys | Asn | Ser | His |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Lys | Val | Gly | Val | Lys | Lys | Ala | Leu | Val | Phe | Tyr | Gly | Gly | Lys | Pro | Pro |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Lys | Gly | Ile | Lys | Thr | Asp | Trp | Ile | Met | His | Glu | Tyr | Arg | Leu | Thr | Asp |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Asn | Leu | Ser | Thr | Ala | Ala | Lys | Pro | Pro | Asp | Leu | Thr | Thr | Thr | Arg |
|     |     |     | 145 |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Asn | Ser | Leu | Arg | Leu | Asp | Asp | Trp | Val | Leu | Cys | Arg | Ile | Tyr | Lys |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Lys | Asn | Ser | Ser | Gln | Xaa | Thr | Thr | Gln | Trp | Arg | Glu | Tyr |     |     |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Asp | Ser | Ser | Ile | Gly | Pro | Gly | His | Pro | His | Leu | Pro | Pro | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Phe | Arg | Phe | His | Pro | Thr | Asp | Glu | Glu | Leu | Val | Val | His | Tyr | Leu | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Lys | Ala | Ala | Ser | Val | Pro | Leu | Pro | Val | Ser | Ile | Ile | Ala | Glu | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Leu | Trp | Lys | Phe | Asp | Pro | Trp | Glu | Leu | Pro | Ser | Lys | Ala | Ser | Phe |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Gly | Glu | His | Glu | Trp | Tyr | Phe | Phe | Ser | Pro | Arg | Asp | Arg | Lys | Tyr | Pro |
| 65  |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asn | Gly | Val | Arg | Pro | Asn | Arg | Ala | Ala | Thr | Ser | Gly | Tyr | Trp | Lys | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Gly | Thr | Asp | Lys | Pro | Ile | Phe | Thr | Cys | Asn | Ser | His | Lys | Val | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Lys | Lys | Ala | Leu | Val | Phe | Tyr | Gly | Gly | Lys | Pro | Pro | Lys | Gly | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Thr | Asp | Trp | Ile | Met | His | Glu | Tyr | Arg | Leu | Thr | Asp | Gly | Asn | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Thr | Ala | Ala | Lys | Pro | Pro | Asp | Leu | Thr | Thr | Thr | Arg | Lys | Asn | Ser |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Arg | Leu | Asp | Asp | Trp | Val | Leu | Cys | Arg | Ile | Tyr | Lys | Lys | Asn | Ser |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Gln | Xaa | Thr | Thr | Gln | Trp | Arg | Glu | Tyr |     |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1213:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1569329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gly | Met | Leu | Ser | Lys | Ser | Ser | Ala | Asn | Ser | Ser | Ser | Thr | Ser |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Leu | Asp | Asn | Asn | Asp | Asn | Asn | Xaa | Asn | Asn | Lys | Glu | His | Phe |     |
|     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Phe | Asp | Gly | Met | Val | Val | Ser | Ser | Asp | Lys | Arg | Ser | Leu | Cys | Gly | Gln |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Tyr | Arg | Met | Gly | Asp | Glu | Ala | Ser | Gly | Ser | Ser | Ser | Phe | Gly | Ser | Phe |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Leu | Ser | Ser | Lys | Arg | Phe | His | His | Thr | Gly | Asp | Leu | Asn | Asn | Asp | Asn |
| 65  |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Tyr | Asn | Val | Ser | Phe | Val | Ser | Met | Leu | Ser | Glu | Ile | Pro | Gln | Ser | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Phe | His | Ala | Asn | Gly | Val | Met | Asp | Thr | Thr | Ser | Ser | Leu | Ala | Asp |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| His | Gly | Val | Leu | Arg | Gln | Ala | Phe | Gln | Leu | Pro | Asn | Met | Asn | Trp | His |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1214:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 718 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..718

(D) OTHER INFORMATION: / Ceres Seq. ID 1569338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| aattgaaaga  | cggtgggggg | tttctcacta | cccagaaatt | atcatcatcc  | acagagaaaac | 60  |
| ccaaaagaga  | ttgaagaaga | tgcattacat | gggtttgttt | agtagagctg  | gaaacatatt  | 120 |
| taggcagcct  | agagcgtttg | aggcctcaaa | cgctatgtta | cagggcaatc  | tttcatat    | 180 |
| tccatccaaa  | atctttgttg | gaggtctctc | accatctact | gatgtggagc  | tcttgaaaga  | 240 |
| agcttttggc  | agttttggaa | aaattgttga | tgcggtagtg | gttttggacc  | gtgaaagtgg  | 300 |
| tttatcaagg  | ggctttgggt | tcgtaacata | tgattcgatc | gaagttgcta  | ataacgcaat  | 360 |
| cgaaagctatg | caaaataaag | agcttgatgg | gcgaataatt | ggagtgcatc  | cagctgattc  | 420 |
| agghgtgtgt  | nggsggyvgt | ggtgggtttg | caagaagggg | agggttatggt | ggtggctgtg  | 480 |
| ggggatagtc  | tcgtgggtga | tttggtcgcg | gtggatttgg | tgggtgtggc  | tatggcttgg  | 540 |
| ttcgttaact  | ggacatccag | atatgtctac | gcgcaagatt | gattagctctg | tggtttaatt  | 600 |
| ttctcttcac  | aaagaccact | attttgttat | aacaacgctc | ttatgcttga  | acaaacatat  | 660 |
| caagcggtga  | aagttggcaa | aaacatttgt | tgattcaatt | ggtattttgat | acaaattc    |     |

(2) INFORMATION FOR SEQ ID NO:1215:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..194

(D) OTHER INFORMATION: / Ceres Seq. ID 1569339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Glu | Arg | Arg | Trp | Gly | Val | Ser | His | Tyr | Pro | Glu | Ile | Ile | Ile | Ile |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |  |
| His | Arg | Glu | Thr | Gln | Lys | Arg | Leu | Lys | Lys | Met | His | Tyr | Met | Gly | Leu |  |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |  |
| Phe | Ser | Arg | Ala | Gly | Asn | Ile | Phe | Arg | Gln | Pro | Arg | Ala | Leu | Gln | Ala |  |
|     |     |     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |  |
| Ser | Asn | Ala | Met | Leu | Gln | Gly | Asn | Leu | Ser | Leu | Thr | Pro | Ser | Lys | Ile |  |
|     |     |     | 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |     |  |
| Phe | Val | Gly | Gly | Leu | Ser | Pro | Ser | Thr | Asp | Val | Glu | Leu | Leu | Lys | Glu |  |
|     |     |     | 65  |     |     |     |     |     | 70  |     |     |     | 75  |     | 80  |  |
| Ala | Phe | Gly | Ser | Phe | Gly | Lys | Ile | Val | Asp | Ala | Val | Val | Val | Leu | Asp |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |  |
| Arg | Glu | Ser | Gly | Leu | Ser | Arg | Gly | Phe | Gly | Phe | Val | Thr | Tyr | Asp | Ser |  |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |  |
| Ile | Glu | Val | Ala | Asn | Asn | Ala | Met | Gln | Ala | Met | Gln | Asn | Lys | Glu | Leu |  |
|     |     |     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |     |  |
| Asp | Gly | Arg | Ile | Ile | Gly | Val | His | Pro | Ala | Asp | Ser | Xaa | Xaa | Gly | Xaa |  |
|     |     |     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |  |
| Xaa | Xaa | Trp | Trp | Phe | Cys | Lys | Lys | Gly | Arg | Leu | Trp | Trp | Trp | Ser | Trp |  |
|     |     |     | 145 |     |     |     |     |     | 150 |     |     |     | 155 |     | 160 |  |
| Gly | Ile | Cys | Ser | Trp | Trp | Ile | Trp | Ser | Arg | Trp | Ile | Trp | Trp | Trp | Trp |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |  |
| Leu | Trp | Leu | Cys | Ser | Leu | Thr | Gly | His | Pro | Asp | Met | Ser | Thr | Ala | Lys |  |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |  |
| Ile | Asp |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..168  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1569340  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:  
Met His Tyr Met Gly Leu Phe Ser Arg Ala Gly Asn Ile Phe Arg Gln  
1                  5                  10                  15  
Pro Arg Ala Leu Gln Ala Ser Asn Ala Met Leu Gln Gly Asn Leu Ser  
                  20                  25                  30  
Leu Thr Pro Ser Lys Ile Phe Val Gly Gly Leu Ser Pro Ser Thr Asp  
                  35                  40                  45  
Val Glu Leu Leu Lys Glu Ala Phe Gly Ser Phe Gly Lys Ile Val Asp  
50                  55                  60  
Ala Val Val Val Leu Asp Arg Glu Ser Gly Leu Ser Arg Gly Phe Gly  
65                  70                  75                  80  
Phe Val Thr Tyr Asp Ser Ile Glu Val Ala Asn Asn Ala Met Gln Ala  
                  85                  90                  95  
Met Gln Asn Lys Glu Leu Asp Gly Arg Ile Ile Gly Val His Pro Ala  
                  100                 105                 110  
Asp Ser Xaa Xaa Gly Xaa Xaa Xaa Trp Trp Phe Cys Lys Lys Gly Arg  
                 115                 120                 125  
Leu Trp Trp Trp Ser Trp Gly Ile Cys Ser Trp Trp Ile Trp Ser Arg  
130                 135                 140  
Trp Ile Trp Trp Trp Trp Leu Trp Leu Cys Ser Leu Thr Gly His Pro  
145                 150                 155                 160  
Asp Met Ser Thr Ala Lys Ile Asp  
                 165

(2) INFORMATION FOR SEQ ID NO:1217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:

Met Gly Leu Phe Ser Arg Ala Gly Asn Ile Phe Arg Gln Pro Arg Ala  
1                  5                  10                  15  
Leu Gln Ala Ser Asn Ala Met Leu Gln Gly Asn Leu Ser Leu Thr Pro  
                  20                  25                  30  
Ser Lys Ile Phe Val Gly Gly Leu Ser Pro Ser Thr Asp Val Glu Leu  
                  35                  40                  45  
Leu Lys Glu Ala Phe Gly Ser Phe Gly Lys Ile Val Asp Ala Val Val  
50                  55                  60  
Val Leu Asp Arg Glu Ser Gly Leu Ser Arg Gly Phe Gly Phe Val Thr  
65                  70                  75                  80  
Tyr Asp Ser Ile Glu Val Ala Asn Asn Ala Met Gln Ala Met Gln Asn  
                  85                  90                  95  
Lys Glu Leu Asp Gly Arg Ile Ile Gly Val His Pro Ala Asp Ser Xaa  
                 100                 105                 110  
Xaa Gly Xaa Xaa Xaa Trp Trp Phe Cys Lys Lys Gly Arg Leu Trp Trp  
                 115                 120                 125  
Trp Ser Trp Gly Ile Cys Ser Trp Trp Ile Trp Ser Arg Trp Ile Trp  
130                 135                 140  
Trp Trp Trp Leu Trp Leu Cys Ser Leu Thr Gly His Pro Asp Met Ser  
145                 150                 155                 160

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Arg | Ser | Arg | Val | Thr | Arg | Glu | Ala | Pro | Thr | Gly | Thr | Arg | Ile |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Leu | Ala | Ser | Leu | Ser | Ala | Met | Val | Ala | Glu | Ser | Val | Thr | Phe | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Asp | Leu | Thr | Lys | Thr | Arg | Met | Gln | Leu | His | Gly | Ser | Gly | Ser | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Gly | Ala | His | Arg | Ile | Gly | Ala | Phe | Gly | Val | Val | Ser | Glu | Ile | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Lys | Glu | Gly | Val | Ile | Gly | Leu | Tyr | Lys | Gly | Leu | Ser | Pro | Ala | Ile |
|     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Arg | His | Leu | Phe | Tyr | Thr | Pro | Ile | Arg | Ile | Ile | Gly | Tyr | Glu | Asn |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Leu | Lys | Gly | Leu | Ile | Val | Arg | Ser | Glu | Thr | Asn | Asn | Ser | Glu | Ser | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Pro Leu Ala Thr Lys Ala Leu Val Gly Gly Phe Ser Gly Val Ile Ala  
115 120 125  
Gln Lys Cys Arg  
130

(2) INFORMATION FOR SEQ ID NO:1220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Val | Val | Ala | Ser | Pro | Ala | Asp | Leu | Val | Lys | Val | Arg | Met | Gln |     |
| 1   |     |     |     |     | 5   |     |     |     |     |     | 10  |     |     | 15  |     |     |
| Ala | Asp | Gly | Arg | Gly | Leu | Val | Ser | Gln | Gly | Leu | Lys | Pro | Arg | Tyr | Ser | Gly |
|     |     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ile | Glu | Ala | Phe | Thr | Lys | Ile | Leu | Gln | Ser | Glu | Gly | Val | Lys | Gly |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Leu | Trp | Lys | Gly | Val | Leu | Pro | Asn | Ile | Gln | Arg | Ala | Phe | Leu | Val | Asn |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Met | Gly | Glu | Leu | Ala | Cys | Tyr | Asp | His | Ala | Lys | His | Phe | Val | Ile | Asp |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |     |
| Lys | Lys | Ile | Ala | Glu | Asp | Asn | Ile | Phe | Ala | His | Thr | Leu | Ala | Ser | Ile |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Met | Ser | Gly | Leu | Ala | Ser | Thr | Ser | Leu | Ser | Cys | Pro | Ala | Asp | Val | Val |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Lys | Thr | Arg | Met | Met | Asn | Gln | Gly | Glu | Asn | Ala | Val | Tyr | Arg | Asn | Ser |     |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |     |
| Tyr | Asp | Cys | Leu | Val | Lys | Thr | Val | Lys | Phe | Glu | Gly | Ile | Arg | Ala | Leu |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Trp | Lys | Gly | Phe | Phe | Pro | Thr | Trp | Ala | Arg | Leu | Gly | Pro | Trp | Gln | Phe |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |     |
| Val | Phe | Trp | Val | Ser | Tyr | Glu | Lys | Phe | Arg | Leu | Leu | Ala | Gly | Ile | Ser |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |

Ser Phe

(2) INFORMATION FOR SEQ ID NO:1221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gln | Ala | Asp | Gly | Arg | Leu | Val | Ser | Gln | Gly | Leu | Lys | Pro | Arg | Tyr |  |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser | Gly | Pro | Ile | Glu | Ala | Phe | Thr | Lys | Ile | Leu | Gln | Ser | Glu | Gly | Val |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Lys | Gly | Leu | Trp | Lys | Gly | Val | Leu | Pro | Asn | Ile | Gln | Arg | Ala | Phe | Leu |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Val | Asn | Met | Gly | Glu | Leu | Ala | Cys | Tyr | Asp | His | Ala | Lys | His | Phe | Val |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Ile | Asp | Lys | Lys | Ile | Ala | Glu | Asp | Asn | Ile | Phe | Ala | His | Thr | Leu | Ala |  |



|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 65                                                              | 70  | 75  | 80  |
| Ser Ile Met Ser Gly Leu Ala Ser Thr Ser Leu Ser Cys Pro Ala Asp |     |     |     |
|                                                                 | 85  | 90  | 95  |
| Val Val Lys Thr Arg Met Met Asn Gln Gly Glu Asn Ala Val Tyr Arg |     |     |     |
|                                                                 | 100 | 105 | 110 |
| Asn Ser Tyr Asp Cys Leu Val Lys Thr Val Lys Phe Glu Gly Ile Arg |     |     |     |
|                                                                 | 115 | 120 | 125 |
| Ala Leu Trp Lys Gly Phe Phe Pro Thr Trp Ala Arg Leu Gly Pro Trp |     |     |     |
|                                                                 | 130 | 135 | 140 |
| Gln Phe Val Phe Trp Val Ser Tyr Glu Lys Phe Arg Leu Leu Ala Gly |     |     |     |
|                                                                 | 145 | 150 | 155 |
| Ile Ser Ser Phe                                                 |     |     | 160 |

(2) INFORMATION FOR SEQ ID NO:1222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1595 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1595
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:

|            |             |             |            |             |             |      |
|------------|-------------|-------------|------------|-------------|-------------|------|
| acaagagcca | tttgcaatta  | ggcataatat  | atgtcctaac | tcaccaaccc  | octcaaaatt  | 60   |
| gccaccaact | tcaaatcttc  | ctccctttaa  | cccttctcaa | tcattcttct  | tctgcttgg   | 120  |
| aatcctgac  | atggcgctct  | ctccacttc   | caaatccatt | ctcggaacca  | ccaaaccggg  | 180  |
| ttctctctct | cttccctcgg  | agctccgtcg  | tctttcttct | cccgccgttc  | agatctctct  | 240  |
| ccgtacccaa | accaggaaga  | acttccagat  | acaagctact | ggaagtctat  | atggggactca | 300  |
| ttttgagtt  | tcaacttttg  | gagaatcaca  | tggaggagga | gttggttgta  | tcattgatgg  | 360  |
| ttgtctctct | cgtattccac  | ttaactgaat  | tgatttgcaa | ttcgatctcg  | atagaaggag  | 420  |
| acctggtcac | agcaggatga  | caactcctag  | aaaggagact | gatacttgcc  | ggatactctc  | 480  |
| tgaggtctcc | gaaggaaatg  | cgacaggaac  | acctatccat | gtgtttgtgc  | ctaacacaga  | 540  |
| tcagagagga | cttgattaca  | gtgaaatgtc  | ggttgcctat | agaccatgcg  | atgctgatgc  | 600  |
| aacttatgac | atgaagtatg  | gtgtcagatc  | agtgcagggt | ggaggaaagt  | cttcagctag  | 660  |
| agagaccatt | ggaagagtgt  | ctcctggagc  | tttggccaa  | aaaaatttga  | agcaatttgc  | 720  |
| aggaactgag | attcttgctc  | atgtctcgca  | agttcaccat | gttgtaacttc | cagaagaatt  | 780  |
| ggtagaccac | gagaatttaa  | cactcgaaac  | gatagaaaa  | aacattgtca  | gagccctaa   | 840  |
| tcccagatag | cggaaaaaga  | tgatagctgc  | gattgatgct | gtcaggacaa  | aagggaactc  | 900  |
| ttgttggtgt | gtttgtacct  | cgattgttgc  | gaatgctcca | ctcgggcttg  | gtacaccggt  | 960  |
| tttcgataaa | cttgaagcag  | aactggtcaa  | agcttgtatg | tcgttaacctg | caacaagggg  | 1020 |
| atttgagtgt | ggaagcggct  | tttcaggtac  | ctttttgact | gtgtctgaac  | acaatgatga  | 1080 |
| gttctatacc | gcagaataat  | gaagaataac  | taccagaaca | aaccgatctg  | gtggaaattca | 1140 |
| gggagggatc | tcaaatgggtg | aaataataaa  | catgagagta | gccttcaagc  | caacatcaac  | 1200 |
| aattggaagg | aagcagaata  | cggttaaccag | agacaaggta | gaaacccgaa  | tgattgcgcg  | 1260 |
| ttgtgtcatc | gatccttggt  | tgttctctcg  | agctgtgcca | atggttgaat  | caatggtggc  | 1320 |
| tttagttctt | gtggatcaat  | tgatggcgca  | atacgacaaa | tgccatttgt  | ttccaataaa  | 1380 |
| tcacagtggt | caggaacctc  | tcacagatag  | gcagccccaa | aatgctactg  | cttttgtaag  | 1440 |
| aaaactcgag | aagataaagag | tcagagacag  | taaggYttcg | ctttgtgtgt  | gtgattatta  | 1500 |
| ttatgaataa | aaaaaatggt  | aattttgtac  | ccaccagaga | aacaaaaaac  | atgatttttt  | 1560 |
| tgtaacagga | tttgtactcta | tatcattatt  | cagct      |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1569359

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ala | Pro | Pro | Pro | Ala | Ile | Arg | His | Asn | Ile | Cys | Pro | Asn | Ser | Pro | Thr |
| 1   | 10  | 5   |     |     |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Pro | Ser | Lys | Leu | Pro | Pro | Thr | Ser | Asn | Phe | Ser | Pro | Leu | Asn | Leu | Ser |     |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gln | Ser | Ser | Phe | Phe | Cys | Leu | Gly | Ile | Leu | Ile | Met | Ala | Ser | Ser | Ser | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Thr | Ser | Lys | Ser | Ile | Leu | Gly | Ser | Thr | Lys | Pro | Gly | Ser | Ser | Ser | Ser | Leu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Pro | Ser | Glu | Leu | Arg | Arg | Leu | Ser | Ser | Pro | Ala | Val | Gln | Ile | Ser | Ser | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Arg | Thr | Gln | Thr | Arg | Lys | Asn | Phe | Gln | Ile | Gln | Ala | Thr | Gly | Ser | Ser |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Tyr | Gly | Thr | His | Phe | Arg | Val | Ser | Thr | Phe | Gly | Glu | Ser | His | Gly | Gly |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Gly | Val | Gly | Cys | Ile | Ile | Asp | Gly | Cys | Pro | Pro | Arg | Ile | Pro | Leu | Thr |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Glu | Ser | Asp | Leu | Gln | Phe | Asp | Leu | Asp | Arg | Arg | Arg | Pro | Gly | Gln | Ser |     |
|     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |     |
| Arg | Ile | Thr | Thr | Pro | Arg | Lys | Glu | Thr | Asp | Thr | Cys | Arg | Ile | Ser | Ser |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Gly | Val | Ser | Glu | Gly | Met | Thr | Thr | Gly | Thr | Pro | Ile | His | Val | Phe | Val |     |
|     |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Pro | Asn | Thr | Asp | Gln | Arg | Gly | Leu | Asp | Tyr | Ser | Glu | Met | Ser | Val | Ala |     |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Tyr | Arg | Pro | Ser | His | Ala | Asp | Ala | Thr | Tyr | Asp | Met | Lys | Tyr | Gly | Val |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Arg | Ser | Val | Gln | Ser | Gly | Gly | Arg | Ser | Ser | Ala | Arg | Glu | Thr | Ile | Gly |     |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Arg | Val | Ala | Pro | Gly | Ala | Leu | Ala | Lys | Lys | Ile | Leu | Lys | Gln | Phe | Ala |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Gly | Thr | Glu | Ile | Leu | Ala | Tyr | Val | Ser | Gln | Val | His | His | Val | Val | Leu |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Pro | Glu | Glu | Leu | Val | Asp | His | Glu | Asn | Leu | Thr | Leu | Glu | Gln | Ile | Glu |     |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Asn | Asn | Ile | Val | Arg | Cys | Pro | Asn | Pro | Glu | Tyr | Ala | Glu | Lys | Met | Ile |     |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Ala | Ala | Ile | Asp | Ala | Val | Arg | Thr | Lys | Gly | Asn | Ser | Val | Gly | Gly | Val |     |
|     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |     |
| Val | Thr | Cys | Ile | Val | Arg | Asn | Ala | Pro | Arg | Gly | Leu | Gly | Thr | Pro | Val |     |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |
| Phe | Asp | Lys | Leu | Glu | Ala | Glu | Leu | Ala | Lys | Ala | Cys | Met | Ser | Leu | Pro |     |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Ala | Thr | Lys | Gly | Phe | Glu | Phe | Gly | Ser | Gly | P   |     |     |     |     |     |     |

Glu Pro Leu Gln Ile Glu Gln Pro Gln Asn Ala Thr Ala Leu  
465 470 475

(2) INFORMATION FOR SEQ ID NO:1224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 435 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..435

(D) OTHER INFORMATION: / Ceres Seq. ID 1569360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Ser | Leu | Thr | Ser | Lys | Ser | Ile | Leu | Gly | Ser | Thr | Lys | Pro |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ser | Ser | Ser | Leu | Pro | Ser | Glu | Leu | Arg | Arg | Leu | Ser | Ser | Pro | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Gln | Ile | Ser | Leu | Arg | Thr | Gln | Thr | Arg | Lys | Asn | Phe | Gln | Ile | Gln |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Thr | Gly | Ser | Ser | Tyr | Gly | Thr | His | Phe | Arg | Val | Ser | Thr | Phe | Gly |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Ser | His | Gly | Gly | Gly | Val | Gly | Cys | Ile | Ile | Asp | Gly | Cys | Pro | Pro |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Ile | Pro | Leu | Thr | Glu | Ser | Asp | Leu | Gln | Phe | Asp | Leu | Asp | Arg | Arg |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | Pro | Gly | Gln | Ser | Arg | Ile | Thr | Thr | Pro | Arg | Lys | Glu | Thr | Asp | Thr |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Cys | Arg | Ile | Ser | Ser | Gly | Val | Ser | Glu | Gly | Met | Thr | Thr | Gly | Thr | Pro |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | His | Val | Phe | Val | Pro | Asn | Thr | Asp | Gln | Arg | Gly | Leu | Asp | Tyr | Ser |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Met | Ser | Val | Ala | Tyr | Arg | Pro | Ser | His | Ala | Asp | Ala | Thr | Tyr | Asp |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Met | Lys | Tyr | Gly | Val | Arg | Ser | Val | Gln | Gly | Gly | Gly | Arg | Ser | Ser | Ala |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Arg | Glu | Thr | Ile | Gly | Arg | Val | Ala | Pro | Gly | Ala | Leu | Ala | Lys | Lys | Ile |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Leu | Lys | Gln | Phe | Ala | Gly | Thr | Glu | Ile | Leu | Ala | Tyr | Val | Ser | Gln | Val |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| His | His | Val | Val | Leu | Pro | Glu | Glu | Leu | Val | Asp | His | Glu | Asn | Leu | Thr |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Glu | Gln | Ile | Glu | Asn | Asn | Ile | Val | Arg | Cys | Pro | Asn | Pro | Glu | Tyr |
|     |     |     | 225 |     |     | 230 |     |     |     | 235 |     |     |     | 240 |     |
| Ala | Glu | Lys | Met | Ile | Ala | Ala | Ile | Asp | Ala | Val | Arg | Thr | Lys | Gly | Asn |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Ser | Val | Gly | Gly | Val | Val | Thr | Cys | Ile | Val | Arg | Asn | Ala | Pro | Arg | Gly |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Leu | Gly | Thr | Pro | Val | Phe | Asp | Lys | Leu | Glu | Ala | Glu | Leu | Ala | Lys | Ala |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Cys | Met | Ser | Leu | Pro | Ala | Thr | Lys | Gly | Phe | Glu | Phe | Gly | Ser | Gly | Phe |
|     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ala | Gly | Thr | Phe | Leu | Thr | Gly | Leu | Glu | His | Asn | Asp | Glu | Phe | Tyr | Thr |
|     |     |     | 305 |     |     | 310 |     |     |     | 315 |     |     |     | 320 |     |
| Asp | Glu | Asn | Gly | Arg | Ile | Arg | Thr | Arg | Thr | Asn | Arg | Ser | Gly | Gly | Ile |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Gln | Gly | Gly | Ile | Ser | Asn | Gly | Glu | Ile | Ile | Asn | Met | Arg | Val | Ala | Phe |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     |     | 350 |     |     |
| Lys | Pro | Thr | Ser | Thr | Ile | Gly | Arg | Lys | Gln | Asn | Thr | Val | Thr | Arg | Asp |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Lys | Val | Glu | Thr | Glu | Met | Ile | Ala | Arg | Gly | Arg | His | Asp | Pro | Cys | Val |

|                     |                                             |     |
|---------------------|---------------------------------------------|-----|
| 370                 | 375                                         | 380 |
| Val Pro Arg Ala Val | Pro Met Val Glu Ser Met Val Ala Leu Val Leu |     |
| 385                 | 390                                         | 395 |
| Val Asp Gln Leu Met | Ala Gln Tyr Ala Gln Cys His Leu Phe Pro Ile | 400 |
|                     | 405                                         | 410 |
| Asn Pro Glu Leu Gln | Glu Pro Leu Gln Ile Glu Gln Pro Gln Asn Ala | 415 |
|                     | 420                                         | 425 |
| Thr Ala Leu         |                                             | 430 |
| 435                 |                                             |     |

(2) INFORMATION FOR SEQ ID NO:1225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..313

(D) OTHER INFORMATION: / Ceres Seq. ID 1569361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Thr Thr Gly Thr Pro Ile His Val Phe Val Pro Asn Thr Asp Gln |     |
| 1                                                               | 5   |
| Arg Gly Leu Asp Tyr Ser Glu Met Ser Val Ala Tyr Arg Pro Ser His | 10  |
|                                                                 | 20  |
| Ala Asp Ala Thr Tyr Asp Met Lys Tyr Gly Val Arg Ser Val Gln Gly | 25  |
|                                                                 | 35  |
| Gly Gly Arg Ser Ser Ala Arg Glu Thr Ile Gly Arg Val Ala Pro Gly | 40  |
|                                                                 | 50  |
| Ala Leu Ala Lys Lys Ile Leu Lys Gln Phe Ala Gly Thr Glu Ile Leu | 55  |
|                                                                 | 65  |
| Ala Tyr Val Ser Gln Val His His Val Val Leu Pro Glu Glu Leu Val | 70  |
|                                                                 | 85  |
| Asp His Glu Asn Leu Thr Leu Glu Gln Ile Glu Asn Asn Ile Val Arg | 90  |
|                                                                 | 100 |
| Cys Pro Asn Pro Glu Tyr Ala Glu Lys Met Ile Ala Ala Ile Asp Ala | 105 |
|                                                                 | 115 |
| Val Arg Thr Lys Gly Asn Ser Val Gly Gly Val Val Thr Cys Ile Val | 120 |
|                                                                 | 130 |
| Arg Asn Ala Pro Arg Gly Leu Gly Thr Pro Val Phe Asp Lys Leu Glu | 135 |
|                                                                 | 145 |
| Ala Glu Leu Ala Lys Ala Cys Met Ser Leu Pro Ala Thr Lys Gly Phe | 150 |
|                                                                 | 165 |
| Glu Phe Gly Ser Gly Phe Ala Gly Thr Phe Leu Thr Gly Leu Glu His | 170 |
|                                                                 | 180 |
| Asn Asp Glu Phe Thr Thr Asp Glu Asn Gly Arg Ile Arg Thr Arg Thr | 185 |
|                                                                 | 195 |
| Asn Arg Ser Gly Gly Ile Gln Gly Gly Ile Ser Asn Gly Glu Ile Ile | 200 |
|                                                                 | 210 |
| Asn Met Arg Val Ala Phe Lys Pro Thr Ser Thr Ile Gly Arg Lys Gln | 215 |
|                                                                 | 225 |
| Asn Thr Val Thr Arg Asp Lys Val Glu Thr Glu Met Ile Ala Arg Gly | 230 |
|                                                                 | 245 |
| Arg His Asp Pro Cys Val Val Pro Arg Ala Val Pro Met Val Glu Ser | 250 |
|                                                                 | 260 |
| Met Val Ala Leu Val Leu Val Asp Gln Leu Met Ala Gln Tyr Ala Gln | 265 |
|                                                                 | 275 |
| Cys His Leu Phe Pro Ile Asn Pro Glu Leu Gln Glu Pro Leu Gln Ile | 280 |
|                                                                 | 290 |
| Glu Gln Pro Gln Asn Ala Thr Ala Leu                             | 295 |
| 305                                                             | 310 |

(2) INFORMATION FOR SEQ ID NO:1226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 925 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..925  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| acaacacaaa | acaagaacaa  | cagacacata | gagatgagcc | gctgcggctc | tottgggctc  | 60  |
| tatgccccaa | atgctttgcc  | atctctctcc | ttgaagccac | gcagtttcaa | atctccttcc  | 120 |
| tgtattacat | ctcacaccaa  | accccaacac | actcttcttc | ataatgttaa | caagatgaga  | 180 |
| gcaaaaggcc | gtgatatact  | tggagcaaa  | aagacaatct | tggcagctca | actcggggca  | 240 |
| gttcttgcca | cgattgacca  | tccagcctta | gcaataacag | gagttaacaa | ccagcaggaa  | 300 |
| ttgagcagtg | ttgtgctcga  | tatcgggatc | atatccgttt | ggatcttcc  | agtaatgcca  | 360 |
| ccaatcatca | tgaactggct  | aagagtaaga | tggtagacaa | ggaagattag | aacttgcaaa  | 420 |
| aaatggcttc | caaggctttg  | attctgttag | gtctcttctc | agttcttctc | gtcgtctccg  | 480 |
| aagtgtctgc | cgcaaggCaa  | Wtcgggcatg | gtgaagcCag | agagtGagg  | aaactgtgca  | 540 |
| Acctgaagtg | tatgtcgggtR | GScCacggag | gacatggtgg | tcacggaggg | ggaggaggcc  | 600 |
| acggacatgg | aggacacaac  | ggaggagggg | gccacggact | tgacggatac | ggaggagggtg | 660 |
| gaggacacta | tggaggaggt  | ggaggacact | acggaggagg | tggaggacac | tacggaggag  | 720 |
| gtggaggaca | ctacggagga  | ggtggtggag | gacacggagg | tggaggacac | tacggagggtg | 780 |
| gtggaggagg | atacggaggt  | ggaggaggac | accacggagg | aggaggccac | gggctaaacg  | 840 |
| aacctgttca | gactaagcgg  | ggtgtttaa  | actatataat | atcttcta   | ccatgcatga  | 900 |
| ttgcataat  | atatatacgs  | ttatg      |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:1227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..146  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Thr | Lys | Asn | Lys | Asn | Asn | Arg | His | Ile | Glu | Met | Ser | Arg | Cys | Gly |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Leu | Gly | Leu | Tyr | Ala | Pro | Asn | Ala | Leu | Pro | Ser | Leu | Ser | Leu | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Arg | Ser | Phe | Lys | Ser | Pro | Phe | Cys | Ile | Thr | Ser | His | Thr | Lys | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Asp | Thr | Leu | Leu | His | Asn | Val | Asn | Lys | Met | Arg | Ala | Lys | Ala | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Ile | Leu | Gly | Ala | Lys | Lys | Thr | Ile | Leu | Ala | Ala | Gln | Leu | Gly | Ala |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Val | Leu | Ala | Thr | Ile | Asp | His | Pro | Ala | Leu | Ala | Ile | Thr | Gly | Val | Asn |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Gln | Gln | Glu | Leu | Ser | Ser | Val | Val | Leu | Asp | Ile | Gly | Ile | Ile | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Trp | Tyr | Phe | Leu | Val | Met | Pro | Pro | Ile | Ile | Met | Asn | Trp | Leu | Arg |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Val | Arg | Trp | Tyr | Arg | Arg | Lys | Ile | Arg | Thr | Cys | Lys | Lys | Trp | Leu | Pro |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1228:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 135 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..135  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569372  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:  
Met Ser Arg Cys Gly Ser Leu Gly Leu Tyr Ala Pro Asn Ala Leu Pro  
1 5 10 15  
Ser Leu Ser Leu Lys Pro Arg Ser Phe Lys Ser Pro Phe Cys Ile Thr  
20 25 30  
Ser His Thr Lys Pro Asn Asp Thr Leu Leu His Asn Val Asn Lys Met  
35 40 45  
Arg Ala Lys Ala Cys Asp Ile Leu Gly Ala Lys Lys Thr Ile Leu Ala  
50 55 60  
Ala Gln Leu Gly Ala Val Leu Ala Thr Ile Asp His Pro Ala Leu Ala  
65 70 75 80  
Ile Thr Gly Val Asn Asn Gln Gln Glu Leu Ser Ser Val Val Leu Asp  
85 90 95  
Ile Gly Ile Ile Ser Val Trp Tyr Phe Leu Val Met Pro Pro Ile Ile  
100 105 110  
Met Asn Trp Leu Arg Val Arg Trp Tyr Arg Arg Lys Ile Arg Thr Cys  
115 120 125  
Lys Lys Trp Leu Pro Arg Leu  
130 135  
(2) INFORMATION FOR SEQ ID NO:1229:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 148 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..148  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569373  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:  
Met Ala Ser Lys Ala Leu Ile Leu Leu Gly Leu Phe Ser Val Leu Leu  
1 5 10 15  
Val Val Ser Glu Val Ser Ala Ala Arg Gln Xaa Gly His Gly Glu Ala  
20 25 30  
Arg Glu Trp Arg Lys Leu Cys Asn Leu Lys Val Met Ala Xaa Xaa His  
35 40 45  
Gly Gly His Gly Gly His Gly Gly Gly Gly His Gly His Gly Gly  
50 55 60  
His Asn Gly Gly Gly Gly His Gly Leu Asp Gly Tyr Gly Gly Gly Gly  
65 70 75 80  
Gly His Tyr Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly His  
85 90 95  
Tyr Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly His Gly  
100 105 110  
Gly Gly Gly His Tyr Gly Gly Gly Gly Tyr Gly Gly Gly Gly  
115 120 125  
Gly His His Gly Gly Gly His Gly Leu Asn Glu Pro Val Gln Thr  
130 135 140  
Lys Pro Gly Val  
145

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..810

(D) OTHER INFORMATION: / Ceres Seq. ID 1569378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:

|              |             |            |             |             |             |     |
|--------------|-------------|------------|-------------|-------------|-------------|-----|
| agacaacaaac  | aaacaaaaag  | tcatgtctcc | gacgacgaca  | tctgttacgat | ccctaagctt  | 60  |
| actcgtctttac | tgcgtcttcta | attctactcc | gattttctaca | ccaattaggt  | cccgacagtt  | 120 |
| cctaggtctta  | tgcagtagat  | tctacggtgt | gtctctcttg  | agctcttctt  | ctctccctaac | 180 |
| tactctctct   | tctatgcggaa | atctcttctt | ctctacaagg  | aactcagctc  | tctccgttaa  | 240 |
| gtcccaagcg   | ttaStgctga  | aacccgacag | ccaataatggt | gggagagaa   | atcgaggcca  | 300 |
| aacatgatgt   | acattacctc  | agctcagcag | ttcttcaacg  | cgtttaaaga  | tgcggagat   | 360 |
| agattagatt   | tctgtagatt  | ttaocgaaat | tggttggtgt  | tcttcgctgt  | aattgttcca  | 420 |
| aagctctgca   | aaacggcgaa  | agacacccct | gacatcttgt  | tccttaaagt  | aaactttgac  | 480 |
| gagacaaga    | ctctctcgaa  | aaagcttaac | gtcaaggtgt  | tacgattgt   | ccactctac   | 540 |
| cgcggtctgt   | atggccaagt  | gaactctctc | tcatgtcttc  | tgcgaagt    | ccagaaattc  | 600 |
| agagagcgca   | tagagagaca  | caatgatgca | agatcagta   | acatctcttc  | ttaagattct  | 660 |
| gagaaagtgt   | aagattcaag  | tgaattatga | atgcctgggt  | cagattgcta  | acagattatt  | 720 |
| ttgttaaattc  | gtctccctgt  | ataatgtgt  | actgcatttt  | ccatgtgggt  | cateataatt  | 780 |

(2) INFORMATION FOR SEQ ID NO:1231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..101
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1569379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1232:

(1) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1569380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:

Met	Ser	Pro	Thr	Thr	Thr	Ser	Leu	Arg	Ser	Leu	Ser	Phe	Ser	Leu	Tyr
1				5					10					15	
Ala	Ser	Ser	Asn	Ser	Thr	Pro	Ile	Ser	Thr	Pro	Ile	Glu	Ala	Arg	Gln
			20					25						30	
Leu	Leu	Ser	Ser	Cys	Ser	Arg	Phe	Tyr	Gly	Leu	Ser	Ser	Ser	Ser	Ser
			35				40						45		
Ser	Ser	Ser	Leu	Thr	Thr	Ser	Ser	Leu	Ile	Gly	Asn	Leu	Val	Phe	Ser
			50			55					60				
Ser	Arg	Asn	Gln	Ser	Leu	Ser	Val	Lys	Val	Gln	Ala	Leu	Xaa	Leu	Lys
			65		70				75					80	
Pro	Asn	Ser	Gln	Asn	Gly	Gly	Arg	Gly	Lys	Gln	Gly	Gln	Thr		
			85					90							

(2) INFORMATION FOR SEQ ID NO:1233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1569381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:

Met	Ile	Asp	Ile	Thr	Ser	Ala	Glu	Gln	Phe	Leu	Asn	Ala	Leu	Lys	Asp
1				5					10					15	
Ala	Gly	Asp	Arg	Leu	Val	Ile	Val	Asp	Phe	Tyr	Gly	Thr	Trp	Cys	Gly
			20					25					30		
Ser	Cys	Arg	Ala	Met	Phe	Pro	Lys	Leu	Cys	Lys	Thr	Ala	Lys	Glu	His
			35				40				45				
Pro	Asp	Ile	Leu	Phe	Leu	Lys	Val	Asn	Phe	Asp	Glu	Asn	Lys	Ser	Leu
			50			55				60					
Cys	Lys	Ser	Leu	Asn	Val	Lys	Val	Leu	Pro	Tyr	Phe	His	Phe	Tyr	Arg
			65		70				75					80	
Gly	Ala	Asp	Gly	Gln	Val	Glu	Ser	Phe	Ser	Cys	Ser	Leu	Ala	Lys	Phe
			85					90						95	
Gln	Lys	Leu	Arg	Glu	Ala	Ile	Glu	Arg	His	Asn	Val	Gly	Ser	Ile	Ser
			100				105						110		
Asn	Ile	Ser	Ser	Ser	Ala	Ser	Glu	Lys	Val	Glu	Asp	Ser	Ser	Glu	
			115			120					125				

(2) INFORMATION FOR SEQ ID NO:1234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1854 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1854

(D) OTHER INFORMATION: / Ceres Seq. ID 1569385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:

atatactttc	tctgtttaca	ttctgttttc	cgaggagaaa	agtctgcgac	ttctgtgatct	60
ggggttttgt	ttgggtttggg	gttgactcgg	ttttgactcg	ggacaaagtcg	tctcgtgaga	120
tgatgtcttc	tcgttttatta	gtatctcttt	gagagtcgtg	ctttctgggt	tcaatagatt	180
cttatagttt	cgcttagaaa	cacgcacaaa	aagatgtcgt	tgaagcatca	tcacagagga	240
ttagagctct	ctgtcttgaa	gagttttgtc	tcaaagaagt	ggactttatt	tctctgtatc	300
ggtttcttct	gcgcaggaat	tctcttcttc	gacagaatgt	ggccagagcc	tgaatccaat	360

gttgatcaaa	gggacacagt	agcatcagat	gaacggctgc	ggttagagtc	tgaggactgt	420
gattcatcaa	aaaaggggtt	taaagcgtga	atcgaaagac	atccttggag	atgtttacaa	480
gagtcacag	gcaattcaaa	cgcttgataa	aacgatttca	aagctggaaa	cagaactggc	540
cgatgcgaag	gctgcgcaag	aattctatcat	gaatgggttca	ccagtttctg	atgactttaa	600
gctccctgaa	actgtcaacta	aaagaaaagta	tctgatgggtt	gttgggtgta	atactgcggt	660
tagcagcaga	aagcgcaggg	attcagtcgg	tgctacttgg	atgcctcccg	gtgaggagag	720
aaagaagctc	gaggaagaga	aagggatcgt	galgcgggtt	gtgataggcc	atagtcttac	780
tcccggttga	attcttgata	gagcgattca	ggctgaagaa	agataaacatg	gagacttctt	840
gaggtcgatg	catgttgaag	gttatctcga	gctgtcagca	aagactaaaa	cttactttac	900
cacggctttt	gcaatgtggg	atcgagactt	ctacgtcaaa	gtcgatgatg	atgtgcgatg	960
aaatatagcc	acgcttggag	cagaattagc	aagataccgg	atgaagcccc	gagtgatcat	1020
tggttgcatg	aaatctggac	ctgtttcttg	tcagaaaagga	gtgagatatt	atgaaccoga	1080
atactgtgaaa	tttggagaag	agggtaacaa	atacttcocg	catgccacag	gtcagctcta	1140
tgcaataatc	agggagttgg	cgctttacat	atcgataaac	caaaaactac	ttcacaaaata	1200
tgatgaatga	gatgtctctt	taggatcatg	gtttcttggg	ttgatgtggg	agcatgtaga	1260
tgaccgtagg	ctatgtttgtg	gtacaaacaga	ttgtgagtg	aaggcgcagg	cgggcaacat	1320
ctgtgttgcc	tggttcgatt	ggagctgcag	tggtgattgt	agatcagcgg	ataggatgaa	1380
ggatgttcat	cgtaggtgtg	gagaaggtga	aaaggccott	ctggctgcac	ctttctgaaA	1440
cacaataact	aaagaaacac	attgaggaag	aagagtacag	agacaaaatcc	gctgcacagt	1500
ctacacttgg	tagtatagac	acacagtcac	actctctcta	tatatgtatg	tatgtatgta	1560
tgtagtcttc	ttgtgaactg	agatgagaag	ggtgcttttt	ggcctccctt	cttgtttctt	1620
tatgcttttc	tcaattctct	gaaggtctgg	agttctttgc	acacagaaaa	tcgagatttt	1680
agctgcaaaag	gcggactcca	tgagtgaccc	ttcagagtcca	tttcattgat	gcgttttctc	1740
tgcccttttga	gcttttcttc	ttcatttctt	tttgattttt	gcctattttg	ttcatttttt	1800
cccttgccat	gattgtgggt	aaacatgggt	tgtttatgtg	tgtacttgaa	acgc	

(2) INFORMATION FOR SEQ ID NO:1235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..289

(D) OTHER INFORMATION: / Ceres Seq. ID 1569386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:

Met	Asn	Gly	Ser	Pro	Val	Ser	Asp	Asp	Phe	Lys	Leu	Pro	Glu	Thr	Val
1			5						10				15		
Thr	Lys	Arg	Lys	Tyr	Leu	Met	Val	Val	Gly	Val	Asn	Thr	Ala	Phe	Ser
			20					25					30		
Ser	Arg	Lys	Lys	Arg	Asp	Ser	Val	Arg	Ala	Thr	Trp	Met	Pro	Pro	Gly
			35				40					45			
Glu	Glu	Arg	Lys	Lys	Leu	Glu	Glu	Glu	Lys	Gly	Ile	Val	Met	Arg	Phe
	50					55					60				
Val	Ile	Gly	His	Ser	Ser	Thr	Pro	Gly	Gly	Ile	Leu	Asp	Arg	Ala	Ile
	65					70				75					80
Gln	Ala	Glu	Glu	Ser	Lys	His	Gly	Asp	Phe	Leu	Arg	Leu	Asp	His	Val
			85					90					95		
Glu	Gly	Tyr	Leu	Glu	Leu	Ser	Ala	Lys	Thr	Lys	Thr	Tyr	Phe	Thr	Thr
			100					105					110		
Ala	Phe	Ala	Met	Trp	Asp	Ala	Asp	Phe	Thr	Val	Lys	Val	Asp	Asp	Asp
			115				120					125			
Val	His	Val	Asn	Ile	Ala	Thr	Leu	Gly	Ala	Glu	Leu	Ala	Arg	Tyr	Arg
			130				135				140				
Met	Lys	Pro	Arg	Val	Tyr	Ile	Gly	Cys	Met	Lys	Ser	Gly	Pro	Val	Leu
			145			150				155					160
Ala	Gln	Lys	Gly	Val	Arg	Tyr	His	Glu	Pro	Glu	Tyr	Trp	Lys	Phe	Gly
			165					170					175		
Glu	Glu	Gly	Asn	Lys	Tyr	Phe	Arg	His	Ala	Thr	Gly	Gln	Leu	Tyr	Ala
			180					185					190		

Ile Ser Arg Glu Leu Ala Ser Tyr Ile Ser Ile Asn Gln Asn Val Leu
195 200 205
His Lys Tyr Val Asn Glu Asp Val Ser Leu Gly Ser Trp Phe Leu Gly
210 215 220
Leu Asp Val Glu His Val Asp Asp Arg Arg Leu Cys Cys Gly Thr Thr
225 230 235 240
Asp Cys Glu Trp Lys Ala Gln Ala Gly Asn Ile Cys Val Ala Ser Phe
245 250 255
Asp Trp Ser Cys Ser Gly Ile Cys Arg Ser Ala Asp Arg Met Lys Asp
260 265 270
Val His Arg Arg Cys Gly Glu Gly Glu Lys Ala Leu Leu Ala Ala Ser
275 280 285
Phe

(2) INFORMATION FOR SEQ ID NO:1236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..267

(D) OTHER INFORMATION: / Ceres Seq. ID 1569387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:

Met Val Val Gly Val Asn Thr Ala Phe Ser Ser Arg Lys Arg Asp
1 5 10 15
Ser Val Arg Ala Thr Trp Met Pro Pro Gly Glu Glu Arg Lys Lys Leu
20 25 30
Glu Glu Glu Lys Gly Ile Val Met Arg Phe Val Ile Gly His Ser Ser
35 40 45
Thr Pro Gly Gly Ile Leu Asp Arg Ala Ile Gln Ala Glu Glu Ser Lys
50 55 60
His Gly Asp Phe Leu Arg Leu Asp His Val Glu Gly Tyr Leu Glu Leu
65 70 75 80
Ser Ala Lys Thr Lys Thr Tyr Phe Thr Thr Ala Phe Ala Met Trp Asp
85 90 95
Ala Asp Phe Tyr Val Lys Val Asp Asp Val His Val Asn Ile Ala
100 105 110
Thr Leu Gly Ala Glu Leu Ala Arg Tyr Arg Met Lys Pro Arg Val Tyr
115 120 125
Ile Gly Cys Met Lys Ser Gly Pro Val Leu Ala Gln Lys Gly Val Arg
130 135 140
Tyr His Glu Pro Glu Tyr Trp Lys Phe Gly Glu Gly Asn Lys Tyr
145 150 155 160
Phe Arg His Ala Thr Gly Gln Leu Tyr Ala Ile Ser Arg Glu Leu Ala
165 170 175
Ser Tyr Ile Ser Ile Asn Gln Asn Val Leu His Lys Tyr Val Asn Glu
180 185 190
Asp Val Ser Leu Gly Ser Trp Phe Leu Gly Leu Asp Val Glu His Val
195 200 205
Asp Asp Arg Arg Leu Cys Cys Gly Thr Thr Asp Cys Glu Trp Lys Ala
210 215 220
Gln Ala Gly Asn Ile Cys Val Ala Ser Phe Asp Trp Ser Cys Ser Gly
225 230 235 240
Ile Cys Arg Ser Ala Asp Arg Met Lys Asp Val His Arg Arg Cys Gly
245 250 255
Glu Gly Glu Lys Ala Leu Leu Ala Ala Ser Phe
260 265

(2) INFORMATION FOR SEQ ID NO:1237:

(X1) SEQUENCE DESTRUCTION: SEQ 18 REF 18						
aaaggtgtct	tcgttttoca	gacaaaagaa	acacaaaattc	attccctctc	cctcttcate	60
tatttttcga	atatgatggc	tattattatt	ctgtctccca	tctctgtctc	ccacccggatt	120
aaagattctc	tcatttttgc	cgctctctgc	ctctctcgca	accctctctc	cgctctcttc	180
acctctctct	tcgcttttag	ggctttgatc	ggccaagaaa	cagagacggc	tttcatcaga	240
ggagccgcgc	tttgtgtcat	ctcagggctc	gtctctctca	tgaagctctc	tgaattcttc	300
ctctctctct	ggcaatcoga	ttatcttgga	attgatgctc	ttctctactt	gcatttttag	360

cgggaggcgtt gttcgtgagc gtatcgggtcc tgcaatgcta agtgcggtcc agagtcagat 420
gggagctgtg gaggccaggt tccaagatca tacagacatc tttagacactg ccattttcaaa 480
gggtctcaact ggggactctc tcaacaggat ccctaaggctc cgaatcacag acacctctcc 540
ggagattgtc tcttgcctctg tctgccttca ggaactttcag gtggggagaga cagttagaag 600
tttgccgcac tggcatcata tgttccacct accatgcacg gacaaaaggC ttgcgaggca 660
tgcttcttgt cctcttgcca gaagacatct ttgaattgat tttagaactct tctttctctt 720
cttctttgtg catgaggtat aggcatacac acacacacat atatacacac tagtagtctt 780
ccttgatttt ttttagatta caggttacac agattttgat gcaccaatca ttgtaacttc 840
actcatctct tggagatcct gtttatttat gctacttatt cttggtctcc

(2) INFORMATION FOR SEQ ID NO:1239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:

Lys	Gly	Ser	Phe	Cys	Phe	Gln	Thr	Lys	Lys	Thr	Gln	Ile	His	Ser	Leu
1				5					10					15	
Leu	Leu	Phe	Ile	Ser	Phe	Ala	Asp	Met	Asp	Gly	Tyr	Tyr	Ser	Leu	Ser
			20					25					30		
Pro	Ile	Ser	Val	Leu	His	Arg	Ile	Lys	Asp	Ser	Phe	His	Phe	Ala	Val
			35				40					45			
Ser	Ala	Leu	Leu	Ala	Asn	Leu	Phe	Ser	Ala	Leu	Phe	Thr	Phe	Phe	Phe
			50			55					60				
Ala	Leu	Gly	Ala	Leu	Ile	Gly	Gln	Glu	Thr	Glu	Ser	Gly	Phe	Ile	Arg
			65		70			75					80		
Gly	Ala	Ala	Val	Gly	Ala	Ile	Ser	Gly	Ala	Val	Phe	Ser	Ile	Glu	Val
			85					90					95		
Phe	Glu	Ser	Ser	Leu	Leu	Leu	Trp	Gln	Ser	Asp	Glu	Ser	Gly	Ile	Gly
			100					105					110		
Cys	Leu	Leu	Tyr	Leu	Pro	Phe	Glu	Arg	Glu	Ala	Cys	Ser			
			115			120						125			

(2) INFORMATION FOR SEQ ID NO:1240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:

Met	Asp	Gly	Tyr	Tyr	Ser	Leu	Ser	Pro	Ile	Ser	Val	Leu	His	Arg	Ile
1				5					10					15	
Lys	Asp	Ser	Phe	His	Phe	Ala	Val	Ser	Ala	Leu	Leu	Ala	Asn	Leu	Phe
			20					25					30		
Ser	Ala	Leu	Phe	Thr	Phe	Phe	Phe	Ala	Leu	Gly	Ala	Leu	Ile	Gly	Gln
			35				40				45				
Glu	Thr	Glu	Ser	Gly	Phe	Ile	Arg	Gly	Ala	Ala	Val	Gly	Ala	Ile	Ser
			50			55					60				
Gly	Ala	Val	Phe	Ser	Ile	Glu	Val	Phe	Glu	Ser	Ser	Leu	Leu	Leu	Trp
			65		70			75					80		
Gln	Ser	Asp	Glu	Ser	Gly	Ile	Gly	Cys	Leu	Leu	Tyr	Leu	Pro	Phe	Glu
			85					90					95		

Arg Glu Ala Cys Ser
100

(2) INFORMATION FOR SEQ ID NO:1241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:

Met	Ser	Leu	Glu	Leu	Asp	Ala	Phe	Ser	Thr	Cys	Leu	Leu	Ser	Gly	Arg
1			5						10					15	
Leu	Val	Arg	Glu	Arg	Ile	Gly	Pro	Ala	Met	Leu	Ser	Ala	Val	Gln	Ser
			20				25						30		
Gln	Met	Gly	Ala	Val	Glu	Ser	Gln	Phe	Gln	Asp	His	Thr	Asp	Ile	Phe
			35				40					45			
Asp	Thr	Ala	Ile	Ser	Lys	Gly	Leu	Thr	Gly	Asp	Ser	Leu	Asn	Arg	Ile
			50			55				60					
Pro	Lys	Val	Arg	Ile	Thr	Asp	Thr	Ser	Pro	Glu	Ile	Val	Ser	Cys	Ser
			65			70				75				80	
Val	Cys	Leu	Gln	Asp	Phe	Gln	Val	Gly	Glu	Thr	Val	Arg	Ser	Leu	Pro
			85						90					95	
His	Cys	His	His	Met	Phe	His	Leu	Pro	Cys	Ile	Asp	Lys	Trp	Leu	Arg
			100				105						110		
Arg	His	Ala	Ser	Cys	Pro	Leu	Cys	Arg	Arg	His	Leu				
			115				120								

(2) INFORMATION FOR SEQ ID NO:1242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1580
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

aatagggttca	gtgtttctga	catattgttc	cctctctgaa	tgaacctctc	ccaaatagag	60
aatggccctaa	ccacctatcc	aaccgcatca	aggcacttgg	tttcatcccc	ttgatttttc	120
tcctttttttc	ttttctcttc	gcaggatttt	gtgttcttgg	tttgaatatg	aaatgtttcgt	180
cgatgtgttg	tttgatcttc	ttggcccttt	ctctctctac	cgctctcact	cttgctttctt	240
cgtcaaatgg	tatatagtga	cctttctacg	actctactgc	ctacacagag	tgtagagccg	300
aagcagagaaa	gccactatca	aatggaggaa	tgtctgaagg	ccaaaagcct	tcctgtccca	360
cgaaagactc	ttctcacagg	attgggtgct	gttacacacc	aaattacata	tgtcacatc	420
taactgcca	acactcttat	tgtcttctca	tatgggtgaa	gatagaggct	ggtgctgcgt	480
cagtctcatg	aagagcaagg	ctgagagcag	acaacgccc	attaaactgc	gtcgtgttct	540
taactgcca	acatggttgc	tgtctcttcc	tcaaaggagg	attctctctt	gattctctct	600
gtaaacatc	catctctctc	tttgagacat	cagaggacga	tgttaagatc	caattacaag	660
tgacgagtgc	ctctctctac	ccattccacg	aggagcaatg	gagggaacac	caagattact	720
tcataaatac	cgccagaaaa	cgagcagtg	caattcacgt	gtcaaaaaga	aacggagaga	780
cggttgcaag	agcagaggtg	acagtagagc	agatctctaa	agactctctc	attggtttctg	840
ccattctcaa	aactatcctt	ggaaacattc	cttaccacga	atggtctcgt	aagagattcg	900
acggccacgt	attcgagaa	gagctgaaat	ggtacgcgac	ggagcccgat	caaggcaaac	960
tcaactacac	attggctgat	aagatgatga	atttcgtctg	agccaacaga	atcatcgctc	1020
gcggtcacaa	catattctcg	gaggaatcca	aatacaatcc	cgattggggt	cgtaattctaa	1080
ccggcggaaga	ttctccgctg	gcggttaacc	ggcgaatcaa	gagctctgat	atcgcgtaca	1140

gaggagaggtt cgtgcatttg gacgtgagca acgagatgct tcactttgac ttctacagaga 1200
ctcgactggg gaagaacgag tcgtacggat tcttcgcccg ggctcgtgag attgactcat 1260
tggcgactct gttcttcaat gatttcaacg tgggtggagac ttgcagcgac gagaagtcaa 1320
cggttgacga atacatcgcg aggggtgaggg aactccaacg gtacgacggcg gtaaggatgg 1380
acggaatagg tctcggaggg cacttcaaga cgccaaacgt agcgctgatg agagccatcc 1440
tcgataaacT cgcKtacgct ccagctccca atctgggtca cagagattga tatcagcagc 1500
agcctcgacc accgctctca ggcgatttat ttggagcaag tggttacgtga aggattctcg 1560
caccatcgcg taaacgggtat

(2) INFORMATION FOR SEQ ID NO:1243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..440
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:

Met	Lys	Cys	Ser	Ser	Met	Cys	Cys	Leu	Ile	Leu	Leu	Ala	Leu	Ser	Leu
1			5					10						15	
Leu	Thr	Ala	Phe	Thr	Leu	Ala	Ser	Ser	Asn	Gly	Ile	Asp	Gly	Pro	
			20					25					30		
Phe	Tyr	Asp	Ser	Thr	Ala	Tyr	Thr	Glu	Cys	Arg	Ala	Glu	Ala	Glu	Lys
			35					40					45		
Pro	Leu	Tyr	Asn	Gly	Gly	Met	Leu	Lys	Asp	Gln	Lys	Pro	Ser	Val	Pro
			50				55				60				
Gly	Lys	Asp	Ser	Leu	Thr	Gly	Ile	Gly	Ala	Arg	Tyr	Thr	Pro	Thr	Tyr
			65				70				75				80
Ile	Leu	His	Asn	Leu	Thr	Gln	Asn	Thr	Ile	Tyr	Cys	Phe	Ser	Ile	Trp
			85					90						95	
Val	Lys	Ile	Glu	Ala	Gly	Ala	Ala	Ser	Ala	His	Val	Arg	Ala	Arg	Leu
			100					105					110		
Arg	Ala	Asp	Asn	Ala	Thr	Leu	Asn	Cys	Val	Gly	Ser	Val	Thr	Ala	Lys
			115				120					125			
His	Gly	Cys	Trp	Ser	Phe	Leu	Lys	Gly	Gly	Phe	Leu	Leu	Asp	Ser	Pro
			130				135					140			
Cys	Lys	Gln	Ser	Ile	Leu	Phe	Phe	Glu	Thr	Ser	Glu	Asp	Asp	Gly	Lys
					150					155				160	
Ile	Gln	Leu	Gln	Val	Thr	Ser	Ala	Ser	Leu	Gln	Pro	Phe	Thr	Gln	Glu
			165						170					175	
Gln	Trp	Arg	Asn	Asn	Gln	Asp	Tyr	Phe	Ile	Asn	Thr	Ala	Arg	Lys	Arg
			180					185					190		
Ala	Val	Thr	Ile	His	Val	Ser	Lys	Glu	Asn	Gly	Glu	Ser	Val	Glu	Gly
			195				200					205			
Ala	Glu	Val	Thr	Val	Glu	Gln	Ile	Ser	Lys	Asp	Phe	Ser	Ile	Gly	Ser
			210				215					220			
Ala	Ile	Ser	Lys	Thr	Ile	Leu	Gly	Asn	Ile	Pro	Tyr	Gln	Glu	Trp	Phe
			225				230				235				240
Val	Lys	Arg	Phe	Asp	Ala	Thr	Val	Phe	Glu	Asn	Glu	Leu	Lys	Trp	Tyr
			245						250					255	
Ala	Thr	Glu	Pro	Asp	Gln	Gly	Lys	Leu	Asn	Tyr	Thr	Leu	Ala	Asp	Lys
			260					265					270		
Met	Met	Asn	Phe	Val	Arg	Ala	Asn	Arg	Ile	Ile	Ala	Arg	Gly	His	Asn
			275				280					285			
Ile	Phe	Trp	Glu	Asp	Pro	Lys	Tyr	Asn	Pro	Asp	Trp	Val	Arg	Asn	Leu
			290				295					300			
Thr	Gly	Glu	Asp	Leu	Arg	Ser	Ala	Val	Asn	Arg	Arg	Ile	Lys	Ser	Leu
			305				310				315				320
Met	Thr	Arg	Tyr	Arg	Gly	Glu	Phe	Val	His	Trp	Asp	Val	Ser	Asn	Glu

325 330 335
Met Leu His Phe Asp Phe Tyr Glu Thr Arg Leu Gly Lys Asn Ala Ser
340 345 350
Tyr Gly Phe Phe Ala Ala Ala Arg Glu Ile Asp Ser Leu Ala Thr Leu
355 360 365
Phe Phe Asn Asp Phe Asn Val Val Glu Thr Cys Ser Asp Glu Lys Ser
370 375 380
Thr Val Asp Glu Tyr Ile Ala Arg Val Arg Glu Leu Gln Arg Tyr Asp
385 390 395 400
Gly Val Arg Met Asp Gly Ile Gly Leu Glu Gly His Phe Thr Thr Pro
405 410 415
Asn Val Ala Leu Met Arg Ala Ile Leu Asp Lys Leu Xaa Tyr Ala Pro
420 425 430
Ala Pro Asn Leu Ala His Arg Asp
435 440
(2) INFORMATION FOR SEQ ID NO:1244:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 435 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..435
(D) OTHER INFORMATION: / Ceres Seq. ID 1569405
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:
Met Cys Cys Leu Ile Leu Leu Ala Leu Ser Leu Leu Thr Ala Phe Thr
1 5 10 15
Leu Ala Ser Ser Ser Asn Gly Ile Asp Gly Pro Phe Tyr Asp Ser Thr
20 25 30
Ala Tyr Thr Glu Cys Arg Ala Glu Ala Glu Lys Pro Leu Tyr Asn Gly
35 40 45
Gly Met Leu Lys Asp Gln Lys Pro Ser Val Pro Gly Lys Asp Ser Leu
50 55 60
Thr Gly Ile Gly Ala Arg Tyr Thr Pro Thr Tyr Ile Leu His Asn Leu
65 70 75 80
Thr Gln Asn Thr Ile Tyr Cys Phe Ser Ile Trp Val Lys Ile Glu Ala
85 90 95
Gly Ala Ala Ser Ala His Val Arg Ala Arg Leu Arg Ala Asp Asn Ala
100 105 110
Thr Leu Asn Cys Val Gly Ser Val Thr Ala Lys His Gly Cys Trp Ser
115 120 125
Phe Leu Lys Gly Gly Phe Leu Leu Asp Ser Pro Cys Lys Gln Ser Ile
130 135 140
Leu Phe Phe Glu Thr Ser Glu Asp Asp Gly Lys Ile Gln Leu Gln Val
145 150 155 160
Thr Ser Ala Ser Leu Gln Pro Phe Thr Gln Glu Gln Trp Arg Asn Asn
165 170 175
Gln Asp Tyr Phe Ile Asn Thr Ala Arg Lys Arg Ala Val Thr Ile His
180 185 190
Val Ser Lys Glu Asn Gly Glu Ser Val Glu Gly Ala Glu Val Thr Val
195 200 205
Glu Gln Ile Ser Lys Asp Phe Ser Ile Gly Ser Ala Ile Ser Lys Thr
210 215 220
Ile Leu Gly Asn Ile Pro Tyr Gln Glu Trp Phe Val Lys Arg Phe Asp
225 230 235 240
Ala Thr Val Phe Glu Asn Glu Leu Lys Trp Tyr Ala Thr Glu Pro Asp
245 250 255
Gln Gly Lys Leu Asn Tyr Thr Leu Ala Asp Lys Met Met Asn Phe Val
260 265 270

Arg Ala Asn Arg Ile Ile Ala Arg Gly His Asn Ile Phe Trp Glu Asp
275 280 285
Pro Lys Tyr Asn Pro Asp Trp Val Arg Asn Leu Thr Gly Glu Asp Leu
290 295 300
Arg Ser Ala Val Asn Arg Arg Ile Lys Ser Leu Met Thr Arg Tyr Arg
305 310 315
Gly Glu Phe Val His Trp Asp Val Ser Asn Glu Met Leu His Phe Asp
325 330 335
Phe Tyr Glu Thr Arg Leu Gly Lys Asn Ala Ser Tyr Gly Phe Phe Ala
340 345 350
Ala Ala Arg Glu Ile Asp Ser Leu Ala Thr Leu Phe Phe Asn Asp Phe
355 360 365
Asn Val Val Glu Thr Cys Ser Asp Glu Lys Ser Thr Val Asp Glu Tyr
370 375 380
Ile Ala Arg Val Arg Glu Leu Gln Arg Tyr Asp Gly Val Arg Met Asp
385 390 395
Gly Ile Gly Leu Glu Gly His Phe Thr Thr Pro Asn Val Ala Leu Met
405 410 415
Arg Ala Ile Leu Asp Lys Leu Xaa Tyr Ala Pro Ala Pro Asn Leu Ala
420 425 430
His Arg Asp
435

(2) INFORMATION FOR SEQ ID NO:1245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..386
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:

Met Leu Lys Asp Gln Lys Pro Ser Val Pro Gly Lys Asp Ser Leu Thr
1 5 10 15
Gly Ile Gly Ala Arg Tyr Thr Pro Thr Tyr Ile Leu His Asn Leu Thr
20 25 30
Gln Asn Thr Ile Tyr Cys Phe Ser Ile Trp Val Lys Ile Glu Ala Gly
35 40 45
Ala Ala Ser Ala His Val Arg Ala Arg Leu Arg Ala Asp Asn Ala Thr
50 55 60
Leu Asn Cys Val Gly Ser Val Thr Ala Lys His Gly Cys Trp Ser Phe
65 70 75 80
Leu Lys Gly Gly Phe Leu Leu Asp Ser Pro Cys Lys Gln Ser Ile Leu
85 90 95
Phe Phe Glu Thr Ser Glu Asp Asp Gly Lys Ile Gln Leu Gln Val Thr
100 105 110
Ser Ala Ser Leu Gln Pro Phe Thr Gln Glu Gln Trp Arg Asn Asn Gln
115 120 125
Asp Tyr Phe Ile Asn Thr Ala Arg Lys Arg Ala Val Thr Ile His Val
130 135 140
Ser Lys Glu Asn Gly Glu Ser Val Glu Gly Ala Glu Val Thr Val Glu
145 150 155 160
Gln Ile Ser Lys Asp Phe Ser Ile Gly Ser Ala Ile Ser Lys Thr Ile
165 170 175
Leu Gly Asn Ile Pro Tyr Gln Glu Trp Phe Val Lys Arg Phe Asp Ala
180 185 190
Thr Val Phe Glu Asn Glu Leu Lys Trp Tyr Ala Thr Glu Pro Asp Gln
195 200 205
Gly Lys Leu Asn Tyr Thr Leu Ala Asp Lys Met Met Asn Phe Val Arg

210	215	220
Ala Asn Arg Ile Ile Ala Arg Gly His Asn Ile Phe Trp Glu Asp Pro		
225	230	235
Lys Tyr Asn Pro Asp Trp Val Arg Asn Leu Thr Gly Glu Asp Leu Arg		
	245	250
Ser Ala Val Asn Arg Arg Ile Lys Ser Leu Met Thr Arg Tyr Arg Gly		
	260	265
Glu Phe Val His Trp Asp Val Ser Asn Glu Met Leu His Phe Asp Phe		
	275	280
Tyr Glu Thr Arg Leu Gly Lys Asn Ala Ser Tyr Gly Phe Phe Ala Ala		
	290	295
Ala Arg Glu Ile Asp Ser Leu Ala Thr Leu Phe Phe Asn Asp Phe Asn		
305	310	315
Val Val Glu Thr Cys Ser Asp Glu Lys Ser Thr Val Asp Glu Tyr Ile		
	325	330
Ala Arg Val Arg Glu Leu Gln Arg Tyr Asp Gly Val Arg Met Asp Gly		
	340	345
Ile Gly Leu Glu Gly His Phe Thr Thr Pro Asn Val Ala Leu Met Arg		
	355	360
Ala Ile Leu Asp Lys Leu Xaa Tyr Ala Pro Ala Pro Asn Leu Ala His		
	370	375
Arg Asp		380
385		

(2) INFORMATION FOR SEQ ID NO:1246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1362
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:

aatttcattc	gtctctttatc	aacaacacac	tctctctctt	ctatcaaacac	tttctttcat	60
ctctgcgcgg	aaaaaacccat	aaccacaaca	atggccaccg	aaacccaaaat	cgaatcggga	120
gtaatggggt	gcgcgcgatat	cgctcgaaaa	gtctctcgag	caatccacct	cgctcccaac	180
gccacaatct	ccggcgtaGc	aagccgggtct	ttagaaaaag	ccaaagcctt	tgccaccggc	240
aataactacc	cagaatcaac	caaaatccac	ggctcttacg	aatctctctt	cgaagatcca	300
gagatcgatg	cgctctatgt	tctctctccc	actagtcctc	acgttgagtg	ggctattaaa	360
cgagctgaga	aagggaaca	tatccttttg	gagaagcctg	ttgctatgaa	cgtaactgag	420
tttgataaga	ttgttgatgc	ttgtgaagct	aatgggtgtc	agattatgga	tggtactatg	480
tgggttcaat	atctagaac	tgctttgctt	aaagagtttc	tttctgattc	tgaacgtttt	540
ggtcagctta	aaactgtaca	gagttgtttc	tcatttgcgt	gagatgaaga	ttttcttaa	600
aacgataacc	gtgtgaaacc	tggtcttgac	gggcttggtg	cgctaggaga	tgccgggtgg	660
tacgcgatca	gagcaactct	tttagctaat	aaatttgagc	ttccgaaaac	ttgtaactgt	720
ttcccgcgtg	ctgtgttgaa	tgaagcagga	ttgatacttt	ccctggagac	atctttgagt	780
tgggaagtat	gacgaactgc	aactatata	ttgtctattc	tggttaacct	aaacaaggag	840
ataactgccca	ttggaacgaa	aggcacaact	cggtgtacacg	acttcattat	cccgataaag	900
gagactgagg	cgctgtttac	cacgagcact	aaagcttggt	tcaatgaact	tgtgactggc	960
tggtgttagtc	ccccgagtga	gcatacgggt	aagacagagc	ttccacaaga	ggcatgtatg	1020
gtgagagagt	ttgtctgatt	gggttgagaa	atcaagaaca	atggtgcmaa	gcctgatggg	1080
tactggccta	gtattagccg	aaagacgcag	ctagtgtgtg	atgctgttaa	agagcttggt	1140
gataaaaact	atcaacagat	tagtctctct	ggctcgttga	ggaaggagct	cagactataa	1200
atgttgtcgt	gtgtctctct	ctctctcgt	ctctatgttc	aaactctgat	caaccgttta	1260
agtgcttggt	accacttacc	aatatgttct	gtctctctct	gtgtccgctc	gtatgtatgt	1320
taattgtttt	agactccaat	tactagcctt	caattactaa	gc		

(2) INFORMATION FOR SEQ ID NO:1247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..392

(D) OTHER INFORMATION: / Ceres Seq. ID 1569408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

Asn	Phe	Ile	Arg	Ser	Leu	Ser	Thr	Thr	Leu	Ser	Leu	Phe	Ser	Ile	Asn
1					5				10					15	
Thr	Phe	Phe	His	Leu	Ser	Pro	Glu	Lys	Pro	Ile	Thr	Thr	Thr	Met	Ala
			20					25					30		
Thr	Glu	Thr	Gln	Ile	Arg	Ile	Gly	Val	Met	Gly	Cys	Ala	Asp	Ile	Ala
			35				40					45			
Arg	Lys	Val	Ser	Arg	Ala	Ile	His	Leu	Ala	Pro	Asn	Ala	Thr	Ile	Ser
	50					55				60					
Gly	Val	Ala	Ser	Arg	Ser	Leu	Glu	Lys	Ala	Lys	Ala	Phe	Ala	Thr	Ala
65					70				75					80	
Asn	Asn	Tyr	Pro	Glu	Ser	Thr	Lys	Ile	His	Gly	Ser	Tyr	Glu	Ser	Leu
			85					90					95		
Leu	Glu	Asp	Pro	Glu	Ile	Asp	Ala	Leu	Tyr	Val	Pro	Leu	Pro	Thr	Ser
			100				105					110			
Leu	His	Val	Glu	Trp	Ala	Ile	Lys	Ala	Ala	Glu	Lys	Gly	Lys	His	Ile
	115						120					125			
Leu	Leu	Glu	Lys	Pro	Val	Ala	Met	Asn	Val	Thr	Glu	Phe	Asp	Lys	Ile
	130					135					140				
Val	Asp	Ala	Cys	Glu	Ala	Asn	Gly	Val	Gln	Ile	Met	Asp	Gly	Thr	Met
145					150					155				160	
Trp	Val	His	Asn	Pro	Arg	Thr	Ala	Leu	Leu	Lys	Glu	Phe	Leu	Ser	Asp
			165				170						175		
Ser	Glu	Arg	Phe	Gly	Gln	Leu	Lys	Thr	Val	Gln	Ser	Cys	Phe	Ser	Phe
	180						185					190			
Ala	Gly	Asp	Glu	Asp	Phe	Leu	Lys	Asn	Asp	Ile	Arg	Val	Lys	Pro	Gly
	195					200					205				
Leu	Asp	Gly	Leu	Gly	Ala	Leu	Gly	Asp	Ala	Gly	Trp	Tyr	Ala	Ile	Arg
	210					215					220				
Ala	Thr	Leu	Leu	Ala	Asn	Asn	Phe	Glu	Leu	Pro	Lys	Thr	Val	Thr	Ala
225					230					235				240	
Phe	Pro	Gly	Ala	Val	Leu	Asn	Glu	Ala	Gly	Leu	Ile	Leu	Ser	Cys	Gly
			245						250					255	
Ala	Ser	Leu	Ser	Trp	Glu	Asp	Gly	Arg	Thr	Ala	Thr	Ile	Tyr	Cys	Ser
			260				265					270			
Phe	Leu	Ala	Asn	Leu	Thr	Met	Glu	Ile	Thr	Ala	Ile	Gly	Thr	Lys	Gly
	275						280					285			
Thr	Leu	Arg	Val	His	Asp	Phe	Ile	Ile	Pro	Tyr	Lys	Glu	Thr	Glu	Ala
	290					295					300				
Ser	Phe	Thr	Thr	Ser	Thr	Lys	Ala	Trp	Phe	Asn	Asp	Leu	Val	Thr	Ala
305					310					315				320	
Trp	Val	Ser	Pro	Pro	Ser	Glu	His	Thr	Val	Lys	Thr	Glu	Leu	Pro	Gln
			325						330				335		
Glu	Ala	Cys	Met	Val	Arg	Glu	Phe	Ala	Arg	Leu	Val	Gly	Glu	Ile	Lys
			340				345					350			
Asn	Asn	Gly	Ala	Lys	Pro	Asp	Gly	Tyr	Trp	Pro	Ser	Ile	Ser	Arg	Lys
			355				360					365			
Thr	Gln	Leu	Val	Val	Asp	Ala	Val	Lys	Glu	Ser	Val	Asp	Lys	Asn	Tyr
	370					375					380				
Gln	Gln	Ile	Ser	Leu	Ser	Gly	Arg								
385					390										

(2) INFORMATION FOR SEQ ID NO:1248:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..362
(D) OTHER INFORMATION: / Ceres Seq. ID 1569409
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:
Met Ala Thr Glu Thr Gln Ile Arg Ile Gly Val Met Gly Cys Ala Asp
1 5 10 15
Ile Ala Arg Lys Val Ser Arg Ala Ile His Leu Ala Pro Asn Ala Thr
20 25 30
Ile Ser Gly Val Ala Ser Arg Ser Leu Glu Lys Ala Lys Ala Phe Ala
35 40 45
Thr Ala Asn Asn Tyr Pro Glu Ser Thr Lys Ile His Gly Ser Tyr Glu
50 55 60
Ser Leu Leu Glu Asp Pro Glu Ile Asp Ala Leu Tyr Val Pro Leu Pro
65 70 75 80
Thr Ser Leu His Val Glu Trp Ala Ile Lys Ala Ala Glu Lys Gly Lys
85 90 95
His Ile Leu Leu Glu Lys Pro Val Ala Met Asn Val Thr Glu Phe Asp
100 105 110
Lys Ile Val Asp Ala Cys Glu Ala Asn Gly Val Gln Ile Met Asp Gly
115 120 125
Thr Met Trp Val His Asn Pro Arg Thr Ala Leu Leu Lys Glu Phe Leu
130 135 140
Ser Asp Ser Glu Arg Phe Gly Gln Leu Lys Thr Val Gln Ser Cys Phe
145 150 155 160
Ser Phe Ala Gly Asp Glu Asp Phe Leu Lys Asn Asp Ile Arg Val Lys
165 170 175
Pro Gly Leu Asp Gly Leu Gly Ala Leu Gly Asp Ala Gly Trp Tyr Ala
180 185 190
Ile Arg Ala Thr Leu Leu Ala Asn Asn Phe Glu Leu Pro Lys Thr Val
195 200 205
Thr Ala Phe Pro Gly Ala Val Leu Asn Glu Ala Gly Leu Ile Leu Ser
210 215 220
Cys Gly Ala Ser Leu Ser Trp Glu Asp Gly Arg Thr Ala Thr Ile Tyr
225 230 235 240
Cys Ser Phe Leu Ala Asn Leu Thr Met Glu Ile Thr Ala Ile Gly Thr
245 250 255
Lys Gly Thr Leu Arg Val His Asp Phe Ile Ile Pro Tyr Lys Glu Thr
260 265 270
Glu Ala Ser Phe Thr Thr Ser Thr Lys Ala Trp Phe Asn Asp Leu Val
275 280 285
Thr Ala Trp Val Ser Pro Pro Ser Glu His Thr Val Lys Thr Glu Leu
290 295 300
Pro Gln Glu Ala Cys Met Val Arg Glu Phe Ala Arg Leu Val Gly Glu
305 310 315 320
Ile Lys Asn Asn Gly Ala Lys Pro Asp Gly Tyr Trp Pro Ser Ile Ser
325 330 335
Arg Lys Thr Gln Leu Val Val Asp Ala Val Lys Glu Ser Val Asp Lys
340 345 350
Asn Tyr Gln Gln Ile Ser Leu Ser Gly Arg
355 360
(2) INFORMATION FOR SEQ ID NO:1249:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..351
(D) OTHER INFORMATION: / Ceres Seq. ID 1569410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:

Met Gly Cys Ala Asp Ile Ala Arg Lys Val Ser Arg Ala Ile His Leu
1 5 10 15
Ala Pro Asn Ala Thr Ile Ser Gly Val Ala Ser Arg Ser Leu Glu Lys
20 25 30
Ala Lys Ala Phe Ala Thr Ala Asn Asn Tyr Pro Glu Ser Thr Lys Ile
35 40 45
His Gly Ser Tyr Glu Ser Leu Leu Glu Asp Pro Glu Ile Asp Ala Leu
50 55 60
Tyr Val Pro Leu Pro Thr Ser Leu His Val Glu Trp Ala Ile Lys Ala
65 70 75 80
Ala Glu Lys Gly Lys His Ile Leu Leu Glu Lys Pro Val Ala Met Asn
85 90 95
Val Thr Glu Phe Asp Lys Ile Val Asp Ala Cys Glu Ala Asn Gly Val
100 105 110
Gln Ile Met Asp Gly Thr Met Trp Val His Asn Pro Arg Thr Ala Leu
115 120 125
Leu Lys Glu Phe Leu Ser Asp Ser Glu Arg Phe Gly Gln Leu Lys Thr
130 135 140
Val Gln Ser Cys Phe Ser Phe Ala Gly Asp Glu Asp Phe Leu Lys Asn
145 150 155 160
Asp Ile Arg Val Lys Pro Gly Leu Asp Gly Leu Gly Ala Leu Gly Asp
165 170 175
Ala Gly Trp Tyr Ala Ile Arg Ala Thr Leu Leu Ala Asn Asn Phe Glu
180 185 190
Leu Pro Lys Thr Val Thr Ala Phe Pro Gly Ala Val Leu Asn Glu Ala
195 200 205
Gly Leu Ile Leu Ser Cys Gly Ala Ser Leu Ser Trp Glu Asp Gly Arg
210 215 220
Thr Ala Thr Ile Tyr Cys Ser Phe Leu Ala Asn Leu Thr Met Glu Ile
225 230 235 240
Thr Ala Ile Gly Thr Lys Gly Thr Leu Arg Val His Asp Phe Ile Ile
245 250 255
Pro Tyr Lys Glu Thr Glu Ala Ser Phe Thr Thr Ser Thr Lys Ala Trp
260 265 270
Phe Asn Asp Leu Val Thr Ala Trp Val Ser Pro Pro Ser Glu His Thr
275 280 285
Val Lys Thr Glu Leu Pro Gln Glu Ala Cys Met Val Arg Glu Phe Ala
290 295 300
Arg Leu Val Gly Glu Ile Lys Asn Asn Gly Ala Lys Pro Asp Gly Tyr
305 310 315 320
Trp Pro Ser Ile Ser Arg Lys Thr Gln Leu Val Val Asp Ala Val Lys
325 330 335
Glu Ser Val Asp Lys Asn Tyr Gln Gln Ile Ser Leu Ser Gly Arg
340 345 350

(2) INFORMATION FOR SEQ ID NO:1250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1202

(D) OTHER INFORMATION: / Ceres Seq. ID 1569411
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:

aacgcagatt	gccatccagg	agaggggaga	agaagaattt	gtattctcaa	gtgtgcgata	60
tgagagagat	gaagtccaga	acacgtttgt	gagagaacag	cttttagatg	tgattgtgga	120
tcagattctc	aaagactttt	cgcgaaagat	ctctgatcct	taaatcgctt	ctctctcgct	180
tgacctcatt	tcgtctgcga	aatcagatcc	gtgtgaaaaa	gccgaaacag	gatatggaga	240
agatggagct	tcgttaagaac	ttccgttaag	tttggcatac	cgattctacc	cacagtatcc	300
agaacgatac	tccttatgtg	tgcttcgctg	ttgtgtgtgc	cccttgatga	tcatacttgc	360
ttcgcaagcg	tgccgctttc	gatgatattg	caaggtacgt	ctgtctgtgc	ggttacatgc	420
cttgtagtgt	taggtgtgga	gaagccaaat	gtcctcaact	ttgtcttgcc	actgaggtct	480
cttgcgtgct	tgcaaacctc	gtggcctcaa	ctcgttttct	cttgcgaagt	gagttccaaa	540
ttcagacgac	aaaatgtgac	aactgcatac	ttgttttcat	ggtttgcttc	agccaaagtgg	600
cttgcataatt	ctccatagtt	gcattgtatt	tcggtatgga	tgagctttca	gaagcttctc	660
agatactcac	atgtgtcctt	gacatgggtg	actgcacggt	ttgcgcatgt	atgcagacac	720
aacacaagat	ggaaatggac	aagagggagc	gtaagtctgg	gccacagcca	atggcagatgc	780
ctccggctca	gcataatgtc	cggtttgatc	aagccacccc	acccgcagtc	ggttatcttc	840
cacaacaagg	ttatccacct	ttcgtttacc	ctcaacaccc	tcacaagggt	tatccacctt	900
ctggctatcc	tcaaaaaccc	ctccctcag	cttattctca	ataccctctc	ggggcttacc	960
ctcctctccc	cgcttaccac	aagtgtatcc	cttttgccctg	ttttctctcc	cgattggaaa	1020
attttttttc	atcttttttt	aattgctgct	tgttacgggt	caagaattga	acgttgcgtg	1080
attgtttttg	ggctgtttgt	tgatgatgat	tttgacctca	catgtgtgtg	ttttctgaaa	1140
cgctcctctt	ggactaagag	atttcattgc	tttttctctt	cttttttaaa	ttctcttttt	1200

tc

(2) INFORMATION FOR SEQ ID NO:1251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..255

(D) OTHER INFORMATION: / Ceres Seq. ID 1569412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:

Met	Pro	Lys	Gln	Asp	Met	Glu	Lys	Met	Glu	Leu	Arg	Lys	Asn	Phe	Arg
1			5					10					15		
Asn	Val	Trp	His	Thr	Asp	Leu	Thr	His	Ser	Ile	Gln	Asn	Asp	Thr	Pro
			20					25					30		
Tyr	Cys	Cys	Phe	Ala	Leu	Trp	Cys	Ala	Pro	Cys	Ala	Ser	Tyr	Leu	Leu
		35					40					45			
Arg	Lys	Arg	Ala	Leu	Tyr	Asp	Asp	Met	Ser	Arg	Tyr	Val	Cys	Cys	Ala
	50					55					60				
Gly	Tyr	Met	Pro	Cys	Ser	Gly	Arg	Cys	Gly	Gly	Ala	Lys	Cys	Pro	Gln
	65				70				75					80	
Leu	Cys	Leu	Ala	Thr	Glu	Val	Phe	Cys	Cys	Phe	Ala	Asn	Ser	Val	Ala
			85						90				95		
Ser	Thr	Arg	Phe	Leu	Leu	Gln	Asp	Glu	Phe	Gln	Ile	Gln	Thr	Thr	Lys
			100					105					110		
Cys	Asp	Asn	Cys	Ile	Ile	Gly	Phe	Met	Val	Cys	Leu	Ser	Glu	Val	Ala
	115					120						125			
Cys	Ile	Phe	Ser	Ile	Val	Ala	Cys	Ile	Val	Gly	Met	Asp	Glu	Leu	Ser
	130					135				140					
Glu	Ala	Ser	Gln	Ile	Leu	Thr	Cys	Cys	Ser	Asp	Met	Val	Tyr	Cys	Thr
	145				150				155					160	
Val	Cys	Ala	Cys	Met	Gln	Thr	Gln	His	Lys	Met	Glu	Met	Asp	Lys	Arg
			165					170					175		
Asp	Gly	Lys	Phe	Gly	Pro	Gln	Pro	Met	Ala	Val	Pro	Pro	Ala	Gln	Gln
			180					185					190		
Met	Ser	Arg	Phe	Asp	Gln	Ala	Thr	Pro	Pro	Ala	Val	Gly	Tyr	Pro	Pro
	195					200					205				

Gln	Gln	Gly	Tyr	Pro	Pro	Ser	Gly	Tyr	Pro	Gln	His	Pro	Pro	Gln	Gly
	210					215					220				
Tyr	Pro	Pro	Ser	Gly	Tyr	Pro	Gln	Asn	Pro	Pro	Pro	Ser	Ala	Tyr	Ser
225				230					235					240	
Gln	Tyr	Pro	Pro	Gly	Ala	Tyr	Pro	Pro	Pro	Pro	Ala	Tyr	Pro	Lys	
				245					250					255	

(2) INFORMATION FOR SEQ ID NO:1252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..250

(D) OTHER INFORMATION: / Ceres Seq. ID 1569413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

Met	Glu	Lys	Met	Glu	Leu	Arg	Lys	Asn	Phe	Arg	Asn	Val	Trp	His	Thr
1				5					10					15	
Asp	Leu	Thr	His	Ser	Ile	Gln	Asn	Asp	Thr	Pro	Tyr	Cys	Cys	Phe	Ala
			20					25					30		
Leu	Trp	Cys	Ala	Pro	Cys	Ala	Ser	Tyr	Leu	Leu	Arg	Lys	Arg	Ala	Leu
		35					40					45			
Tyr	Asp	Asp	Met	Ser	Arg	Tyr	Val	Cys	Cys	Ala	Gly	Tyr	Met	Pro	Cys
	50					55					60				
Ser	Gly	Arg	Cys	Gly	Glu	Ala	Lys	Cys	Pro	Gln	Leu	Cys	Leu	Ala	Thr
65				70					75					80	
Glu	Val	Phe	Cys	Cys	Phe	Ala	Asn	Ser	Val	Ala	Ser	Thr	Arg	Phe	Leu
				85					90				95		
Leu	Gln	Asp	Glu	Phe	Gln	Ile	Gln	Thr	Thr	Lys	Cys	Asp	Asn	Cys	Ile
			100					105					110		
Ile	Gly	Phe	Met	Val	Cys	Leu	Ser	Gln	Val	Ala	Cys	Ile	Phe	Ser	Ile
		115						120					125		
Val	Ala	Cys	Ile	Val	Gly	Met	Asp	Glu	Leu	Ser	Glu	Ala	Ser	Gln	Ile
	130					135					140				
Leu	Thr	Cys	Cys	Ser	Asp	Met	Val	Tyr	Cys	Thr	Val	Cys	Ala	Cys	Met
	145				150					155				160	
Gln	Thr	Gln	His	Lys	Met	Glu	Met	Asp	Lys	Arg	Asp	Gly	Lys	Phe	Gly
			165					170						175	
Pro	Gln	Pro	Met	Ala	Val	Pro	Pro	Ala	Gln	Gln	Met	Ser	Arg	Phe	Asp
			180					185					190		
Gln	Ala	Thr	Pro	Pro	Ala	Val	Gly	Tyr	Pro	Pro	Gln	Gln	Gly	Tyr	Pro
		195					200					205			
Pro	Ser	Gly	Tyr	Pro	Gln	His	Pro	Pro	Gln	Gly	Tyr	Pro	Pro	Ser	Gly
	210					215					220				
Tyr	Pro	Gln	Asn	Pro	Pro	Ser	Ala	Tyr	Ser	Gln	Tyr	Pro	Pro	Gly	
225				230					235					240	
Ala	Tyr	Pro	Pro	Pro	Pro	Ala	Tyr	Pro	Lys						
				245					250						

(2) INFORMATION FOR SEQ ID NO:1253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..247

(D) OTHER INFORMATION: / Ceres Seq. ID 1569414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

```

Met Glu Leu Arg Lys Asn Phe Arg Asn Val Trp His Thr Asp Leu Thr
1      5      10      15
His Ser Ile Gln Asn Asp Thr Pro Tyr Cys Cys Phe Ala Leu Trp Cys
20     25     30
Ala Pro Cys Ala Ser Tyr Leu Leu Arg Lys Arg Ala Leu Tyr Asp Asp
35     40     45
Met Ser Arg Tyr Val Cys Cys Ala Gly Tyr Met Pro Cys Ser Gly Arg
50     55     60
Cys Gly Glu Ala Lys Cys Pro Gln Leu Cys Leu Ala Thr Glu Val Phe
65     70     75     80
Cys Cys Phe Ala Asn Ser Val Ala Ser Thr Arg Phe Leu Leu Gln Asp
85     90     95
Glu Phe Gln Ile Gln Thr Thr Lys Cys Asp Asn Cys Ile Ile Gly Phe
100    105    110
Met Val Cys Leu Ser Gln Val Ala Cys Ile Phe Ser Ile Val Ala Cys
115    120    125
Ile Val Gly Met Asp Glu Leu Ser Glu Ala Ser Gln Ile Leu Thr Cys
130    135    140
Cys Ser Asp Met Val Tyr Cys Thr Val Cys Ala Cys Met Gln Thr Gln
145    150    155    160
His Lys Met Glu Met Asp Lys Arg Asp Gly Lys Phe Gly Pro Gln Pro
165    170    175
Met Ala Val Pro Pro Ala Gln Gln Met Ser Arg Phe Asp Gln Ala Thr
180    185    190
Pro Pro Ala Val Gly Tyr Pro Pro Gln Gln Gly Tyr Pro Pro Ser Gly
195    200    205
Tyr Pro Gln His Pro Pro Gln Gly Tyr Pro Pro Ser Gly Tyr Pro Gln
210    215    220
Asn Pro Pro Pro Ser Ala Tyr Ser Gln Tyr Pro Pro Gly Ala Tyr Pro
225    230    235    240
Pro Pro Pro Ala Tyr Pro Lys
245

```

(2) INFORMATION FOR SEQ ID NO:1254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1348
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:

```

aaaaactcgaa aaaaagatgg cggcggtttt gcaaaactaac atccgtctgg agatcatacc 60
gggaagatcac agttctctca ccatcataaa gtttcgtcgg ccgtatcgaa ttagtgcgc 120
cgccgcttca cccgtgaaaa aacggtataa catcactctg ctccocggcg atgggtatcgg 180
tccagaagtt atatctgttg ctaagaatgt gcttcagaaa gctggatttc tccaaggact 240
agagtttgat ttccaggaga tgccctttcg cggaGcagct ttggattttg tcggagttcc 300
attgcggagg gaaacttcca ctgctgctaa acagtctgat gccattctc ttggagctat 360
cggagggtac aaatgggaca agaattgaga acatctgaga cctgagatgg gctctgctaa 420
cattcgaaga gatctcaatg tctttgctaa ttgagacct gctacagttt taccacagct 480
agttgatcgt tccacactga agaaagaagt agcacaggt gttgatata tgatttgtaag 540
ggagctcact ggaggtatatt accttggaga gccaaaggcg attacgatca acgaaaaatgg 600
cgaagaagtc ggttttaata cagagatcta cgctgctcac agatttgaca gaattgctcg 660
tgttgcattc gagactgcga ggaaggcg tggaagctg tgttctgttg acaaaagccaa 720
tgctttgatg gcatcaatat tctggaggaa aagagtaaca gctttagctt ctgaatatcc 780
agatgttgaa ctatcacata tgtatgtoga taatgStgcg atccagcttg tccgtgaccc 840
gaacagttt gacacaatcg tcaccaataa catttttgg gatataattg ctgatgaagc 900
ttcaatgatc actggttagca ttgggatgct tccatctgca agtcttggg aatcgggacc 960

```

tggactcttt gaacctatac atgggttcagc accagatata gctggacaag acaaggcaaa 1020
cccattggcc accattctca gtgcggcgat gcttctcaag tatggacttg gagaagaaaa 1080
ggctgcaaaag atgattgaag acgcggctgt ggatgctctg aacaaagggt tcagaaccgg 1140
agacatctac tcccccgaa ataaactggt gggatgcaag gaaatgggtg agggagttct 1200
caaatcagtg gactccaaag ttctgttta aaaaaagtgt gtaccccttg gttttactgt 1260
tactttttg ctaatacatg tattagaaac tgtattcttg tagcttttat aataataaaa 1320
tatttgggat cgattctgca attcaaa

(2) INFORMATION FOR SEQ ID NO:1255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 409 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..409

(D) OTHER INFORMATION: / Ceres Seq. ID 1569428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:

Lys Leu Glu Lys Lys Met Ala Ala Phe Leu Gln Thr Asn Ile Arg Leu
1 5 10 15
Glu Ile Ile Pro Gly Arg Tyr Ser Ser Leu Thr Asp His Lys Phe Arg
20 25 30
Ala Pro Tyr Arg Ile Arg Cys Ala Ala Ser Pro Val Lys Lys Arg
35 40 45
Tyr Asn Ile Thr Leu Leu Pro Gly Asp Gly Ile Gly Pro Glu Val Ile
50 55 60
Ser Val Ala Lys Asn Val Leu Gln Lys Ala Gly Phe Leu Gln Gly Leu
65 70 75 80
Glu Phe Asp Phe Gln Glu Met Pro Phe Gly Gly Ala Ala Leu Asp Leu
85 90 95
Val Gly Val Pro Leu Pro Glu Glu Thr Ser Thr Ala Ala Lys Gln Ser
100 105 110
Asp Ala Ile Leu Leu Gly Ala Ile Gly Gly Tyr Lys Trp Asp Lys Asn
115 120 125
Glu Lys His Leu Arg Pro Glu Met Gly Leu Leu Asn Ile Arg Arg Asp
130 135 140
Leu Asn Val Phe Ala Asn Leu Arg Pro Ala Thr Val Leu Pro Gln Leu
145 150 155
Val Asp Ala Ser Thr Leu Lys Lys Glu Val Ala Gln Gly Val Asp Met
160 165 170 175
Met Ile Val Arg Glu Leu Thr Gly Gly Ile Tyr Phe Gly Glu Pro Arg
180 185 190
Gly Ile Thr Ile Asn Glu Asn Gly Glu Glu Val Gly Phe Asn Thr Glu
195 200 205
Ile Tyr Ala Ala His Glu Ile Asp Arg Ile Ala Arg Val Ala Phe Glu
210 215 220
Thr Ala Arg Lys Arg Arg Gly Lys Leu Cys Ser Val Asp Lys Ala Asn
225 230 235 240
Val Leu Asp Ala Ser Ile Leu Trp Arg Lys Arg Val Thr Ala Leu Ala
245 250 255
Ser Glu Tyr Pro Asp Val Glu Leu Ser His Met Tyr Val Asp Asn Xaa
260 265 270
Ala Met Gln Leu Val Arg Asp Pro Lys Gln Phe Asp Thr Ile Val Thr
275 280 285
Asn Asn Ile Phe Gly Asp Ile Leu Ser Asp Glu Ala Ser Met Ile Thr
290 295 300
Gly Ser Ile Gly Met Leu Pro Ser Ala Ser Leu Gly Glu Ser Gly Pro
305 310 315 320
Gly Leu Phe Glu Pro Ile His Gly Ser Ala Pro Asp Ile Ala Gly Gln
325 330 335

Asp Lys Ala Asn Pro Leu Ala Thr Ile Leu Ser Ala Ala Met Leu Leu
340 345 350
Lys Tyr Gly Leu Gly Glu Glu Lys Ala Ala Lys Met Ile Glu Asp Ala
355 360 365
Val Val Asp Ala Leu Asn Lys Gly Phe Arg Thr Gly Asp Ile Tyr Ser
370 375 380
Pro Gly Asn Lys Leu Val Gly Cys Lys Glu Met Gly Glu Glu Val Leu
385 390 395 400
Lys Ser Val Asp Ser Lys Val Pro Val
405

(2) INFORMATION FOR SEQ ID NO:1256:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 404 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..404

(D) OTHER INFORMATION: / Ceres Seq. ID 1569429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:

Met Ala Ala Phe Leu Gln Thr Asn Ile Arg Leu Glu Ile Ile Pro Gly
1 5 10 15
Arg Tyr Ser Ser Leu Thr Asp His Lys Phe Arg Ala Pro Tyr Arg Ile
20 25 30
Arg Cys Ala Ala Ala Ser Pro Val Lys Lys Arg Tyr Asn Ile Thr Leu
35 40 45
Leu Pro Gly Asp Gly Ile Gly Pro Glu Val Ile Ser Val Ala Lys Asn
50 55 60
Val Leu Gln Lys Ala Gly Phe Leu Gln Gly Leu Glu Phe Asp Phe Gln
65 70 75 80
Glu Met Pro Phe Gly Gly Ala Ala Leu Asp Leu Val Gly Val Pro Leu
85 90 95
Pro Glu Glu Thr Ser Thr Ala Ala Lys Gln Ser Asp Ala Ile Leu Leu
100 105 110
Gly Ala Ile Gly Gly Tyr Lys Trp Asp Lys Asn Glu Lys His Leu Arg
115 120 125
Pro Glu Met Gly Leu Leu Asn Ile Arg Arg Asp Leu Asn Val Phe Ala
130 135 140
Asn Leu Arg Pro Ala Thr Val Leu Pro Gln Leu Val Asp Ala Ser Thr
145 150 155 160
Leu Lys Lys Glu Val Ala Gln Gly Val Asp Met Met Ile Val Arg Glu
165 170 175
Leu Thr Gly Gly Ile Tyr Phe Gly Glu Pro Arg Gly Ile Thr Ile Asn
180 185 190
Glu Asn Gly Glu Glu Val Gly Phe Asn Thr Glu Ile Tyr Ala Ala His
195 200 205
Glu Ile Asp Arg Ile Ala Arg Val Ala Phe Glu Thr Ala Arg Lys Arg
210 215 220
Arg Gly Lys Leu Cys Ser Val Asp Lys Ala Asn Val Leu Asp Ala Ser
225 230 235 240
Ile Leu Trp Arg Lys Arg Val Thr Ala Leu Ala Ser Glu Tyr Pro Asp
245 250 255
Val Glu Leu Ser His Met Tyr Val Asp Asn Xaa Ala Met Gln Leu Val
260 265 270
Arg Asp Pro Lys Gln Phe Asp Thr Ile Val Thr Asn Asn Ile Phe Gly
275 280 285
Asp Ile Leu Ser Asp Glu Ala Ser Met Ile Thr Gly Ser Ile Gly Met
290 295 300
Leu Pro Ser Ala Ser Leu Gly Glu Ser Gly Pro Gly Leu Phe Glu Pro

305		310		315		320
Ile His Gly Ser Ala Pro Asp Ile Ala Gly Gln Asp Lys Ala Asn Pro						
	325			330		335
Leu Ala Thr Ile Leu Ser Ala Ala Met Leu Leu Lys Tyr Gly Leu Gly						
	340			345		350
Glu Glu Lys Ala Ala Lys Met Ile Glu Asp Ala Val Val Asp Ala Leu						
	355			360		365
Asn Lys Gly Phe Arg Thr Gly Asp Ile Tyr Ser Pro Gly Asn Lys Leu						
	370			375		380
Val Gly Cys Lys Glu Met Gly Glu Glu Val Leu Lys Ser Val Asp Ser						
	385			390		400
Lys Val Pro Val						

(2) INFORMATION FOR SEQ ID NO:1257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..323
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:

Met Pro Phe Gly Gly Ala Ala Leu Asp Leu Val Gly Val Pro Leu Pro						
1	5			10		15
Glu Glu Thr Ser Thr Ala Ala Lys Gln Ser Asp Ala Ile Leu Leu Gly						
	20			25		30
Ala Ile Gly Gly Tyr Lys Trp Asp Lys Asn Glu Lys His Leu Arg Pro						
	35			40		45
Glu Met Gly Leu Leu Asn Ile Arg Arg Asp Leu Asn Val Phe Ala Asn						
	50			55		60
Leu Arg Pro Ala Thr Val Leu Pro Gln Leu Val Asp Ala Ser Thr Leu						
	65			70		75
Lys Lys Glu Val Ala Gln Gly Val Asp Met Met Ile Val Arg Glu Leu						
	85			90		95
Thr Gly Gly Ile Tyr Phe Gly Glu Pro Arg Gly Ile Thr Ile Asn Glu						
	100			105		110
Asn Gly Glu Glu Val Gly Phe Asn Thr Glu Ile Tyr Ala Ala His Glu						
	115			120		125
Ile Asp Arg Ile Ala Arg Val Ala Phe Glu Thr Ala Arg Lys Arg Arg						
	130			135		140
Gly Lys Leu Cys Ser Val Asp Lys Ala Asn Val Leu Asp Ala Ser Ile						
	145			150		155
Leu Trp Arg Lys Arg Val Thr Ala Leu Ala Ser Glu Tyr Pro Asp Val						
	165			170		175
Glu Leu Ser His Met Tyr Val Asp Asn Xaa Ala Met Gln Leu Val Arg						
	180			185		190
Asp Pro Lys Gln Phe Asp Thr Ile Val Thr Asn Asn Ile Phe Gly Asp						
	195			200		205
Ile Leu Ser Asp Glu Ala Ser Met Ile Thr Gly Ser Ile Gly Met Leu						
	210			215		220
Pro Ser Ala Ser Leu Glu Gly Ser Gly Pro Gly Leu Phe Glu Pro Ile						
	225			230		235
His Gly Ser Ala Pro Asp Ile Ala Gly Gln Asp Lys Ala Asn Pro Leu						
	245			250		255
Ala Thr Ile Leu Ser Ala Ala Met Leu Leu Lys Tyr Gly Leu Gly Glu						
	260			265		270
Glu Lys Ala Ala Lys Met Ile Glu Asp Ala Val Val Asp Ala Leu Asn						
	275			280		285

Lys Gly Phe Arg Thr Gly Asp Ile Tyr Ser Pro Gly Asn Lys Leu Val
290 295 300
Gly Cys Lys Glu Met Gly Glu Glu Val Leu Lys Ser Val Asp Ser Lys
305 310 315 320
Val Pro Val

(2) INFORMATION FOR SEQ ID NO:1258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1475 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1475
(D) OTHER INFORMATION: / Ceres Seq. ID 1569435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:

gtgatctatc tttagaatctc aaaagcatac ttgagagaga tctgtttcga taatttgctt 60
caatcacogt gttaattggcg gccgtagGag tggaggcgag acctcctgtg acagcgatgg 120
aggaaacctg caacgtttaag ggagcgcgcg cgaaacaagg agaaggcttt aacaagtact 180
acctccagca tctcgatgag ctccagcgcc tgcaacgcga aaagtctgat aaccttaatc 240
gtcttgaagc tcagaggaat gaactcaatt ctcgagtacg aatgctcaga gaagagttac 300
agctcctcca agaacctggg tcttatgttg gtgaagtgtg aaaagtgatg ggaaaaaaca 360
agggttttgt taaggttcat ccagagggga agtatgttgt cgatattgac aaaagtatag 420
acataacgaa acctactcca tcaacgagag tgcctctccg taatgatagc tatgttctcc 480
acctgttctc gccaaagtaa gtatagccct tgggttaacct tatgaaagtg gagaagggtc 540
cagactccac atatgacatg attggtggtc ttgaccagca aatcaaggaa ataaaggagg 600
tcattgaact gccaatcaag catcctgaat tgtttgagtc tcttggaatt gcgcagccaa 660
agggtgtgtt gttgtacggt ccacctggaa ctgggaagac actattggct cgggctgtgg 720
cacatcacac tgaactgtact ttcacagag tttctggttc tgagctggtc cagaataaca 780
ttggagaagg ttctagaatg gtcagagaaac tttttgtgat ggcaaggagg catgcaccat 840
caatcatctt catggatgaa atcgatagta tcgggtctgc tcgtatggaa tctgttagtg 900
gaaatggtga cagtgaggtg caaaggacta tgcctgagct tctcaatcaa ctgacggatc 960
tcgagggcgtc aaacaaaatc aaggttttga tggctacaaa tcgtattgat attctggatc 1020
aagctcttct ccggcctgga aggattgata ggaaaaatga atttctaata cctaagtaag 1080
agtcacgttt tgatatcttg aagatacact caaggaaaaa gaatttgatg cgtggaatcg 1140
atctgaaaaa gattgcagag aagatgaatg gtgcttcagg tgctgagctg aaggctgtat 1200
gcacggagcg gggcatgttt gcacttcgtg agaggagagt acatgtgact caggaagact 1260
ttgagatggc tgtggcgaag gtaatgaaga aagacacaga gaagaacatg tctctgcgta 1320
agctctggaa gtaggaaatt cagagtcaca gattaatttc ttctactctg 1380
ctgtggttct ttctgaaacc ttttcggcta gcgctttaaag cttttctaaa caatgtttgt 1440
acactagttc ctattcattc aattggttgt tcagc

(2) INFORMATION FOR SEQ ID NO:1259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..419
(D) OTHER INFORMATION: / Ceres Seq. ID 1569436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:

Met Ala Ala Val Gly Val Glu Ala Arg Pro Val Thr Ala Met Glu
1 5 10 15
Glu Thr Cys Asn Val Lys Gly Ala Ala Lys Gln Gly Glu Leu
20 25 30
Asn Lys Tyr Tyr Leu Gln His Leu Asp Glu Leu Gln Arg
35 40 45

Glu	Lys	Ser	Tyr	Asn	Leu	Asn	Arg	Leu	Glu	Ala	Gln	Arg	Asn	Glu	Leu
50						55					60				
Asn	Ser	Arg	Val	Arg	Met	Leu	Arg	Glu	Glu	Leu	Gln	Leu	Leu	Gln	Glu
65					70					75				80	
Pro	Gly	Ser	Tyr	Val	Gly	Glu	Val	Val	Lys	Val	Met	Gly	Lys	Asn	Lys
				85					90					95	
Val	Leu	Val	Lys	Val	His	Pro	Glu	Gly	Lys	Tyr	Val	Val	Asp	Ile	Asp
				100					105				110		
Lys	Ser	Ile	Asp	Ile	Thr	Lys	Leu	Thr	Pro	Ser	Thr	Arg	Val	Ala	Leu
				115				120				125			
Arg	Asn	Asp	Ser	Tyr	Val	Leu	His	Leu	Val	Leu	Pro	Ser	Lys	Val	Asp
				130				135			140				
Pro	Leu	Val	Asn	Leu	Met	Lys	Val	Glu	Lys	Val	Pro	Asp	Ser	Thr	Tyr
				145				150			155				160
Asp	Met	Ile	Gly	Gly	Leu	Asp	Gln	Gln	Ile	Lys	Glu	Ile	Lys	Glu	Val
				165					170					175	
Ile	Glu	Leu	Pro	Ile	Lys	His	Pro	Glu	Leu	Phe	Glu	Ser	Leu	Gly	Ile
				180					185					190	
Ala	Gln	Pro	Lys	Gly	Val	Leu	Leu	Tyr	Gly	Pro	Pro	Gly	Thr	Gly	Lys
				195				200					205		
Thr	Leu	Leu	Ala	Arg	Ala	Val	Ala	His	His	Thr	Asp	Cys	Thr	Phe	Ile
				210				215				220			
Arg	Val	Ser	Gly	Ser	Glu	Leu	Val	Gln	Lys	Tyr	Ile	Gly	Glu	Gly	Ser
				225				230			235				240
Arg	Met	Val	Arg	Glu	Leu	Phe	Val	Met	Ala	Arg	Glu	His	Ala	Pro	Ser
				245					250					255	
Ile	Ile	Phe	Met	Asp	Glu	Ile	Asp	Ser	Ile	Gly	Ser	Ala	Arg	Met	Glu
				260					265					270	
Ser	Gly	Ser	Gly	Asn	Gly	Asp	Ser	Glu	Val	Gln	Arg	Thr	Met	Leu	Glu
				275				280					285		
Leu	Leu	Asn	Gln	Leu	Asp	Gly	Phe	Glu	Ala	Ser	Asn	Lys	Ile	Lys	Val
				290				295				300			
Leu	Met	Ala	Thr	Asn	Arg	Ile	Asp	Ile	Leu	Asp	Gln	Ala	Leu	Leu	Arg
				305				310				315			320
Pro	Gly	Arg	Ile	Asp	Arg	Lys	Ile	Glu	Phe	Pro	Asn	Pro	Asn	Glu	Glu
				325					330					335	
Ser	Arg	Phe	Asp	Ile	Leu	Lys	Ile	His	Ser	Arg	Lys	Met	Asn	Leu	Met
				340					345				350		
Arg	Gly	Ile	Asp	Leu	Lys	Lys	Ile	Ala	Glu	Lys	Met	Asn	Gly	Ala	Ser
				355					360				365		
Gly	Ala	Glu	Leu	Lys	Ala	Val	Cys	Thr	Glu	Ala	Gly	Met	Phe	Ala	Leu
				370				375				380			
Arg	Glu	Arg	Arg	Val	His	Val	Thr	Gln	Glu	Asp	Phe	Glu	Met	Ala	Val
				385				390			395				400
Ala	Lys	Val	Met	Lys	Lys	Asp	Thr	Glu	Lys	Asn	Met	Ser	Leu	Arg	Lys
				405					410					415	

(2) INFORMATION FOR SEQ ID NO:1260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..405

(D) OTHER INFORMATION: / Ceres Seq. ID 1569437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:

Met Glu Glu Thr Cys Asn Val Lys Gly Ala Ala Ala Lys Gln Gly Glu

1	5	10	15
Gly Leu Asn Lys Tyr Tyr Leu Gln His Leu Asp Glu Leu Gln Arg Leu	20	25	30
Gln Arg Glu Lys Ser Tyr Asn Leu Asn Arg Leu Glu Ala Gln Arg Asn	35	40	45
Glu Leu Asn Ser Arg Val Arg Met Leu Arg Glu Glu Leu Gln Leu Leu	50	55	60
Gln Glu Pro Gly Ser Tyr Val Gly Glu Val Val Lys Val Met Gly Lys	65	70	75
Asn Lys Val Leu Val Lys Val His Pro Glu Gly Lys Tyr Val Val Asp	85	90	95
Ile Asp Lys Ser Ile Asp Ile Thr Lys Leu Thr Pro Ser Thr Arg Val	100	105	110
Ala Leu Arg Asn Asp Ser Tyr Val Leu His Leu Val Leu Pro Ser Lys	115	120	125
Val Asp Pro Leu Val Asn Leu Met Lys Val Glu Lys Val Pro Asp Ser	130	135	140
Thr Tyr Asp Met Ile Gly Gly Leu Asp Gln Gln Ile Lys Glu Ile Lys	145	150	155
Glu Val Ile Glu Leu Pro Ile Lys His Pro Glu Leu Phe Glu Ser Leu	165	170	175
Gly Ile Ala Gln Pro Lys Gly Val Leu Leu Tyr Gly Pro Pro Gly Thr	180	185	190
Gly Lys Thr Leu Leu Ala Arg Ala Val Ala His His Thr Asp Cys Thr	195	200	205
Phe Ile Arg Val Ser Gly Ser Glu Leu Val Gln Lys Tyr Ile Gly Glu	210	215	220
Gly Ser Arg Met Val Arg Glu Leu Phe Val Met Ala Arg Glu His Ala	225	230	235
Pro Ser Ile Ile Phe Met Asp Glu Ile Asp Ser Ile Gly Ser Ala Arg	245	250	255
Met Glu Ser Gly Ser Gly Asn Gly Asp Ser Glu Val Gln Arg Thr Met	260	265	270
Leu Glu Leu Leu Asn Gln Leu Asp Gly Phe Glu Ala Ser Asn Lys Ile	275	280	285
Lys Val Leu Met Ala Thr Asn Arg Ile Asp Ile Leu Asp Gln Ala Leu	290	295	300
Leu Arg Pro Gly Arg Ile Asp Arg Lys Ile Glu Phe Pro Asn Pro Asn	305	310	315
Glu Glu Ser Arg Phe Asp Ile Leu Lys Ile His Ser Arg Lys Met Asn	325	330	335
Leu Met Arg Gly Ile Asp Leu Lys Lys Ile Ala Glu Lys Met Asn Gly	340	345	350
Ala Ser Gly Ala Glu Leu Lys Ala Val Cys Thr Glu Ala Gly Met Phe	355	360	365
Ala Leu Arg Glu Arg Arg Val His Val Thr Gln Glu Asp Phe Glu Met	370	375	380
Ala Val Ala Lys Val Met Lys Lys Asp Thr Glu Lys Asn Met Ser Leu	385	390	395
Arg Lys Leu Trp Lys	405		400

(2) INFORMATION FOR SEQ ID NO:1261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..350

(D) OTHER INFORMATION: / Ceres Seq. ID 1569438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:

Met	Leu	Arg	Glu	Glu	Leu	Gln	Leu	Leu	Gln	Pro	Gly	Ser	Tyr	Val
1			5						10				15	
Gly	Glu	Val	Val	Lys	Val	Met	Gly	Lys	Asn	Lys	Val	Leu	Val	Lys
			20				25					30		
His	Pro	Glu	Gly	Lys	Tyr	Val	Val	Asp	Ile	Asp	Lys	Ser	Ile	Asp
		35					40				45			
Thr	Lys	Leu	Thr	Pro	Ser	Thr	Arg	Val	Ala	Leu	Arg	Asn	Asp	Ser
	50				55					60				
Val	Leu	His	Leu	Val	Leu	Pro	Ser	Lys	Val	Asp	Pro	Leu	Val	Asn
65				70					75					80
Met	Lys	Val	Glu	Lys	Val	Pro	Asp	Ser	Thr	Tyr	Asp	Met	Ile	Gly
			85						90				95	
Leu	Asp	Gln	Gln	Ile	Lys	Glu	Ile	Lys	Glu	Val	Ile	Glu	Leu	Pro
			100				105					110		
Lys	His	Pro	Glu	Leu	Phe	Glu	Ser	Leu	Gly	Ile	Ala	Gln	Pro	Lys
		115				120					125			
Val	Leu	Leu	Tyr	Gly	Pro	Pro	Gly	Thr	Gly	Lys	Thr	Leu	Leu	Ala
	130				135					140				
Ala	Val	Ala	His	His	Thr	Asp	Cys	Thr	Phe	Ile	Arg	Val	Ser	Gly
145				150					155					160
Glu	Leu	Val	Gln	Lys	Tyr	Ile	Gly	Glu	Gly	Ser	Arg	Met	Val	Arg
			165				170						175	
Leu	Phe	Val	Met	Ala	Arg	Glu	His	Ala	Pro	Ser	Ile	Ile	Phe	Met
		180				185						190		
Glu	Ile	Asp	Ser	Ile	Gly	Ser	Ala	Arg	Met	Glu	Ser	Gly	Ser	Gly
	195					200					205			
Gly	Asp	Ser	Glu	Val	Gln	Arg	Thr	Met	Leu	Glu	Leu	Leu	Asn	Gln
	210					215				220				
Asp	Gly	Phe	Glu	Ala	Ser	Asn	Lys	Ile	Lys	Val	Leu	Met	Ala	Thr
225				230						235				240
Arg	Ile	Asp	Ile	Leu	Asp	Gln	Ala	Leu	Leu	Arg	Pro	Gly	Arg	Ile
			245						250				255	
Arg	Lys	Ile	Glu	Phe	Pro	Asn	Pro	Asn	Glu	Glu	Ser	Arg	Phe	Asp
		260				265						270		
Leu	Lys	Ile	His	Ser	Arg	Lys	Met	Asn	Leu	Met	Arg	Gly	Ile	Asp
		275				280					285			
Lys	Lys	Ile	Ala	Glu	Lys	Met	Asn	Gly	Ala	Ser	Gly	Ala	Glu	Leu
	290				295				300					
Ala	Val	Cys	Thr	Glu	Ala	Gly	Met	Phe	Ala	Leu	Arg	Glu	Arg	Val
305				310					315					320
His	Val	Thr	Gln	Glu	Asp	Phe	Glu	Met	Ala	Val	Ala	Lys	Val	Met
		325					330					335		
Lys	Asp	Thr	Glu	Lys	Asn	Met	Ser	Leu	Arg	Lys	Leu	Trp	Lys	
	340					345					350			

(2) INFORMATION FOR SEQ ID NO:1262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1188 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1188

(D) OTHER INFORMATION: / Ceres Seq. ID 1569439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:

aatctagaac	aagaaaccaa	aacatacacc	actctgttt	ttaaaggtaa	aaaagatcaa	60
gaagaaacca	aagaaatca	gacagcaaca	agaaaagatc	agtttttaag	agaaggaaag	120
taggaaacgg	gtcagattgt	tggatagaga	gaggaagcga	aaaaagagtc	gcagtgttct	180

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ttttccactg cgtgggtttg gtataatcag ctgtggctac aacgaggagg cataatctac 240
cgacgtcgga ttccggtgag ttaccgact gggcgggcac gacgacgaca cttcccgctg 300
ccaccgagga ttcctctctt ggtttcaatg ctggttccctc cgtcatccac ggtgggtttag 360
gctcagcttc agtcgcgcgc ggCgttccat catggcctccc gggatctctt gtccgtttacg 420
gcctacacctc ttccggcgggc gcgacggaga tgggcatggt tgggtctaaga gatgttttcc 480
ttgttgctcc gggtttatcac caccagaacg ccggagtgat atctggatcc gatcatatga 540
acagtaatgc agctgcggcg gcggcgctcg ctgtcggagt gattcctcta ctccacggcgg 600
gtccaccgca gcaaaacgtg gaagactccg acattaaact cctcggaaac aaccggagat 660
ggcagaataa caacaacaac caccgaaacgc agtatcttca cttcaagagt actaacgaga 720
caacggtcgg aacgagctcg aacaactcgg ggtctggctc aggcgcatac ggaaccggcca 780
cgtgtcaaga ctgtggaaat caggcggaaga aagaatgtaa gcagaggcgg ttaggactt 840
gctgcgaagg cgtggctctt gatgtttcta ctacagtgaa gagcacgtgg gtctctgctg 900
ctcggcgagg agagaggcag gtcattGctta ccggcgctaa tccaacggct ggctctgctc 960
tttcgacctc ctccgggagc aagaagccga ggatcgtagg gtctcaacaa caacaacaac 1020
aacaacaaca aacaacaagc acttctcata cttcaacttc taacacacca cctcaaaagt 1080
tcgagaccag ctccagccga caaggtagtt ttacattttc attagtatac atagctacat 1140
gattttatgt atgtatatat atgcataata cactattagc ccttcttg

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(2) INFORMATION FOR SEQ ID NO:1263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..230

(D) OTHER INFORMATION: / Ceres Seq. ID 1569440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:

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Met Gly Met Val Gly Leu Arg Asp Val Phe Leu Val Ala Pro Ala Tyr
1 5 10 15
His His Gln Asn Ala Gly Val Ile Ser Gly Ser Asp His Met Asn Ser
20 25 30
Asn Ala Ala Ala Ala Ala Leu Ala Val Gly Val Ile Pro Leu Leu
35 40 45
Thr Ala Gly Pro Pro Gln Gln Asn Val Glu Asp Ser Asp Ile Asn Phe
50 55 60
Leu Gly Asn Asn Arg Arg Trp Gln Asn Asn Asn Asn His Glu Thr
65 70 75 80
Gln Tyr Leu His Phe Pys Ser Thr Asn Gln Thr Thr Val Gly Thr Ser
85 90 95
Ser Asn Asn Ser Gly Ser Gly Ser Gly Ala Ser Gly Thr Ala Thr Cys
100 105 110
Gln Asp Cys Gly Asn Gln Ala Lys Lys Glu Cys Lys Gln Arg Arg Cys
115 120 125
Arg Thr Cys Cys Lys Ser Arg Gly Phe Asp Cys Ser Thr His Val Lys
130 135 140
Ser Thr Trp Val Ser Ala Ala Arg Arg Arg Glu Arg Gln Val Met Pro
145 150 155 160
Thr Gly Ala Asn Pro Thr Ala Gly Ser Ser Leu Ser Thr Ser Ser Gly
165 170 175
Thr Lys Lys Pro Arg Ile Val Gly Ser Gln Gln Gln Gln Gln Gln
180 185 190
Gln Gln Gln Gln Ala Thr Ser His Thr Ser Thr Ser Asn Thr Pro Pro
195 200 205
Gln Ser Phe Glu Thr Ser Ser Ser Arg Gln Gly Ser Phe Thr Phe Ser
210 215 220
Leu Val Tyr Ile Ala Thr
225 230

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(2) INFORMATION FOR SEQ ID NO:1264:

(i) SEQUENCE CHARACTERISTICS:

SEQUENCE LISTING

- (A) LENGTH: 228 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..228
(D) OTHER INFORMATION: / Ceres Seq. ID 1569441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:

Met Val Gly Leu Arg Asp Val Phe Leu Val Ala Pro Ala Tyr His His
1 5 10 15
Gln Asn Ala Gly Val Ile Ser Gly Ser Asp His Met Asn Ser Asn Ala
20 25 30
Ala Ala Ala Ala Ala Leu Ala Val Gly Val Ile Pro Leu Leu Thr Ala
35 40 45
Gly Pro Pro Gln Gln Asn Val Glu Asp Ser Asp Ile Asn Phe Leu Gly
50 55 60
Asn Asn Arg Arg Trp Gln Asn Asn Asn Asn His Glu Thr Gln Tyr
65 70 75 80
Leu His Phe Lys Ser Thr Asn Gln Thr Thr Val Gly Thr Ser Ser Asn
85 90 95
Asn Ser Gly Ser Gly Ser Gly Ala Ser Gly Thr Ala Thr Cys Gln Asp
100 105 110
Cys Gly Asn Gln Ala Lys Lys Glu Cys Lys Gln Arg Arg Cys Arg Thr
115 120 125
Cys Cys Lys Ser Arg Gly Phe Asp Cys Ser Thr His Val Lys Ser Thr
130 135 140
Trp Val Ser Ala Ala Arg Arg Arg Glu Arg Gln Val Met Pro Thr Gly
145 150 155 160
Ala Asn Pro Thr Ala Gly Ser Ser Leu Ser Thr Ser Ser Gly Thr Lys
165 170 175
Lys Pro Arg Ile Val Gly Ser Gln Gln Gln Gln Gln Gln Gln
180 185 190
Gln Gln Ala Thr Ser His Thr Ser Thr Ser Asn Thr Pro Pro Gln Ser
195 200 205
Phe Glu Thr Ser Ser Ser Arg Gln Gly Ser Phe Thr Phe Ser Leu Val
210 215 220
Tyr Ile Ala Thr
225

(2) INFORMATION FOR SEQ ID NO:1265:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..201
(D) OTHER INFORMATION: / Ceres Seq. ID 1569442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:

Met Asn Ser Asn Ala Ala Ala Ala Ala Ala Leu Ala Val Gly Val Ile
1 5 10 15
Pro Leu Leu Thr Ala Gly Pro Pro Gln Gln Asn Val Glu Asp Ser Asp
20 25 30
Ile Asn Phe Leu Gly Asn Asn Arg Arg Trp Gln Asn Asn Asn Asn Asn
35 40 45
His Glu Thr Gln Tyr Leu His Phe Lys Ser Thr Asn Gln Thr Thr Val
50 55 60
Gly Thr Ser Ser Asn Asn Ser Gly Ser Gly Ser Gly Ala Ser Gly Thr

65	70	75	80
Ala Thr Cys Gln Asp Cys Gly Asn Gln Ala Lys Lys Glu Cys Lys Gln			
	85	90	95
Arg Arg Cys Arg Thr Cys Cys Lys Ser Arg Gly Phe Asp Cys Ser Thr			
	100	105	110
His Val Lys Ser Thr Trp Val Ser Ala Ala Arg Arg Arg Glu Arg Gln			
	115	120	125
Val Met Pro Thr Thr Gly Ala Asn Pro Thr Ala Gly Ser Ser Leu Ser Thr			
	130	135	140
Ser Ser Gly Thr Lys Lys Pro Arg Ile Val Gly Ser Gln Gln Gln Gln			
	145	150	155
Gln Gln Gln Gln Gln Gln Gln Ala Thr Ser His Thr Ser Thr Ser Asn			
	165	170	175
Thr Pro Pro Gln Ser Phe Glu Thr Ser Ser Ser Arg Gln Gly Ser Phe			
	180	185	190
Thr Phe Ser Leu Val Tyr Ile Ala Thr			
	195	200	

(2) INFORMATION FOR SEQ ID NO:1266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1210
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:

tcaatggtga	tacttttgat	gagaaatcca	ggattctcga	tcctaataagg	atgattcgag	60
cttacactca	atctgcagct	actttgaato	ttcttagagc	ctttgccact	ggaggttacg	120
ctgctattca	aagagttact	caatggaacc	tgatttttgt	tgaacaaagt	gagcaagctg	180
acaggtacca	ggagtttagc	aacagggttg	atgagccctt	ggggttcatg	ctctcatgtg	240
gacttggcac	ggatcatcca	cttatgacta	caactgattt	ctacacatcc	catgagtgtt	300
tgcttctgcc	ttatgaacag	tcccttacc	ggttggattc	aactcttgtt	ctctactatg	360
attgtttctg	acacatggct	tggtgcggag	agcgtaccag	acaattggat	ggcgctcatg	420
tcgagtttct	cagggggatt	gctaactctc	tgggcattaa	gggtgagcac	aaaatggatc	480
ccaatgagct	ggttaaagct	gtagaaatcc	tgaatcctaa	taacaagcct	ggaagaatca	540
ctgtaattgt	gagaatgggt	gctgagaaca	tgagagttaa	ggttccccac	ctgatcaagag	600
cagtcgccag	atcaggccag	attgtgacat	gggtctgcga	tccaatgcac	ggaacaccca	660
tcaaagcaCc	ttgcggtctt	aaaacacgtg	cccttgactc	aatactggct	gaagtcccgag	720
cattctctga	tgtagcacag	caagaaggaa	gtcacgcggg	cggatctcat	ctcgagatga	780
caggtcaagaa	cgtgacagaa	gtgattggag	gggtccgcac	gtgacactac	gatgacctca	840
gttctogcta	ccacacacac	tgtgacccaa	ggctgaacgc	gtcacagtct	cttgaaactg	900
cttctattgt	tgacgaacgc	ctcaggaaga	gaagaacggg	tagccagcgt	gtgtctttgag	960
tcoggtttct	cccttttata	cactttttga	ttccaaacaa	ctctttttct	tttgtcttgt	1020
gaactgtgag	tggtgtcttt	atgacttaag	ttaaaagccc	aaaagcctct	ctaggaggag	1080
taaaacctgt	ttctgtgtgtg	acagaccatg	tcagtctcat	gttcttttag	ttactcttaa	1140
tgtaacaacg	tgtagcttac	actagtgtat	atttattttt	acgtatctac	acaaacatga	1200
aacttggtct						

(2) INFORMATION FOR SEQ ID NO:1267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..318
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

Asn Gly Asp Thr Phe Asp Glu Lys Ser Arg Ile Pro Asp Pro Asn Arg
1 5 10 15
Met Ile Arg Ala Tyr Thr Gln Ser Ala Ala Thr Leu Asn Leu Leu Arg
20 25 30
Ala Phe Ala Thr Gly Gly Tyr Ala Ala Ile Gln Arg Val Thr Gln Trp
35 40 45
Asn Leu Asp Phe Val Glu Gln Ser Glu Gln Ala Asp Arg Tyr Gln Glu
50 55 60
Leu Ala Asn Arg Val Asp Glu Ala Leu Gly Phe Met Ser Ala Cys Gly
65 70 75 80
Leu Gly Thr Asp His Pro Leu Met Thr Thr Asp Phe Tyr Thr Ser
85 90 95
His Glu Cys Leu Leu Leu Pro Tyr Glu Gln Ser Leu Thr Arg Leu Asp
100 105 110
Ser Thr Ser Gly Leu Tyr Tyr Asp Cys Ser Ala His Met Val Trp Cys
115 120 125
Gly Glu Arg Thr Arg Gln Leu Asp Gly Ala His Val Glu Phe Leu Arg
130 135 140
Gly Ile Ala Asn Pro Leu Gly Ile Lys Val Ser Asn Lys Met Asp Pro
145 150 155 160
Asn Glu Leu Val Lys Leu Val Glu Ile Leu Asn Pro Asn Asn Lys Pro
165 170 175
Gly Arg Ile Thr Val Ile Val Arg Met Gly Ala Glu Asn Met Arg Val
180 185 190
Lys Leu Pro His Leu Ile Arg Ala Val Arg Arg Ser Gly Gln Ile Val
195 200 205
Thr Trp Val Cys Asp Pro Met His Gly Asn Thr Ile Lys Ala Pro Cys
210 215 220
Gly Leu Lys Thr Arg Ala Phe Asp Ser Ile Leu Ala Glu Val Arg Ala
225 230 235 240
Phe Leu Asp Val His Glu Gln Glu Gly Ser His Ala Gly Gly Ile His
245 250 255
Leu Glu Met Thr Gly Gln Asn Val Thr Glu Cys Ile Gly Gly Ser Arg
260 265 270
Thr Val Thr Tyr Asp Asp Leu Ser Ser Arg Tyr His Thr His Cys Asp
275 280 285
Pro Arg Leu Asn Ala Ser Gln Ser Leu Glu Leu Ala Phe Ile Val Ala
290 295 300
Glu Arg Leu Arg Lys Arg Arg Thr Gly Ser Gln Arg Val Ser
305 310 315

(2) INFORMATION FOR SEQ ID NO:1268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..302
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:

Met Ile Arg Ala Tyr Thr Gln Ser Ala Ala Thr Leu Asn Leu Arg
1 5 10 15
Ala Phe Ala Thr Gly Gly Tyr Ala Ala Ile Gln Arg Val Thr Gln Trp
20 25 30
Asn Leu Asp Phe Val Glu Gln Ser Glu Gln Ala Asp Arg Tyr Gln Glu
35 40 45
Leu Ala Asn Arg Val Asp Glu Ala Leu Gly Phe Met Ser Ala Cys Gly
50 55 60

Leu Gly Thr Asp His Pro Leu Met Thr Thr Thr Asp Phe Tyr Thr Ser
65 70 75 80
His Glu Cys Leu Leu Pro Tyr Glu Gln Ser Leu Thr Arg Leu Asp
85 90 95
Ser Thr Ser Gly Leu Tyr Tyr Asp Cys Ser Ala His Met Val Trp Cys
100 105 110
Gly Glu Arg Thr Arg Gln Leu Asp Gly Ala His Val Glu Phe Leu Arg
115 120 125
Gly Ile Ala Asn Pro Leu Gly Ile Lys Val Ser Asn Lys Met Asp Pro
130 135 140
Asn Glu Leu Val Lys Leu Val Glu Ile Leu Asn Pro Asn Asn Lys Pro
145 150 155 160
Gly Arg Ile Thr Val Ile Val Arg Met Gly Ala Glu Asn Met Arg Val
165 170 175
Lys Leu Pro His Leu Ile Arg Ala Val Arg Arg Ser Gly Gln Ile Val
180 185 190
Thr Trp Val Cys Asp Pro Met His Gly Asn Thr Ile Lys Ala Pro Cys
195 200 205
Gly Leu Lys Thr Arg Ala Phe Asp Ser Ile Leu Ala Glu Val Arg Ala
210 215 220
Phe Leu Asp Val His Glu Gln Glu Gly Ser His Ala Gly Gly Ile His
225 230 235 240
Leu Glu Met Thr Gly Gln Asn Val Thr Glu Cys Ile Gly Gly Ser Arg
245 250 255
Thr Val Thr Tyr Asp Asp Leu Ser Ser Arg Tyr His Thr His Cys Asp
260 265 270
Pro Arg Leu Asn Ala Ser Gln Ser Leu Glu Leu Ala Phe Ile Val Ala
275 280 285
Glu Arg Leu Arg Lys Arg Arg Thr Gly Ser Gln Arg Val Ser
290 295 300

(2) INFORMATION FOR SEQ ID NO:1269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..243
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:

Met Ser Ala Cys Gly Leu Gly Thr Asp His Pro Leu Met Thr Thr Thr
1 5 10 15
Asp Phe Tyr Thr Ser His Glu Cys Leu Leu Pro Tyr Glu Gln Ser
20 25 30
Leu Thr Arg Leu Asp Ser Thr Ser Gly Leu Tyr Tyr Asp Cys Ser Ala
35 40 45
His Met Val Trp Cys Gly Glu Arg Thr Arg Gln Leu Asp Gly Ala His
50 55 60
Val Glu Phe Leu Arg Gly Ile Ala Asn Pro Leu Gly Ile Lys Val Ser
65 70 75 80
Asn Lys Met Asp Pro Asn Glu Leu Val Lys Leu Val Glu Ile Leu Asn
85 90 95
Pro Asn Asn Lys Pro Gly Arg Ile Thr Val Ile Val Arg Met Gly Ala
100 105 110
Glu Asn Met Arg Val Lys Leu Pro His Leu Ile Arg Ala Val Arg Arg
115 120 125
Ser Gly Gln Ile Val Thr Trp Trp Lys Cys Asp Pro Met His Gly Asn Thr
130 135 140
Ile Lys Ala Pro Cys Gly Leu Lys Thr Arg Ala Phe Asp Ser Ile Leu

145	150	155	160
Ala Glu Val Arg	Ala Phe Leu Asp Val	His Glu Gln Glu Gly Ser His	
	165	170	175
Ala Gly Gly Ile	His Leu Glu Met Thr	Gly Gln Asn Val Thr	Glu Cys
	180	185	190
Ile Gly Gly Ser	Arg Thr Val Thr Tyr	Asp Asp Leu Ser Ser	Arg Tyr
	195	200	205
His Thr His Cys	Asp Pro Arg Leu Asn Ala Ser	Gln Ser Leu Glu Leu	
	210	215	220
Ala Phe Ile Val	Ala Glu Arg Leu Arg Lys	Arg Thr Gly Ser Gln	
	225	230	235
Arg Val Ser			240

(2) INFORMATION FOR SEQ ID NO:1270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1748
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:

aggtccagca	cacgataccta	aatcctgtga	gcacgtcttc	catcgctggt	cttccattat	60
tgacgaatct	cttttgccttt	ttttcttctt	tcttaaacaa	acccaattcg	atttcaacga	120
acgcctcttc	tctctcaact	tctttcgatt	tggtctttgc	cggagctcgt	agtgtaacgg	180
tgatccgcgg	cggagagagt	gctcctaagt	atccataaaa	agccgttggt	ggcggcgcaa	240
gtggttttct	cgcctctctt	gcttcgtcga	tctccaattt	gggatctgct	atgaccaaat	300
cagtttaagt	tttggttccc	tatgagggac	ttgaagttaa	caatctcgaa	ggaagtacag	360
atgatctgga	ggaggaagca	agcagaggaa	gatggaagca	agaggatcga	gatgctgatt	420
ggaagatgat	gcagaagtac	ataggatctg	atgttacatc	aattggtgac	cttcctgtga	480
ttatttttga	accaatgaca	atgcttcaga	aaatggcgga	gttgatggaA	tactcgcatc	540
tgctagacat	ggcagacaaa	accgaggacc	cttattttgc	catggtgtat	gcatactcgt	600
gggctatata	cgtgtattat	gctttccaac	gtacctggaa	accattcaat	ccaatccttg	660
gtgagactta	tgagatggct	aattacaatg	gtgttaactt	catatctgaa	caggtcagcc	720
atccaccacc	aatgagtgtc	ggctcatgct	aaaatagaca	ttttacgtat	gattgtactt	780
caaaactgaa	aacaaaattt	ttgggcaatt	ccattgacgt	ttaccagta	ggaaggacac	840
gggtgacact	taaaagagat	ggagtgtgtc	ttgacttggt	acctctctgc	accaaagtcc	900
acaacctata	ctttggcaga	attcgggtgc	attcgctcgt	ggaattatgc	atgacaaaac	960
agaccaccgg	tgacaaagtc	gtgctttact	tcaaacctat	tggtctgttc	ggatctgtgc	1020
gatataaggt	ggatggatat	gtctataaac	cctctgagga	gcctaagata	ctcatgactc	1080
gcaaatggaa	cgagtccatg	agttatcagc	cgtgtgatgt	tgaaggtgaa	ccctctccag	1140
gcaccgaact	gaaagaggta	tggaaaactgc	ctgatgtgoc	aaagatgac	aaatatcaat	1200
acactcactt	tgctcacaa	attaaatagct	tcgacactgc	cccgaaaaag	ctgtttgcct	1260
ctgattcacg	gttacgaact	gatagatacg	cacttgagat	gggcgcacgt	tccaaatcag	1320
gctatgagaa	gagcagcatg	gaagagagac	agagagctga	aaagagaagc	cgcgaagaga	1380
aaggccaacg	cttctactca	aaatggttcg	atgtaacgga	agaagtcaat	gctacacact	1440
ggggtgatct	ggaagtttac	caattcaatg	gaaagtactc	ggaacatcgt	cgagctgcgg	1500
ataactctga	agataaacac	gacctaaagt	cgatccaatt	caacccatgc	caattccaag	1560
atctgtctac	ttaaatgtat	cgtcccaaaa	gacagaaaag	atcaaatctt	tttgaaaaca	1620
aattgtattc	tattctctcg	tagttacaaa	aaactttgtt	ctacatctgc	tagctttccc	1680
attgctttct	ctagtattag	tgtacaactt	ctactgtttt	gtcttaaaat	cattcaaatc	1740
ttctcttg						

(2) INFORMATION FOR SEQ ID NO:1271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..523
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569471
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:

Val	Gln	His	Thr	Ile	Leu	Asn	Pro	Val	Ser	Ile	Val	Ser	Ile	Ala	Gly
1				5					10					15	
Leu	Pro	Leu	Leu	Thr	Asn	Leu	Phe	Ala	Phe	Phe	Ser	Ser	Phe	Leu	Asn
				20				25					30		
Lys	Pro	Asn	Ser	Ile	Ser	Thr	Asn	Ala	Ser	Ser	Leu	Ser	Leu	Ser	Phe
		35					40				45				
Asp	Leu	Phe	Phe	Ala	Gly	Ala	Arg	Ser	Val	Ser	Val	Ile	Arg	Gly	Gly
	50					55					60				
Glu	Met	Ala	Pro	Asn	Asp	Pro	Lys	Lys	Ala	Val	Gly	Gly	Gly	Gly	Ser
	65			70					75				80		
Gly	Phe	Phe	Ala	Ser	Leu	Ala	Ser	Ser	Ile	Ser	Asn	Leu	Gly	Ser	Ala
			85						90				95		
Met	Thr	Lys	Ser	Val	Asn	Gly	Leu	Val	Pro	Tyr	Glu	Gly	Leu	Glu	Val
			100				105						110		
Ile	Asn	Pro	Glu	Gly	Ser	Thr	Asp	Asp	Ala	Glu	Glu	Glu	Ala	Ser	Arg
		115					120					125			
Gly	Arg	Trp	Lys	Gln	Glu	Asp	Arg	Asp	Gly	Tyr	Trp	Lys	Met	Met	Gln
	130				135						140				
Lys	Tyr	Ile	Gly	Ser	Asp	Val	Thr	Ser	Met	Val	Thr	Leu	Pro	Val	Ile
	145			150						155				160	
Ile	Phe	Glu	Pro	Met	Thr	Met	Leu	Gln	Lys	Met	Ala	Glu	Leu	Met	Glu
			165						170				175		
Tyr	Ser	His	Leu	Leu	Asp	Met	Ala	Asp	Lys	Thr	Glu	Asp	Pro	Tyr	Leu
		180					185						190		
Arg	Met	Val	Tyr	Ala	Ser	Ser	Trp	Ala	Ile	Ser	Val	Tyr	Tyr	Ala	Phe
		195					200					205			
Gln	Arg	Thr	Trp	Lys	Pro	Phe	Asn	Pro	Ile	Leu	Gly	Glu	Thr	Tyr	Glu
	210					215					220				
Met	Ala	Asn	Tyr	Asn	Gly	Val	Asn	Phe	Ile	Ser	Glu	Gln	Val	Ser	His
	225				230				235					240	
His	Pro	Pro	Met	Ser	Ala	Gly	His	Ala	Glu	Asn	Glu	His	Phe	Thr	Tyr
			245						250				255		
Asp	Cys	Thr	Ser	Lys	Leu	Lys	Thr	Lys	Phe	Leu	Gly	Asn	Ser	Ile	Asp
		260					265						270		
Val	Tyr	Pro	Val	Gly	Arg	Thr	Arg	Val	Thr	Leu	Lys	Arg	Asp	Gly	Val
		275					280					285			
Val	Leu	Asp	Leu	Val	Pro	Pro	Leu	Thr	Lys	Val	His	Asn	Leu	Ile	Phe
	290					295					300				
Gly	Arg	Thr	Trp	Val	Asp	Ser	Pro	Gly	Glu	Met	Ile	Met	Thr	Asn	Gln
	305				310				315					320	
Thr	Thr	Gly	Asp	Lys	Val	Val	Leu	Tyr	Phe	Gln	Pro	Cys	Gly	Trp	Phe
			325						330				335		
Gly	Ser	Gly	Arg	Tyr	Glu	Val	Asp	Gly	Tyr	Val	Tyr	Asn	Ala	Ser	Glu
		340					345						350		
Glu	Pro	Lys	Ile	Leu	Met	Thr	Gly	Lys	Trp	Asn	Glu	Ser	Met	Ser	Tyr
		355					360					365			
Gln	Pro	Cys	Asp	Gly	Glu	Gly	Glu	Pro	Leu	Pro	Gly	Thr	Glu	Leu	Lys
	370					375					380				
Glu	Val	Trp	Lys	Leu	Ala	Asp	Val	Pro	Lys	Asp	Asp	Lys	Tyr	Gln	Tyr
	385				390					395				400	
Thr	His	Phe	Ala	His	Lys	Ile	Asn	Ser	Phe	Asp	Thr	Ala	Pro	Lys	Lys
			405						410				415		
Leu	Leu	Pro	Ser	Asp	Ser	Arg	Leu	Arg	Pro	Asp	Arg	Tyr	Ala	Leu	Glu
		420					425					430			
Met	Gly	Asp	Met	Ser	Lys	Ser	Gly	Tyr	Glu	Lys	Ser	Ser	Met	Glu	Glu

(2) INFORMATION FOR SEQ ID NO:1272:

(A) LENGTH: 458 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: 1 in

MOLECULE TYPE: peptide

(18) FEATURE:

(D) NAM

(A) NAME/REF: peptide
(B) LOCATION: 1 458

(D) OTHER INFORMATION

(D) OTHER INFORMATION: / CELES Seq: ID 1505472
SEQUENCE DESCRIPTION: SEQ ID NO:1272:

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:1272:
Ala Pro Arg Arg Pro Lys Lys Ala Val Gly Gl

Phe	Ala	Pro	Asn	5	Pro	Lys	Lys	Ala	Val	Gly	Gly	Gly	Gly	Ser	Gly
1				5					10					15	
Phe	Phe	Ala	Ser	Leu	Ala	Ser	Ser	Ile	Ser	Asn	Leu	Gly	Ser	Ala	Met
			20					25					30		
Thr	Lys	Ser	Val	Asn	Gly	Leu	Val	Pro	Tyr	Glu	Gly	Leu	Glu	Val	Ile
		35					40					45			
Asn	Pro	Glu	Gly	Ser	Thr	Asp	Asp	Ala	Glu	Glu	Glu	Ala	Ser	Arg	Gly
		50				55				60					
Arg	Trp	Lys	Gln	Glu	Asp	Arg	Asp	Gly	Tyr	Trp	Lys	Met	Met	Gln	Lys
65				70					75					80	
Tyr	Ile	Gly	Ser	Asp	Val	Thr	Ser	Met	Val	Thr	Leu	Pro	Val	Ile	Ile
			85						90					95	
Phe	Glu	Pro	Met	Thr	Met	Leu	Gln	Lys	Met	Ala	Glu	Leu	Met	Glu	Tyr
			100					105						110	
Ser	His	Leu	Leu	Asp	Met	Ala	Asp	Lys	Thr	Glu	Asp	Pro	Tyr	Leu	Arg
			115					120				125			
Met	Val	Tyr	Ala	Ser	Ser	Trp	Ala	Ile	Ser	Val	Tyr	Tyr	Ala	Phe	Gln
			130			135						140			
Arg	Thr	Trp	Lys	Pro	Phe	Asn	Pro	Ile	Leu	Gly	Glu	Thr	Tyr	Glu	Met
145					150					155				160	
Ala	Asn	Tyr	Asn	Gly	Val	Asn	Phe	Ile	Ser	Glu	Gln	Val	Ser	His	His
			165					170						175	
Pro	Pro	Met	Ser	Ala	Gly	His	Ala	Glu	Asn	Glu	His	Phe	Thr	Tyr	Asp
			180					185					190		
Cys	Thr	Ser	Lys	Leu	Lys	Thr	Lys	Phe	Leu	Gly	Asn	Ser	Ile	Asp	Val
		195					200					205			
Tyr	Pro	Val	Gly	Arg	Thr	Arg	Val	Thr	Leu	Lys	Arg	Asp	Gly	Val	Val
		210				215					220				
Leu	Asp	Leu	Val	Pro	Pro	Leu	Thr	Lys	Val	His	Asn	Leu	Ile	Phe	Gly
225					230					235				240	
Arg	Thr	Trp	Val	Asp	Ser	Pro	Gly	Glu	Met	Ile	Met	Thr	Asn	Gln	Thr
			245						250					255	
Thr	Gly	Asp	Lys	Val	Val	Leu	Tyr	Phe	Gln	Pro	Cys	Gly	Tyr	Phe	Gly
			260					265					270		
Ser	Gly	Arg	Tyr	Glu	Val	Asp	Gly	Tyr	Val	Tyr	Asn	Ala	Ser	Glu	Glu
		275					280					285			
Pro	Lys	Ile	Leu	Met	Thr	Gly	Lys	Trp	Asn	Glu	Ser	Met	Ser	Tyr	Gln
		290				295					300				

Pro Cys Asp Gly Glu Gly Glu Pro Leu Pro Gly Thr Glu Leu Lys Glu
305 310 315 320
Val Trp Lys Leu Ala Asp Val Pro Lys Asp Asp Lys Tyr Gln Tyr Thr
325 330 335
His Phe Ala His Lys Ile Asn Ser Phe Asp Thr Ala Pro Lys Lys Leu
340 345 350
Leu Pro Ser Asp Ser Arg Leu Arg Pro Asp Arg Tyr Ala Leu Glu Met
355 360 365
Gly Asp Met Ser Lys Ser Gly Tyr Glu Lys Ser Ser Met Glu Glu Arg
370 375 380
Gln Arg Ala Glu Lys Arg Thr Arg Glu Glu Lys Gly Gln Ala Phe Thr
385 390 395 400
Pro Lys Trp Phe Asp Val Thr Glu Glu Val Thr Ala Thr Pro Trp Gly
405 410 415
Asp Leu Glu Val Tyr Gln Phe Asn Gly Lys Tyr Ser Glu His Arg Ala
420 425 430
Ala Ala Asp Asn Ser Glu Asp Asn Thr Asp Pro Lys Ser Ile Gln Phe
435 440 445
Asn Pro Trp Gln Phe Gln Asp Leu Ser Thr
450 455

(2) INFORMATION FOR SEQ ID NO:1273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 427 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..427

(D) OTHER INFORMATION: / Ceres Seq. ID 1569473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:

Met Thr Lys Ser Val Asn Gly Leu Val Pro Tyr Glu Gly Leu Glu Val
1 5 10 15
Ile Asn Pro Glu Gly Ser Thr Asp Asp Ala Glu Glu Glu Ala Ser Arg
20 25 30
Gly Arg Trp Lys Gln Glu Asp Arg Asp Gly Tyr Trp Lys Met Met Gln
35 40 45
Lys Tyr Ile Gly Ser Asp Val Thr Ser Met Val Thr Leu Pro Val Ile
50 55 60
Ile Phe Glu Pro Met Thr Met Leu Gln Lys Met Ala Glu Leu Met Glu
65 70 75 80
Tyr Ser His Leu Leu Asp Met Ala Asp Lys Thr Glu Asp Pro Tyr Leu
85 90 95
Arg Met Val Tyr Ala Ser Ser Trp Ala Ile Ser Val Tyr Tyr Ala Phe
100 105 110
Gln Arg Thr Trp Lys Pro Phe Asn Pro Ile Leu Gly Glu Thr Tyr Glu
115 120 125
Met Ala Asn Tyr Asn Gly Val Asn Phe Ile Ser Glu Gln Val Ser His
130 135 140
His Pro Pro Met Ser Ala Gly His Ala Glu Asn Glu His Phe Thr Tyr
145 150 155 160
Asp Cys Thr Ser Lys Leu Lys Thr Lys Phe Leu Gly Asn Ser Ile Asp
165 170 175
Val Tyr Pro Val Gly Arg Thr Arg Val Thr Leu Lys Arg Asp Gly Val
180 185 190
Val Leu Asp Leu Val Pro Pro Leu Thr Lys Val His Asn Leu Ile Phe
195 200 205
Gly Arg Thr Trp Val Asp Ser Pro Gly Glu Met Ile Met Thr Asn Gln
210 215 220
Thr Thr Gly Asp Lys Val Val Leu Tyr Phe Gln Pro Cys Gly Trp Phe

225				230				235				240			
Gly	Ser	Gly	Arg	Tyr	Glu	Val	Asp	Gly	Tyr	Val	Tyr	Asn	Ala	Ser	Glu
				245				250						255	
Glu	Pro	Lys	Ile	Leu	Met	Thr	Gly	Lys	Trp	Asn	Glu	Ser	Met	Ser	Tyr
			260					265						270	
Gln	Pro	Cys	Asp	Gly	Glu	Gly	Glu	Pro	Leu	Pro	Gly	Thr	Glu	Leu	Lys
			275					280						285	
Glu	Val	Trp	Lys	Leu	Ala	Asp	Val	Pro	Lys	Asp	Asp	Lys	Tyr	Gln	Tyr
			290				295				300				
Thr	His	Phe	Ala	His	Lys	Ile	Asn	Ser	Phe	Asp	Thr	Ala	Pro	Lys	Lys
			305			310				315				320	
Leu	Leu	Pro	Ser	Asp	Ser	Arg	Leu	Arg	Pro	Asp	Arg	Tyr	Ala	Leu	Glu
			325						330					335	
Met	Gly	Asp	Met	Ser	Lys	Ser	Gly	Tyr	Glu	Lys	Ser	Ser	Met	Glu	Glu
			340					345					350		
Arg	Gln	Arg	Ala	Glu	Lys	Arg	Thr	Arg	Glu	Glu	Lys	Gly	Gln	Ala	Phe
			355				360					365			
Thr	Pro	Lys	Trp	Phe	Asp	Val	Thr	Glu	Glu	Val	Thr	Ala	Thr	Pro	Trp
			370			375					380				
Gly	Asp	Leu	Glu	Val	Tyr	Gln	Phe	Asn	Gly	Lys	Tyr	Ser	Glu	His	Arg
			385			390				395				400	
Ala	Ala	Ala	Asp	Asn	Ser	Glu	Asp	Asn	Thr	Asp	Pro	Lys	Ser	Ile	Gln
			405						410					415	
Phe	Asn	Pro	Trp	Gln	Phe	Gln	Asp	Leu	Ser	Thr					
			420												

(2) INFORMATION FOR SEQ ID NO:1274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..606
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274:

atcacaaactc	tcatttttctt	ctctctcgat	tTcttgatat	atcagtaacc	aaaaaAcaca	60
gagaattaaa	acatggctta	cttctccaca	gcgacatctc	ttctctctct	ctgctctctct	120
gtttctcttc	cttatgttca	tggagcctcc	gactgcgaca	cccttgatgt	taccctgttc	180
ccatgtttac	cttttatatc	gatcgggggt	acggccgata	caccaacagc	ttcatgtctc	240
tcacgtctca	aaaatattct	cgatacga	ccgatatgtc	tatgcgaagg	gttgaagaag	300
gcacctttag	gaatcaagga	gaggacacta	cggacgagga	ggaggccacg	gtggtgggtg	360
acactatgga	ggtggaggac	accatggagg	aggaggctac	gggctgaacg	aaactgttca	420
gacgaagccg	ggtgtttaaa	agttataact	atcaataaaa	ttcaccatgc	ataattgcac	480
ctctatatac	acttatgtct	tatatgtatc	catcaaaata	aaccatgggt	agtttgtaat	540
gcagttcctt	cagaaatgtg	tggaaataatg	tttcacaata	ataatagaat	atctctgttg	600
attctg						

(2) INFORMATION FOR SEQ ID NO:1275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275:

His Asn Ser His Phe Leu Leu Ser Arg Phe Leu Asp Ile Ser Val Thr

1	5	10	15
Lys Lys His Arg Glu Leu Lys His Gly Leu Leu Leu His Ser Asp Ile	20	25	30
Ser Ser Pro Pro Arg Pro Leu Cys Phe Leu Ser Leu Cys Ser Trp Ser	35	40	45
Leu Arg Leu Arg His Pro Cys Asp Tyr Pro Val Pro Met Phe Thr Phe	50	55	60
Tyr Ile Asp Arg Gly Tyr Gly Arg Tyr Thr His Ser Phe Met Leu Leu	65	70	75
Gln Ser Gln Lys Tyr Ser Arg Tyr Glu Thr Asp Met Ser Met Arg Arg	85	90	95
Val Glu Glu Gly Thr Phe Arg Asn Gln Gly Glu Asp Thr Thr Asp Glu	100	105	110
Glu Glu Ala Thr Val Val Val Asp Thr Met Glu Val Glu Asp Thr Met	115	120	125
Glu Glu Glu Val Thr Gly			
130			

(2) INFORMATION FOR SEQ ID NO:1276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1569511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:

Met Ala Tyr Phe Ser Thr Ala Thr Ser Leu Leu Leu Val Leu Ser	1	5	10	15
Val Ser Ser Pro Tyr Val His Gly Ala Ser Asp Cys Asp Thr Leu Val	20	25	30	
Ile Thr Leu Phe Pro Cys Leu Pro Phe Ile Ser Ile Gly Thr Ala	35	40	45	
Asp Thr Pro Thr Ala Ser Cys Cys Ser Ser Leu Lys Asn Ile Leu Asp	50	55	60	
Thr Lys Pro Ile Cys Leu Cys Glu Gly Leu Lys Lys Ala Pro Leu Gly	65	70	75	80
Ile Lys Glu Arg Thr Leu Arg Thr Arg Arg Arg Pro Arg Trp Trp Trp	85	90	95	
Thr Leu Trp Arg Trp Arg Thr Pro Trp Arg Arg Arg Ser Arg Ala Glu	100	105	110	
Arg Thr Cys Ser Asp Glu Ala Gly Cys Leu Lys Val Ile Thr Ile Lys	115	120	125	

(2) INFORMATION FOR SEQ ID NO:1277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1569512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:

Met Phe Thr Phe Tyr Ile Asp Arg Gly Tyr Gly Arg Tyr Thr His Ser	1	5	10	15
-----------------------------------------------------------------	---	---	----	----

(2) INFORMATION FOR SEQ ID NO:1278:

(A) LENGTH: 985 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: sin

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (gc)

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(ix) FEATURE:
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(B) LOCATION: 1

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:1278:

ttctca gctccgacaa aaatggctgc aatcaccatt to

acgcctctccg	gctcgtcgaa	gcggcgagc	tctctgaaat	accocctgtga	tcacacctcta	120
agcctctccg	cgctgtgttc	gtccacacatg	tctctgaat	ccocctgtga	tcacacctcta	120
ttcacgcttc	acacgattct	tctctctccc	atctctctcc	ttcacacctc	gtgacacgga	180
tcgcgtctgc	cgctgtcttc	tctttatcgc	ctccgcgcgt	aaatctctaa	cgagacagga	240
cgctgcttcca	atcacagagc	ctgatctcaat	cccgctcgct	ctcggtgtat	acgcgtgtata	300
cgctaaagac	gacgacgattg	agttctgcgt	aaatatctcg	aacatcgctg	cgagttgtctc	360
tgctctatcc	aaatctgtgc	cgagagcttg	tgccctcggt	aaggtgtgaa	tagtagaaga	420
acagataatc	cgagtttttaa	cacaagcattg	gaattatg	ataagaagac	ataataaaag	480
aaactggaaa	cttcgcgcgg	ggaataagtc	agggaaacac	acattttgtc	aacaaactcc	540
gggaagAaa	atgacgacg	cgctctacac	caggtgcgca	ctgttgagct	cacggtttcgt	600
tggaagAac	tgattgaCcg	TttagtGaa	gagagcAag	tggttagctt	cataaaagga	660
ctcaagggtg	ctctccaagt	tgattctcca	cacagaggtg	ttgggattct	tgaagggcaa	720
ggagttgatt	atgaaactgt	tgatgtcttc	gacgatgagt	ataactatgg	gctaaagccaa	780
acgctttaaga	actacagacga	gtgtgccaa	tttccacaga	tatttgttga	agaagaacct	840
gtaggagatg	gtgatatttt	gacctccaag	tatgaaatg	gatattgtgc	ccatctgttg	900
aacagtgttc	atccgatttt	ctctctattt	tctagtgtga	actccaaaa	ttcattatag	960
agataacata	cttgtgattct	cttcc				

(2) INFORMATION FOR SEQ ID NO:1279:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..203

(D) OTHER INFORMATION: / Ceres Seq. ID 1569523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

1	Leu	Phe	Ser	Ala	Pro	Thr	Lys	Met	Ala	Ala	Ile	Thr	Ile	Ser	Ser	Ser
				5						10					15	
1	Leu	His	Ala	Ser	Ser	Ala	Ser	Pro	Arg	Val	Val	Arg	Pro	His	Val	Ser
				20						25					30	
Asn	Thr	Pro	Val	Ile	Thr	Leu	Thr	Ser	Arg	Phe	Thr	Pro	Ser	Phe	Ser	
				35			40					45				
Phe	Pro	Ser	Leu	Ser	Phe	Thr	Leu	Arg	Asp	Thr	Ala	Pro	Ser	Arg	Arg	
	50						55				60					
Arg	Ser	Phe	Phe	Ile	Ala	Ser	Ala	Val	Lys	Ser	Leu	Thr	Glu	Thr	Glu	
	65				70					75					80	
Leu	Leu	Pro	Ile	Thr	Glu	Ala	Asp	Ser	Ile	Pro	Ser	Ala	Ser	Gly	Val	
				85					90					95		

Tyr Ala Val Tyr Asp Lys Ser Asp Glu Leu Gln Phe Val Gly Ile Ser
100 105 110
Arg Asn Ile Ala Ala Ser Val Ser Ala His Leu Lys Ser Val Pro Glu
115 120 125
Leu Cys Gly Ser Val Lys Val Gly Ile Val Glu Glu Pro Asp Lys Ala
130 135 140
Val Leu Thr Gln Ala Trp Lys Leu Trp Ile Glu Glu His Ile Lys Val
145 150 155 160
Thr Gly Lys Val Pro Gly Asn Lys Ser Gly Asn Asn Thr Phe Val
165 170 175
Lys Gln Thr Pro Arg Lys Lys Ile Arg Tyr Pro Ser His Ser Arg Ser
180 185 190
Pro Cys Leu Ser Ser Arg Phe Xaa Trp Arg Asn
195 200

(2) INFORMATION FOR SEQ ID NO:1280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:

Met Ala Ala Ile Thr Ile Ser Ser Ser Leu His Ala Ser Ala Ser Pro
1 5 10 15
Arg Val Val Arg Pro His Val Ser Arg Asn Thr Pro Val Ile Thr Leu
20 25 30
Tyr Ser Arg Phe Thr Pro Ser Phe Ser Phe Pro Ser Leu Ser Phe Thr
35 40 45
Leu Arg Asp Thr Ala Pro Ser Arg Arg Arg Ser Phe Phe Ile Ala Ser
50 55 60
Ala Val Lys Ser Leu Thr Glu Thr Glu Leu Leu Pro Ile Thr Glu Ala
65 70 75 80
Asp Ser Ile Pro Ser Ala Ser Gly Val Tyr Ala Val Tyr Asp Lys Ser
85 90 95
Asp Glu Leu Gln Phe Val Gly Ile Ser Arg Asn Ile Ala Ala Ser Val
100 105 110
Ser Ala His Leu Lys Ser Val Pro Glu Leu Cys Gly Ser Val Lys Val
115 120 125
Gly Ile Val Glu Glu Pro Asp Lys Ala Val Leu Thr Gln Ala Trp Lys
130 135 140
Leu Trp Ile Glu Glu His Ile Lys Val Thr Gly Lys Val Pro Pro Gly
145 150 155 160
Asn Lys Ser Gly Asn Asn Thr Phe Val Lys Gln Thr Pro Arg Lys Lys
165 170 175
Ile Arg Tyr Pro Ser His Ser Arg Ser Pro Cys Leu Ser Ser Arg Phe
180 185 190
Xaa Trp Arg Asn
195

(2) INFORMATION FOR SEQ ID NO:1281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..108
(D) OTHER INFORMATION: / Ceres Seq. ID 1569525
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:
Met Phe Glu Leu Thr Val Xaa Leu Glu Glu Leu Ile Asp Arg Leu Val
1 5 10 15
Lys Glu Ser Lys Val Val Ala Phe Ile Lys Gly Ser Arg Ser Ala Pro
20 25 30
Gln Cys Gly Phe Ser Gln Arg Val Val Gly Ile Leu Glu Ser Gln Gly
35 40 45
Val Asp Tyr Glu Thr Val Asp Val Leu Asp Asp Glu Tyr Asn His Gly
50 55 60
Leu Arg Glu Thr Leu Lys Asn Tyr Ser Asn Trp Pro Thr Phe Pro Gln
65 70 75 80
Ile Phe Val Lys Gly Glu Leu Val Gly Gly Cys Asp Ile Leu Thr Ser
85 90 95
Met Tyr Glu Asn Gly Glu Leu Ala Asn Ile Leu Asn
100 105

(2) INFORMATION FOR SEQ ID NO:1282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..654
(D) OTHER INFORMATION: / Ceres Seq. ID 1569526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:

atatttgaag	ttctgtgatt	ttgaaggatt	tgattggttt	ccatgatcta	gagttttgag	60
aatggcgatg	gtatcaggaa	gacgatctac	tctaaacccc	gacgcacctc	ttttttatcc	120
ggcagctgta	cgacaagtgg	aagatttctc	accggagtgg	tggaatttgg	tgacaacttc	180
gacttggtag	cctgattact	ggatcatgca	gcagcagcaa	ggcgcggatg	gtttctatga	240
caacggagag	aatgagaatg	gtggagggtc	tatcgatgta	gctgatcttc	ttccagaatc	300
atttttat	gatgatatgg	aagatttttt	tgacactgat	gctgctgagt	ttgatcaagg	360
attcgatgga	agaatgtatt	accaagcacc	ttccgaattt	ggctttggaa	agaatggtga	420
gatggttaag	aaatcaagt	gaaacaggag	cccagatcgt	attgtggaac	cagctaaagta	480
tgcggaataa	ccagcgaaat	ggggaaacca	gagggttgct	gctgctccga	gaaacatcca	540
ccagcctcgc	tgaagagata	gtttgttaac	tagtcagaga	agtcagagca	gttcggctcg	600
tgatctctta	gccaccactg	tacctttgta	atYYYtttta	gtatttgcct	ccac	

(2) INFORMATION FOR SEQ ID NO:1283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..163
(D) OTHER INFORMATION: / Ceres Seq. ID 1569527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:

Met Ala Met Val Ser Gly Arg Arg Ser Thr Leu Asn Pro Asp Ala Pro	
1 5 10 15	
Leu Phe Ile Pro Ala Ala Val Arg Gln Val Glu Asp Phe Ser Pro Glu	
20 25 30	
Trp Trp Gln Leu Val Thr Thr Ser Thr Trp Tyr Pro Asp Tyr Trp Ile	
35 40 45	
Ser Gln Gln Gln Gln Gly Ala Asp Gly Phe Tyr Asp Asn Gly Glu Asn	
50 55 60	
Glu Asn Gly Gly Gly His Ile Asp Val Ala Asp Leu Leu Pro Glu Ser	

65		70		75		80
Phe Tyr Phe Asp Asp Met Glu Asp Phe Phe Asp Thr Asp Ala Ala Glu						
	85			90		95
Phe Asp Gln Gly Phe Asp Gly Arg Met Tyr Tyr Gln Ala Pro Ser Glu						
	100			105		110
Phe Gly Phe Gly Lys Asn Gly Glu Met Val Lys Lys Ser Ser Gly Asn						
	115			120		125
Arg Ser Pro Arg Ser Ile Val Glu Pro Ala Lys Tyr Ala Glu Lys Pro						
	130			135		140
Ala Lys Trp Gly Asn Gln Arg Val Ala Ala Ala Pro Arg Asn Ile His						
	145			150		155
						160
Gln Pro Arg						

(2) INFORMATION FOR SEQ ID NO:1284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:

Met Val Ser Gly Arg Arg Ser Thr Leu Asn Pro Asp Ala Pro Leu Phe						
1	5			10		15
Ile Pro Ala Ala Val Arg Gln Val Glu Asp Phe Ser Pro Glu Trp Trp						
	20			25		30
Gln Leu Val Thr Thr Ser Thr Trp Tyr Pro Asp Tyr Trp Ile Ser Gln						
	35			40		45
Gln Gln Gln Gly Ala Asp Gly Phe Tyr Asp Asn Gly Glu Asn Glu Asn						
	50			55		60
Gly Gly Gly His Ile Asp Val Ala Asp Leu Leu Pro Glu Ser Phe Tyr						
	65			70		75
Phe Asp Asp Met Glu Asp Phe Phe Asp Thr Asp Ala Ala Glu Phe Asp						
	85			90		95
Gln Gly Phe Asp Gly Arg Met Tyr Tyr Gln Ala Pro Ser Glu Phe Gly						
	100			105		110
Phe Gly Lys Asn Gly Glu Met Val Lys Lys Ser Ser Gly Asn Arg Ser						
	115			120		125
Pro Arg Ser Ile Val Glu Pro Ala Lys Tyr Ala Glu Lys Pro Ala Lys						
	130			135		140
Trp Gly Asn Gln Arg Val Ala Ala Ala Pro Arg Asn Ile His Gln Pro						
	145			150		155
Arg						160

(2) INFORMATION FOR SEQ ID NO:1285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:

Met Ile Trp Lys Ile Ser Leu Thr Leu Met Leu Leu Ser Leu Ile Lys					
1	5			10	15

Asp Ser Met Glu Glu Cys Ile Thr Lys His Leu Pro Asn Leu Ala Leu
20 25 30
Glu Arg Met Val Arg Trp Leu Arg Asn Gln Val Glu Thr Gly Ala Arg
35 40 45
Asp Arg Leu Trp Asn Gln Leu Ser Met Arg Lys Ser Gln Arg Asn Gly
50 55 60
Glu Thr Arg Gly Leu Leu Leu Arg Glu Thr Ser Thr Ser Leu Ala
65 70 75 80
Glu Glu Ile Cys Cys
85

(2) INFORMATION FOR SEQ ID NO:1286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1195

(D) OTHER INFORMATION: / Ceres Seq. ID 1569530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:

ttttcggcgt	caacggaacc	gcgcgaatat	ggagaatagc	ggcgataaat	gaagctgggt	60
ggtggaaga	tcggaccacc	gtggaagata	tggatctcgc	cgctccgagca	agtcttcgcg	120
gctggaaatt	tctctacctc	ggtgaccttc	aggtgaaaag	tgagcttcca	agtactttta	180
gagccttcgc	ttttcagcaa	catagatggt	cttgtggacc	tgcaaatctc	tttaggaaaa	240
tggttatgga	gatcgtaa	aacaagaaag	tgagattctg	gaagaaaagt	tacgtgatat	300
acagctctct	ctttgtgagg	aaaatcattg	cacatttggt	cacattttgt	ttctactcgc	360
ttgtttcttc	tctcacaaat	ctcgtcccg	agggttaaat	tccgatttgg	gggttcggtt	420
atatcccatc	catcataact	atcctcaatt	ccgtcggta	tcCaaggtca	attcatctgc	480
tgttctattg	gattctatc	gagaatgtga	tgtcgtcgca	ccggacaaa	gccactctca	540
ttggtctggt	tgaggcagga	agggtcaaac	agttggtagt	gactgctaag	cttggaagcg	600
gtcagagcgc	taaaggaaac	actaaaggga	tcaaaaggtt	cccaagaatc	ttcaaattgc	660
ctgatcgatt	gaatacattg	gagcttggat	ttcggcgctt	cttgttcgtg	tgccggatgct	720
atgactttgt	gcacgggaag	aacaattact	tcatctacct	gtttctctag	acaatgtctt	780
tccttcacag	tgggctgggc	tggatcggga	cttatgtccc	gagtttagtag	ttgtgtgtgt	840
tcagagagaa	aagagaatgt	tattaatttt	cttgagaaat	aaagacaatt	ttcattgaaa	900
tgacaaagga	aaattgatag	gggagataga	gacgtaccgg	tacaacaaga	taggaagaaa	960
ggagaagact	tttatcaaa	accaggaaa	aggagaagct	ccaagggttc	ttttgattta	1020
tttttatttt	ttctgtgttt	tatttatata	gctatgggat	tgttgattca	gttgttgtga	1080
gatttttaatt	ttcgtttctt	gttttttatt	ttggtttttg	ggattttttt	cggttttgaaa	1140
gtgttagtct	ttttgttttt	tttttaattt	aaattccaag	taaaaattaa	attccc	

(2) INFORMATION FOR SEQ ID NO:1287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..274

(D) OTHER INFORMATION: / Ceres Seq. ID 1569531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:

Phe Gly Phe Asn Gly Thr Ala Gly Ile Trp Arg Ile Ala Ala Ile Asn	
1 5 10 15	
Glu Ala Gly Gly Trp Lys Asp Arg Thr Thr Val Glu Asp Met Asp Leu	
20 25 30	
Ala Val Arg Ala Ser Leu Arg Gly Trp Lys Phe Leu Tyr Leu Gly Asp	
35 40 45	
Leu Gln Val Lys Ser Glu Leu Pro Ser Thr Phe Arg Ala Phe Arg Phe	

WORLD

(1) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..245

- (D) OTHER INFORMATION: / Ceres Seq. ID 1569532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288:

Met	Asp	Leu	Ala	Val	Arg	Ala	Ser	Leu	Arg	Gly	Trp	Lys	Phe	Leu	Tyr
1				5					10					15	
Leu	Gly	Asp	Leu	Gln	Val	Lys	Ser	Glu	Leu	Pro	Ser	Thr	Phe	Arg	Ala
			20					25					30		
Phe	Arg	Phe	Gln	Gln	His	Arg	Trp	Ser	Cys	Gly	Pro	Ala	Asn	Leu	Phe
		35					40					45			
Arg	Lys	Met	Val	Met	Glu	Ile	Val	Arg	Asn	Lys	Lys	Val	Arg	Phe	Trp
	50					55				60					
Lys	Lys	Val	Tyr	Val	Ile	Tyr	Ser	Phe	Phe	Phe	Val	Arg	Lys	Ile	Ile
65				70						75				80	
Ala	His	Trp	Val	Thr	Phe	Cys	Phe	Tyr	Cys	Val	Val	Leu	Pro	Leu	Thr
				85					90					95	
Ile	Leu	Val	Pro	Glu	Val	Lys	Val	Pro	Ile	Trp	Gly	Ser	Val	Tyr	Ile
			100					105					110		
Pro	Ser	Ile	Ile	Thr	Ile	Leu	Asn	Ser	Val	Gly	Thr	Pro	Arg	Ser	Ile
		115				120						125			
His	Leu	Leu	Phe	Tyr	Trp	Ile	Leu	Phe	Glu	Asn	Val	Met	Ser	Leu	His
	130					135				140					
Arg	Thr	Lys	Ala	Thr	Leu	Ile	Gly	Leu	Phe	Glu	Ala	Gly	Arg	Ala	Asn
145					150					155				160	

Glu Leu Val Val Thr Ala Lys Leu Gly Ser Gly Gln Ser Ala Lys Gly
165 170 175
Asn Thr Lys Gly Ile Lys Arg Phe Pro Arg Ile Phe Lys Leu Pro Asp
180 185 190
Arg Leu Asn Thr Leu Glu Leu Gly Phe Ala Ala Phe Leu Phe Val Cys
195 200 205
Gly Cys Tyr Asp Phe Val His Gly Lys Asn Asn Tyr Phe Ile Tyr Leu
210 215 220
Phe Leu Gln Thr Met Ser Phe Phe Ile Ser Gly Leu Gly Trp Ile Gly
225 230 235 240
Thr Tyr Val Pro Ser
245

(2) INFORMATION FOR SEQ ID NO:1289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..195

(D) OTHER INFORMATION: / Ceres Seq. ID 1569533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289:

Met Val Met Glu Ile Val Arg Asn Lys Lys Val Arg Phe Trp Lys Lys
1 5 10 15
Val Tyr Val Ile Tyr Ser Phe Phe Phe Val Arg Lys Ile Ile Ala His
20 25 30
Trp Val Thr Phe Cys Phe Tyr Cys Val Val Leu Pro Leu Thr Ile Leu
35 40 45
Val Pro Glu Val Lys Val Pro Ile Trp Gly Ser Val Tyr Ile Pro Ser
50 55 60
Ile Ile Thr Ile Leu Asn Ser Val Gly Thr Pro Arg Ser Ile His Leu
65 70 75 80
Leu Phe Tyr Trp Ile Leu Phe Glu Asn Val Met Ser Leu His Arg Thr
85 90 95
Lys Ala Thr Leu Ile Gly Leu Phe Glu Ala Gly Arg Ala Asn Glu Leu
100 105 110
Val Val Thr Ala Lys Leu Gly Ser Gly Gln Ser Ala Lys Gly Asn Thr
115 120 125
Lys Gly Ile Lys Arg Phe Pro Arg Ile Phe Lys Leu Pro Asp Arg Leu
130 135 140
Asn Thr Leu Glu Leu Gly Phe Ala Ala Phe Leu Phe Val Cys Gly Cys
145 150 155 160
Tyr Asp Phe Val His Gly Lys Asn Asn Tyr Phe Ile Tyr Leu Phe Leu
165 170 175
Gln Thr Met Ser Phe Phe Ile Ser Gly Leu Gly Trp Ile Gly Thr Tyr
180 185 190
Val Pro Ser
195

(2) INFORMATION FOR SEQ ID NO:1290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1212

(D) OTHER INFORMATION: / Ceres Seq. ID 1569538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:

gcagacattt	tagacaaagt	tactctcttt	ctttctcatg	ttcttttcgg	acagaaacaaa	60
actcccta	ccaatgtc	attcctttg	tctctctctg	aataatcatc	tctcttccaaa	120
ccctattcca	ttttaactat	cgatctctgg	ctaagtcctc	aatggcgggc	gcggttgctt	180
ctcttcccaa	atttagtg	gtcaattcct	ccagatttcc	cagaagaaga	atcggttttt	240
ctgtctccaa	aaagccctcc	gaagtttgtt	gttcttccgg	caatactcgt	tacactaagc	300
agagaggggc	atttacatca	ttagaaagat	gtgcgatttc	attagcttta	tccggttggtt	360
taatgggttc	agtagctctg	attgtcttgc	ctcccaatgc	tcaogcagtg	gcgaatccag	420
tgtattccaga	tgtttcaagt	ttagatctccg	gtctctccgt	taaagatccg	gaagctttac	480
taagatatgc	attgctctatt	gacaaacaa	ccatcaggga	agtgacaga	ccctcttgagg	540
atgactcaga	tagctctcaag	attgtctggc	ttaaggctct	agattctgtt	gaacgggaatg	600
tgaggcaggc	aagtagaaca	ttgcagcaag	ggaaaaagta	aattgtggca	ggttttgcgt	660
aatcgagaaa	ggaatcatgt	aatgaaatga	ttagaaaagt	ggaagctggg	atgcaagata	720
tgtcttaagt	agtgaagat	cgaaaaagag	acgcagttgc	tccaaaaacag	aaagaaattc	780
tcaaatatgt	tggcggaata	gaagaggata	tgggttgatg	ctttccatat	gaagtgcogg	840
aaagatgatc	Cgaacatgcc	tctctccaag	ggaagagcta	gtgtggacat	gaaggtcaag	900
atcaaggaca	atcccaacat	cgaggactgt	gtgttccgca	tgttttatac	tgtttataac	960
gccccgttta	ccgccggaaa	ctttgtggac	tgtgtagaga	ggcatttcta	cgatgctctt	1020
ccggcgcttc	atatggaaa	ccatcaacca	tatctctctc	tattccatgt	ttctgttttt	1080
tgttttttac	tgtgtattca	atacaatttg	tcttttccct	tctgtcattt	ttgtcagatg	1140
ttatttagtt	ttgttcaagt	taactcttgt	tgtttattct	actttaagag	ctcatatgga	1200
tctgtctctt	cc					

(2) INFORMATION FOR SEQ ID NO:1291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..239
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:

Met	Ala	Ala	Ala	Phe	Ala	Ser	Leu	Pro	Thr	Phe	Ser	Val	Val	Asn	Ser	
1				5					10					15		
Ser	Arg	Phe	Pro	Arg	Arg	Arg	Ile	Gly	Phe	Ser	Cys	Ser	Lys	Lys	Pro	
			20					25					30			
Leu	Glu	Val	Arg	Cys	Ser	Ser	Gly	Asn	Thr	Arg	Tyr	Thr	Lys	Gln	Arg	
			35				40					45				
Gly	Ala	Phe	Thr	Ser	Leu	Lys	Glu	Cys	Ala	Ile	Ser	Leu	Ala	Leu	Ser	
	50					55				60						
Val	Gly	Leu	Met	Val	Ser	Val	Pro	Ser	Ile	Ala	Leu	Pro	Pro	Asn	Ala	
	65					70				75				80		
His	Ala	Val	Ala	Asn	Pro	Val	Ile	Pro	Asp	Val	Ser	Val	Leu	Ile	Ser	
			85					90						95		
Gly	Pro	Pro	Ile	Lys	Asp	Pro	Glu	Ala	Leu	Leu	Arg	Tyr	Ala	Leu	Pro	
			100				105						110			
Ile	Asp	Asn	Lys	Ala	Ile	Arg	Glu	Val	Gln	Lys	Pro	Leu	Glu	Asp	Ile	
	115					120						125				
Thr	Asp	Ser	Leu	Lys	Ile	Ala	Gly	Val	Lys	Ala	Leu	Asp	Ser	Val	Glu	
	130					135						140				
Arg	Asn	Val	Arg	Gln	Ala	Ser	Arg	Thr	Leu	Gln	Gln	Gly	Lys	Ser	Ile	
	145					150				155				160		
Ile	Val	Ala	Gly	Phe	Ala	Glu	Ser	Lys	Lys	Asp	His	Gly	Asn	Glu	Met	
			165							170				175		
Ile	Glu	Lys	Leu	Glu	Ala	Gly	Met	Gln	Asp	Met	Leu	Lys	Ile	Val	Glu	
			180				185					190				
Asp	Arg	Lys	Arg	Asp	Ala	Val	Ala	Pro	Lys	Gln	Lys	Glu	Ile	Leu	Lys	
			195				200					205				
Tyr	Val	Gly	Gly	Ile	Glu	Glu	Asp	Met	Val	Asp	Gly	Phe	Pro	Tyr	Glu	

210 215 220
Val Pro Glu Glu Tyr Arg Glu His Ala Ser Pro Gln Gly Lys Ser
225 230 235
(2) INFORMATION FOR SEQ ID NO:1292:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..172
(D) OTHER INFORMATION: / Ceres Seq. ID 1569540
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:
Met Val Ser Val Pro Ser Ile Ala Leu Pro Pro Asn Ala His Ala Val
1 5 10 15
Ala Asn Pro Val Ile Pro Asp Val Ser Val Leu Ile Ser Gly Pro Pro
20 25 30
Ile Lys Asp Pro Glu Ala Leu Leu Arg Tyr Ala Leu Pro Ile Asp Asn
35 40 45
Lys Ala Ile Arg Glu Val Gln Lys Pro Leu Glu Asp Ile Thr Asp Ser
50 55 60
Leu Lys Ile Ala Gly Val Lys Ala Leu Asp Ser Val Glu Arg Asn Val
65 70 75 80
Arg Gln Ala Ser Arg Thr Leu Gln Gln Gly Lys Ser Ile Ile Val Ala
85 90 95
Gly Phe Ala Glu Ser Lys Lys Asp His Gly Asn Glu Met Ile Glu Lys
100 105 110
Leu Glu Ala Gly Met Gln Asp Met Leu Lys Ile Val Glu Asp Arg Lys
115 120 125
Arg Asp Ala Val Ala Pro Lys Gln Lys Glu Ile Leu Lys Tyr Val Gly
130 135 140
Gly Ile Glu Glu Asp Met Val Asp Gly Phe Pro Tyr Glu Val Pro Glu
145 150 155 160
Glu Tyr Arg Glu His Ala Ser Pro Gln Gly Lys Ser
165 170

(2) INFORMATION FOR SEQ ID NO:1293:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..132
(D) OTHER INFORMATION: / Ceres Seq. ID 1569541
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:
Met Ala Phe His Met Lys Cys Arg Lys Ser Ile Ala Asn Met Pro Leu
1 5 10 15
Leu Lys Gly Arg Ala Ser Val Asp Met Lys Val Lys Ile Lys Asp Asn
20 25 30
Pro Asn Ile Glu Asp Cys Val Phe Arg Ile Val Leu Asp Gly Tyr Asn
35 40 45
Ala Pro Val Thr Ala Gly Asn Phe Val Asp Leu Val Glu Arg His Phe
50 55 60
Tyr Asp Ala Leu Pro Ala Leu His Met Glu Ser His Gln Pro Tyr Pro
65 70 75 80
Pro Leu Phe His Val Ser Val Phe Trp Phe Leu Leu Gly Ile Glu Tyr
85 90 95

Asn Leu Ser Phe Pro Phe Cys His Phe Cys Gln Met Leu Phe Ser Phe
100 105 110
Val Gln Val Asn Ser Cys Trp Leu Ser Tyr Phe Lys Ser Ser Tyr Gly
115 120 125
Ser Arg Ser Ser
130

(2) INFORMATION FOR SEQ ID NO:1294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..684
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:

acatctcaact	gctcaactact	ctcaactgtaa	tcctttagat	ctTcttttca	aattTcaatg	60
gcgtccCggt	gatgttgagt	atcggtgctt	cggtggaggt	ctagcatggg	ccactgatga	120
cagagctctt	gagactgcct	tcgctcaata	cgccgacgtt	attgattcca	agatcattaa	180
cgatcgtgag	actggaagat	caaggggatt	cggtatcgct	accttcaagg	atgagaaaagc	240
catgaagat	gcgattgagg	gaatgaacgg	acaagatctc	gatggccgta	gcatactgt	300
taacgaggt	cagtcagcgt	gaagcgggtg	cgccgggaggc	caccgtggag	gtggtggcgg	360
tgatatacgc	agcggcggtg	gtggaagacg	tgagggagga	ggaggatacg	gtggtgggta	420
aggagaggt	tacggaggaa	gcggtggtgg	tgaggatgg	taattccctt	aattaggttt	480
gggattacca	atgaatgttc	ttctctctgc	ttgttatgct	ttctacttgt	tttgtgtgtt	540
ctctattttg	ttctggtttc	gccttagatt	tgatgttaac	gtctgtgatt	aggtattttg	600
gtatctggaa	acgtaatggt	aagtcacttg	tcattctcta	aataacaaat	ttcttcggag	660
atattatctc	tggtgattga	ttct				

(2) INFORMATION FOR SEQ ID NO:1295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:

His	Leu	Thr	Ala	His	Tyr	Ser	His	Cys	Asn	Pro	Leu	Asp	Leu	Leu	Phe
1				5				10					15		
Lys	Phe	Gln	Trp	Arg	Pro	Gly	Asp	Val	Glu	Tyr	Arg	Cys	Phe	Val	Gly
				20				25					30		
Gly	Leu	Ala	Trp	Ala	Thr	Asp	Asp	Arg	Ala	Leu	Glu	Thr	Ala	Phe	Ala
				35				40					45		
Gln	Tyr	Gly	Asp	Val	Ile	Asp	Ser	Lys	Ile	Ile	Asn	Asp	Arg	Glu	Thr
				50				55					60		
Gly	Arg	Ser	Arg	Gly	Phe	Gly	Phe	Val	Thr	Phe	Lys	Asp	Glu	Lys	Ala
				65				70					75		80
Met	Lys	Asp	Ala	Ile	Glu	Gly	Met	Asn	Gly	Gln	Asp	Leu	Asp	Gly	Arg
				85				90					95		
Ser	Ile	Thr	Val	Asn	Glu	Ala	Gln	Ser	Arg	Gly	Ser	Gly	Gly	Gly	Gly
				100				105					110		
Gly	His	Arg	Gly	Gly	Gly	Gly	Gly	Tyr	Arg	Ser	Gly	Gly	Gly	Gly	Gly
				115				120					125		
Arg	Arg	Glu	Gly	Gly	Gly	Gly	Tyr	Gly	Gly	Gly	Glu	Gly	Gly	Gly	Tyr
				130				135					140		
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Trp							

145 150
(2) INFORMATION FOR SEQ ID NO:1296:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 773 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..773
(D) OTHER INFORMATION: / Ceres Seq. ID 1569552
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:
tccatataaa ttgttccaaa ttctattcgt atcctttccg ctgctgcgcgt cttcgtctct 60
gagataataa ggaacttgtgt atttttccat cgttaaaaagg catttcaaa agacaatatg 120
tcaggatgat aggcctgcccc ttgtgttgtt cctccccccg ttgctgagcc agcgcccatc 180
ccagaggaca tggacttaaat gactgcattg gacttgactc ttaggaaaag cgtgtcctat 240
gggtgtgttg ttctgtgtct ccatgagtggt gctaagctta ttgagaagcg tgtggctcaa 300
ctcgttgtct tggctgaaga ctgcaaccag cctgattatg tcaagcttgt gaagcgtctc 360
tgtgtgatc acgaagtcaag gttgctaaca gttccaagt ccaagaccct tggcgaatgg 420
gctggctctc gcaagattga ttctgagggt aatgccagga aggttggttg atgctcatgt 480
cttgtgttca aggacttcgg cgaggagaca actgccctca gtatcgtaa taagcatatt 540
gcttctcaat aaaatgccat gaagcatatc taaactcgga ttcatatgt ttccaccctc 600
caatgctgtt Attctctctgg tttgtatata ttaactaata tttacgggac agctcttgag 660
atatttttgg aacatgatca agttttgttg ttatctagac ttactcttc caaggccaaa 720
tttgcttgag atttatttgg ctctactact tttcatcataa tttttttttt cct
(2) INFORMATION FOR SEQ ID NO:1297:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..144
(D) OTHER INFORMATION: / Ceres Seq. ID 1569553
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:
Met Ser Gly Asp Glu Ala Ala Pro Val Val Val Pro Pro Val Ala
1 5 10 15
Glu Pro Ala Ala Ile Pro Glu Asp Met Asp Leu Met Thr Ala Leu Glu
20 25 30
Leu Thr Leu Arg Lys Ala Arg Ala Tyr Gly Gly Val Val Arg Gly Leu
35 40 45
His Glu Cys Ala Lys Leu Ile Glu Lys Arg Val Ala Gln Leu Val Val
50 55 60
Leu Ala Glu Asp Cys Asn Gln Pro Asp Tyr Val Lys Leu Val Lys Ala
65 70 75 80
Leu Cys Ala Asp His Glu Val Arg Leu Leu Thr Val Pro Ser Ala Lys
85 90 95
Thr Leu Gly Glu Trp Ala Gly Leu Cys Lys Ile Asp Ser Glu Gly Asn
100 105 110
Ala Arg Lys Val Val Gly Cys Ser Cys Leu Val Val Lys Asp Phe Gly
115 120 125
Glu Glu Thr Thr Ala Leu Ser Ile Val Asn Lys His Ile Ala Ser Gln
130 135 140
(2) INFORMATION FOR SEQ ID NO:1298:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..120
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569554
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:
Met Asp Leu Met Thr Ala Leu Glu Leu Thr Leu Arg Lys Ala Arg Ala
1 5 10 15
Tyr Gly Gly Val Val Arg Gly Leu His Glu Cys Ala Lys Leu Ile Glu
 20 25 30
Lys Arg Val Ala Gln Leu Val Val Leu Ala Glu Asp Cys Asn Gln Pro
 35 40 45
Asp Tyr Val Lys Leu Val Lys Ala Leu Cys Ala Asp His Glu Val Arg
 50 55 60
Leu Leu Thr Val Pro Ser Ala Lys Thr Leu Gly Glu Trp Ala Gly Leu
65 70 75 80
Cys Lys Ile Asp Ser Glu Gly Asn Ala Arg Lys Val Val Gly Cys Ser
 85 90 95
Cys Leu Val Val Lys Asp Phe Gly Glu Glu Thr Thr Ala Leu Ser Ile
 100 105 110
Val Asn Lys His Ile Ala Ser Gln
 115 120
(2) INFORMATION FOR SEQ ID NO:1299:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..117
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569555
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299:
Met Thr Ala Leu Glu Leu Thr Leu Arg Lys Ala Arg Ala Tyr Gly Gly
1 5 10 15
Val Val Arg Gly Leu His Glu Cys Ala Lys Leu Ile Glu Lys Arg Val
 20 25 30
Ala Gln Leu Val Val Leu Ala Glu Asp Cys Asn Gln Pro Asp Tyr Val
 35 40 45
Lys Leu Val Lys Ala Leu Cys Ala Asp His Glu Val Arg Leu Leu Thr
 50 55 60
Val Pro Ser Ala Lys Thr Leu Gly Glu Trp Ala Gly Leu Cys Lys Ile
65 70 75 80
Asp Ser Glu Gly Asn Ala Arg Lys Val Val Gly Cys Ser Cys Leu Val
 85 90 95
Val Lys Asp Phe Gly Glu Glu Thr Thr Ala Leu Ser Ile Val Asn Lys
 100 105 110
His Ile Ala Ser Gln
 115
(2) INFORMATION FOR SEQ ID NO:1300:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1141
(D) OTHER INFORMATION: / Ceres Seq. ID 1569579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:

atttagccct	tgttttctct	acacacatct	cacatccccc	tatctctctc	tctcttcaaa	60
cgtttttagt	ccccaaaaaa	atatcaaaag	aactaaaaag	aaaaccctag	agccogaaga	120
ctctctact	cggtgtcgat	cggatcacct	aactaattac	tcgttgataa	tcattatatac	180
gagaaatag	attaattttg	aggccaacga	gctgagatta	gggtaccggg	gtgggaatca	240
cgaggagaa	atggctggaa	aaaataatgg	taaaagagga	ttttctgaga	ctgttgatct	300
caaacctga	ctttcatcga	cggctatgga	ttcagtttcc	aaagtctgatt	tagagaaat	360
gaaggagaa	gtcgtaaacc	caccagccaa	ggcacaagtt	gtgggatggc	caccggtacg	420
atcttctcgc	aagaaacgtca	tgtccggcca	aaaaccgacc	accggaatg	ccaccgaagg	480
aaacgataag	acttctggca	cgagtggagc	cacctcatcc	gcctccgcgt	gtgccaccgt	540
ggcttatgtg	aaggttagca	tggacgggtg	accgtaccta	cggaaaaattg	acttgaaact	600
ctacaaaact	taccaagatc	tctccaacgc	cttaagcaaa	atgttttagct	cttttaccat	660
aggcaactat	ggaccacaag	gaatgaaga	tttcatgaat	gagagttaaa	tgatcgatct	720
tctaaacgga	tcagattatg	tccaacata	tgaagataaa	gatggcgact	ggatccttgt	780
aggagacgta	ccgtgggaga	tgtttgttta	ttcatgcaaa	cgtatacgaa	taatagaagg	840
atcagaagca	atcggaactg	ctccaaggcg	attagaaaaa	tgcaagaaca	gaagttagt	900
ctcgcagcac	attcttgttt	cttacctaaa	aaaggaaaga	agcctgtttc	gatcgtgttg	960
atatctcgaa	ccgagaaagc	taaacccggc	cgaaaatttt	gttcccgagca	aggagctttg	1020
ttataatatt	aattaataat	aatattaata	ttgtCggtg	attacatttt	aaaaaattaa	1080
atcgtttttg	ttatatgtat	tatatacata	tattaatatg	tatatattaat	taggttgcat	1140

(2) INFORMATION FOR SEQ ID NO:1301:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..298
(D) OTHER INFORMATION: / Ceres Seq. ID 1569580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:

Ph	Ser	Pro	Leu	Phe	Leu	Tyr	Thr	His	Leu	Thr	Ser	Pro	Tyr	Leu	Ser
1				5				10						15	
Leu	Ser	Ser	Asn	Val	Leu	Val	Pro	Gln	Lys	Asn	Ile	Lys	Arg	Thr	Lys
			20				25						30		
Arg	Lys	Thr	Leu	Glu	Ala	Glu	Glu	Ser	Pro	Thr	Arg	Cys	Arg	Ser	Asp
		35					40					45			
His	Leu	Thr	Asn	Tyr	Ser	Leu	Ile	Ile	Ile	Ile	Ser	Arg	Asn	Met	Ile
		50					55					60			
Asn	Phe	Glu	Ala	Thr	Glu	Leu	Arg	Leu	Gly	Leu	Pro	Gly	Gly	Asn	His
65				70					75					80	
Gly	Gly	Glu	Met	Ala	Gly	Lys	Asn	Asn	Gly	Lys	Arg	Gly	Phe	Ser	Glu
			85						90				95		
Thr	Val	Asp	Leu	Lys	Leu	Asn	Leu	Ser	Ser	Thr	Ala	Met	Asp	Ser	Val
			100					105					110		
Ser	Lys	Val	Asp	Leu	Glu	Asn	Met	Lys	Glu	Lys	Val	Val	Lys	Pro	Pro
		115					120						125		
Ala	Lys	Ala	Gln	Val	Val	Gly	Trp	Pro	Pro	Val	Arg	Ser	Phe	Arg	Lys
		130					135					140			
Asn	Val	Met	Ser	Gly	Gln	Lys	Pro	Thr	Thr	Gly	Asp	Ala	Thr	Glu	Gly
		145					150			155				160	
Asn	Asp	Lys	Thr	Ser	Gly	Ser	Ser	Gly	Ala	Thr	Ser	Ser	Ala	Ser	Ala
			165					170					175		
Cys	Ala	Thr	Val	Ala	Tyr	Val	Lys	Val	Ser	Met	Asp	Gly	Ala	Pro	Tyr
		180					185						190		
Leu	Arg	Lys	Ile	Asp	Leu	Lys	Leu	Tyr	Lys	Thr	Tyr	Gln	Asp	Leu	Ser

195	200	205
Asn Ala Leu Ser Lys Met Phe Ser Ser Phe Thr Ile Gly Asn Tyr Gly		
210	215	220
Pro Gln Gly Met Lys Asp Phe Met Asn Glu Ser Lys Leu Ile Asp Leu		
225	230	235
Leu Asn Gly Ser Asp Tyr Val Pro Thr Tyr Glu Asp Lys Asp Gly Asp		
245	250	255
Trp Met Leu Val Gly Asp Val Pro Trp Glu Met Phe Val Asp Ser Cys		
260	265	270
Lys Arg Ile Arg Ile Met Lys Gly Ser Glu Ala Ile Gly Leu Ala Pro		
275	280	285
Arg Ala Leu Glu Lys Cys Lys Asn Arg Ser		
290	295	

(2) INFORMATION FOR SEQ ID NO:1302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..236
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:

Met Ile Asn Phe Glu Ala Thr Glu Leu Arg Leu Gly Leu Pro Gly Gly	
1	5
Asn His Gly Gly Glu Met Ala Gly Lys Asn Asn Gly Lys Arg Gly Phe	
20	25
Ser Glu Thr Val Asp Leu Lys Leu Asn Leu Ser Ser Thr Ala Met Asp	
35	40
Ser Val Ser Lys Val Asp Leu Glu Asn Met Lys Glu Lys Val Val Lys	
50	55
Pro Pro Ala Lys Ala Gln Val Val Gly Trp Pro Val Arg Ser Phe	
65	70
Arg Lys Asn Val Met Ser Gly Gln Lys Pro Thr Thr Gly Asp Ala Thr	
85	90
Glu Gly Asn Asp Lys Thr Ser Gly Ser Ser Gly Ala Thr Ser Ser Ala	
100	105
Ser Ala Cys Ala Thr Val Ala Tyr Val Lys Val Ser Met Asp Gly Ala	
115	120
Pro Tyr Leu Arg Lys Ile Asp Leu Lys Leu Tyr Lys Thr Tyr Gln Asp	
130	135
Leu Ser Asn Ala Leu Ser Lys Met Phe Ser Ser Phe Thr Ile Gly Asn	
145	150
Tyr Gly Pro Gln Gly Met Lys Asp Phe Met Asn Glu Ser Lys Leu Ile	
165	170
Asp Leu Leu Asn Gly Ser Asp Tyr Val Pro Thr Tyr Glu Asp Lys Asp	
180	185
Gly Asp Trp Met Leu Val Gly Asp Val Pro Trp Glu Met Phe Val Asp	
195	200
Ser Cys Lys Arg Ile Arg Ile Met Lys Gly Ser Glu Ala Ile Gly Leu	
210	215
Ala Pro Arg Ala Leu Glu Lys Cys Lys Asn Arg Ser	
225	230
	235

(2) INFORMATION FOR SEQ ID NO:1303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

aaaaacatta	gttacagtcg	gaatttcgaa	aaaccccta	tcagctaaga	ggtgatcgtt	60
gattctaaaa	ctcgagtgat	gcagggaata	tggctcgatc	tactaaaagtt	tcttcctcgc	120
caggttcctc	ctctccgttc	ctcgacacca	tcgtcgcgat	taacaaagtc	catccgacgc	180
cttgtttgtc	ccccaaactc	gatatctgct	ctaaactcgc	gaaaactatt	gtttactgcc	240
tcacaattgt	gtctatccat	cgatttttgc	ttctccaaca	ctctgcgttc	tcacgcgaga	300
agctctctct	cggaaagctg	aggtgaaaat	ggtgttttgc	tagtgaaatt	agaggaagag	360
ttcatcaatg	catgagacaa	agctcaagat	ggatcttttc	catcggtctt	ctatttcaat	420
gcgcctgggt	gtggaccatg	cagggttttc	ttctctgtaa	tcgtggaagt	tagtaaaaaa	480
tatcccgatg	taactacgtg	taaaagctgc	attgatgagg	gcgggatttc	gaacatactc	540
acaagatgtg	atatacaggc	tgtgcccaaa	ctgcattttc	tcaaaagagg	ctcgaagcaa	600
ggcgaggttg	tgggtgcaga	tgtcagcaga	ctgaagaatc	tcattgaaac	gctctacaag	660
tgaagacctg	atccgtctca	gtaaaagaag	tgttgtaaat	tcgtcaagata	gtttaagaat	720
gaaattttga	aatacaatcta	aaaaataatg	attgcgtgaa	ccagcttctg	ctttgttccc	780
ccctcgttgt	tcaggaattg	aaattgccct	tgttttttgt	tgttttcttc	attctcttgc	840
cgcttaattt	ctcaagaatt	gtttgtgttc	ctgggtgaca	attctcaaaa	atatacgaca	900

gtcataactt tttatcaaaa ttttGsmcc

(2) INFORMATION FOR SEQ ID NO:1305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..194
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:

Met	Lys	Gly	Asn	Trp	Ser	Ile	Val	Arg	Lys	Val	Leu	His	Arg	Gln	Phe	
1			5						10					15		
Ser	Thr	Leu	Arg	Ser	Ser	Thr	Pro	Ser	Ser	Arg	Leu	Ser	Thr	Ser	Ile	
		20						25					30			
Arg	Pro	Leu	Val	Leu	Ala	Pro	Asn	Ser	Ile	Ser	Ser	Leu	Ile	Ala	Arg	
		35					40					45				
Asn	Ser	Leu	Phe	Thr	Ala	Ser	Asn	Ile	Gly	Pro	Ser	Ile	Asp	Phe	Asn	
	50					55				60						
Phe	Ser	Asn	Thr	Ser	Leu	Pro	His	Arg	Arg	Ser	Leu	Cys	Ser	Glu	Ala	
	65				70				75						80	
Gly	Gly	Glu	Asn	Gly	Val	Val	Leu	Val	Lys	Ser	Glu	Glu	Glu	Phe	Ile	
			85						90					95		
Asn	Ala	Met	Ser	Lys	Ala	Gln	Asp	Gly	Ser	Leu	Pro	Ser	Val	Phe	Tyr	
		100					105						110			
Phe	Thr	Ala	Ala	Trp	Cys	Gly	Pro	Cys	Arg	Phe	Ile	Ser	Pro	Val	Ile	
		115					120					125				
Val	Glu	Leu	Ser	Lys	Gln	Tyr	Pro	Asp	Val	Thr	Thr	Tyr	Lys	Val	Asp	
	130					135					140					
Ile	Asp	Glu	Gly	Gly	Ile	Ser	Asn	Thr	Ile	Ser	Lys	Leu	Asn	Ile	Thr	
	145				150				155					160		
Ala	Val	Pro	Thr	Leu	His	Phe	Phe	Lys	Gly	Ser	Lys	Gln	Gly	Glu		
		165						170					175			
Val	Val	Gly	Ala	Asp	Val	Thr	Lys	Leu	Lys	Asn	Leu	Met	Glu	Gln	Leu	
		180					185						190			
Tyr	Lys															

(2) INFORMATION FOR SEQ ID NO:1306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1340
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:

gccgcagagt	gttgatgctg	ttacgttttag	tactttgatg	aatgggtatc	ttcaggtttc	60
taagaaagcg	ttggcctttg	atttgttttag	gattatgaga	aaaagtgag	tggtcggttaa	120
tgtcagtacg	ttgcttagct	ttctttcggc	tattagtgat	ctaggagatt	tgctcggagc	180
agaatctgct	catgtgttat	gcatacaagt	tggccttgat	ttagacttgc	atttaatac	240
agctttgata	gggatgtacg	gcaaaactgg	gggtatcagt	tcagcacgca	ggatccttga	300
ttggcccat	cgaaaggatg	tgtttacatg	gaactgtatg	atagaccaat	atgccaaaac	360
gggtctcctt	gaagagtgtg	tatggctact	gaggcagatg	aagtatga	aaatgaaac	420
gaattcatct	acgtttgttg	ctgtgtgttc	ttcctgtgcg	tacagtgaag	cagcatctgt	480
aggacgtact	gttTgctgat	ctattggaag	aggaagaagt	agctttggat	gcaatactgt	540
gaactgcact	cgttgatatg	tatgcataag	taggattgct	tgaaaaagct	gttgagattt	600

tcaatagaat	gaagcataag	gatgtaaaagt	cctggaccgc	gatgatctcg	ggttatggag	660
ctcatggagt	agcaagagaa	gcagtaacac	tattcaataa	gatggaggaa	gagaactgca	720
aagtggagacc	caatgagatt	acctctcttg	ttgtgctgaa	tgcttttagc	catggagggt	780
tggtaatgga	aggaatcaga	tgcttttaaga	ggatggttga	ggcttacacg	ttcacgcccc	840
aagttgaaca	tatatgttgt	gtggttgatc	ttttaggtcg	agcggggcag	tttagaggaa	900
cgtatgagtt	aataaggaac	ttaccgatca	caagtgaattc	aacgggtctgg	cgtgctctgc	960
tagctgcttg	tagagtatac	gggaatgcag	atttggggga	aagtgtgatg	atgagattgg	1020
ctgaaatggg	tgagacacat	cggcagatg	caattcttct	agctggggaca	cacgctggtg	1080
cagggaaccc	acaaaaatca	ttagataatg	agttgaataa	agggagaaaa	gaagctggat	1140
acagcgccat	tgaatataga	tagagttagc	aatctctgac	gttcattcac	ctctgacctt	1200
ttgtttgaaa	actatatcag	caaaatgttg	ttcaataaag	taaacccctg	tatttactct	1260
ttctttatgc	tttaaaacag	taacttatgt	ataaagaaag	gagacaattg	atcttaattga	1320

aacagttttg atggattgtg

(2) INFORMATION FOR SEQ ID NO:1307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..201
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:

Met	Tyr	Ala	Lys	Val	Gly	Leu	Leu	Glu	Lys	Ala	Val	Glu	Ile	Phe	Asn
1			5					10						15	
Arg	Met	Lys	Asp	Lys	Asp	Val	Lys	Ser	Trp	Thr	Ala	Met	Ile	Ser	Gly
		20					25						30		
Tyr	Gly	Ala	His	Gly	Leu	Ala	Arg	Glu	Ala	Val	Thr	Leu	Phe	Asn	Lys
		35					40					45			
Met	Glu	Glu	Glu	Asn	Cys	Lys	Val	Arg	Pro	Asn	Glu	Ile	Thr	Phe	Leu
		50					55				60				
Val	Val	Leu	Asn	Ala	Cys	Ser	His	Gly	Gly	Leu	Val	Met	Glu	Gly	Ile
		65					70				75				80
Arg	Cys	Phe	Lys	Arg	Met	Val	Glu	Ala	Tyr	Ser	Phe	Thr	Pro	Lys	Val
			85						90					95	
Glu	His	Tyr	Gly	Cys	Val	Val	Asp	Leu	Leu	Gly	Arg	Ala	Gly	Gln	Leu
			100					105						110	
Glu	Glu	Ala	Tyr	Glu	Leu	Ile	Arg	Asn	Leu	Pro	Ile	Thr	Ser	Asp	Ser
			115				120						125		
Thr	Ala	Trp	Arg	Ala	Leu	Leu	Ala	Ala	Cys	Arg	Val	Tyr	Gly	Asn	Ala
		130					135					140			
Asp	Leu	Gly	Glu	Ser	Val	Met	Met	Arg	Leu	Ala	Glu	Met	Gly	Glu	Thr
			145				150					155			160
His	Pro	Ala	Asp	Ala	Ile	Leu	Leu	Ala	Gly	Thr	His	Ala	Val	Ala	Gly
			165						170					175	
Asn	Pro	Gln	Lys	Ser	Leu	Asp	Asn	Glu	Leu	Asn	Lys	Gly	Arg	Lys	Glu
			180					185						190	
Ala	Gly	Tyr	Ser	Ala	Ile	Glu	Ile	Glu							
			195				200								

(2) INFORMATION FOR SEQ ID NO:1308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..184

(D) OTHER INFORMATION: / Ceres Seq. ID 1569587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:

Met	Lys	Asp	Lys	Asp	Val	Lys	Ser	Trp	Thr	Ala	Met	Ile	Ser	Gly	Tyr
1			5					10						15	
Gly	Ala	His	Gly	Leu	Ala	Arg	Glu	Ala	Val	Thr	Leu	Phe	Asn	Lys	Met
			20				25						30		
Glu	Glu	Glu	Asn	Cys	Lys	Val	Arg	Pro	Asn	Glu	Ile	Thr	Phe	Leu	Val
			35				40					45			
Val	Leu	Asn	Ala	Cys	Ser	His	Gly	Gly	Leu	Val	Met	Glu	Gly	Ile	Arg
			50			55					60				
Cys	Phe	Lys	Arg	Met	Val	Glu	Ala	Tyr	Ser	Phe	Thr	Pro	Lys	Val	Glu
65					70				75					80	
His	Tyr	Gly	Cys	Val	Val	Asp	Leu	Leu	Gly	Arg	Ala	Gly	Gln	Leu	Glu
				85					90				95		
Glu	Ala	Tyr	Glu	Leu	Ile	Arg	Asn	Leu	Pro	Ile	Thr	Ser	Asp	Ser	Thr
				100			105						110		
Ala	Trp	Arg	Ala	Leu	Leu	Ala	Ala	Cys	Arg	Val	Tyr	Gly	Asn	Ala	Asp
			115			120						125			
Leu	Gly	Glu	Ser	Val	Met	Met	Arg	Leu	Ala	Glu	Met	Gly	Glu	Thr	His
			130			135					140				
Pro	Ala	Asp	Ala	Ile	Leu	Leu	Ala	Gly	Thr	His	Ala	Val	Ala	Gly	Asn
145					150				155					160	
Pro	Gln	Lys	Ser	Leu	Asp	Asn	Glu	Leu	Asn	Lys	Gly	Arg	Lys	Glu	Ala
				165			170							175	
Gly	Tyr	Ser	Ala	Ile	Glu	Ile	Glu								
				180											

(2) INFORMATION FOR SEQ ID NO:1309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1569588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:

Met	Ile	Ser	Gly	Tyr	Gly	Ala	His	Gly	Leu	Ala	Arg	Glu	Ala	Val	Thr
1			5					10						15	
Leu	Phe	Asn	Lys	Met	Glu	Glu	Glu	Asn	Cys	Lys	Val	Arg	Pro	Asn	Glu
			20					25					30		
Ile	Thr	Phe	Leu	Val	Val	Leu	Asn	Ala	Cys	Ser	His	Gly	Gly	Leu	Val
			35			40					45				
Met	Glu	Gly	Ile	Arg	Cys	Phe	Lys	Arg	Met	Val	Glu	Ala	Tyr	Ser	Phe
			50			55					60				
Thr	Pro	Lys	Val	Glu	His	Tyr	Gly	Cys	Val	Val	Asp	Leu	Leu	Gly	Arg
65					70				75					80	
Ala	Gly	Gln	Leu	Glu	Glu	Ala	Tyr	Glu	Leu	Ile	Arg	Asn	Leu	Pro	Ile
			85					90					95		
Thr	Ser	Asp	Ser	Thr	Ala	Trp	Arg	Ala	Leu	Leu	Ala	Ala	Cys	Arg	Val
			100				105					110			
Tyr	Gly	Asn	Ala	Asp	Leu	Gly	Glu	Ser	Val	Met	Met	Arg	Leu	Ala	Glu
			115			120						125			
Met	Gly	Glu	Thr	His	Pro	Ala	Asp	Ala	Ile	Leu	Leu	Ala	Gly	Thr	His
			130			135					140				
Ala	Val	Ala	Gly	Asn	Pro	Gln	Lys	Ser	Leu	Asp	Asn	Glu	Leu	Asn	Lys
145					150				155					160	
Gly	Arg	Lys	Glu	Ala	Gly	Tyr	Ser	Ala	Ile	Glu	Ile	Glu			
				165					170						

(2) INFORMATION FOR SEQ ID NO:1310:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1666 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1666

(D) OTHER INFORMATION: / Ceres Seq. ID 1569589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310:

```

aaatataatt tcaacgacgt gctctctttt cttctccgca tctctctccc gccgagtgaa    60
gccgcgactg tgaatcatgt agaggagtaa aacgcgcgcc catctccgaa tcgaatgact    120
ctccccttaa gaatgcaaaa ccgggtgggg gaatctcttt ttgtactcag aagaatgtgg    180
ccccgatgca gcagagtcga ttaacatcag catcatgtga taaacagagg gctgagttag    240
ctaggaaagca tgtgagactt cttataaacc aattttgtaa ttgggtgcag ttacagctga    300
agaatcatcc tgaatgaact tgggaagatg ggatgaatga ctacattacg catgcttcaa    360
acattcttga aaagttttaa gatgtggtca gctggcttaa agaaaaataa ggaaaggggg    420
agaattttat ccctgaatct cgtggagcag aaaagaaatt agtggctgaa gtcaaagata    480
ccaatgttaa atcattttca aacaatatct cttttgcttc aaacaataca cctgggactt    540
tctcaaaaac tcaatcttcc gatttttcca gtatgcagtc tggtttcttt tcaagccaat    600
ctggagcatt ctccagcagt cttctcgttt taatatccaa tagccagact ggatctttta    660
gcagtgccca gttttgtacg acaaaaagca gccaaaccaag cctatttttc ggcagtcaga    720
ccggagcaat ctcttaagtc caacctggaa ctttctccag cagtctctct ggtataaacat    780
ctaatagcca gacgggatct tttagtgtg gccaatattg tcagacaaaa agcagccaac    840
caagcctact ttccggcagt caagcaggag taatctctag tagccaacct tcttttcaat    900
tttctaaacg tcaatccccct ttacatctcg cagtacctcc agtgtccata ccggcaaaag    960
aggatcactc agatgatgcg gatgtgtgag acgaacaatc tcacccgagc agccactctg    1020
tcaaaaagac ggaagaaaaa ggtattactg tggttcatga agtcaaatgc aaactttatg    1080
tcaagtcaag tgaccacgca gataaaaggt ggaagactgg aaactctaca    1140
taaatgtcaa agaaggagtc gacaaggagg caaaagaatc aaaaaccaca attcttgtcc    1200
gaaaagatgt tggaaaaact cttctgtaat cactactgta cgtctggaat agacaagacc    1260
cacagaagaa cgctcttgtt gcaatatctt actcctcgga tgattccaac gagaatgtaa    1320
caccgagaac ctttctgata aggacaaaag acgcagaagc tagagataat tttagcaacg    1380
ccatccaaga atacgcccct tcttcataga ttgcccraag ccaggttgag atcttctact    1440
taacttttaa aagccttatc gactcgtcct ctctctatat ttttttctct atttgtaata    1500
ttaggaaggg tcttaagact aacgtaaaag ttgataaagg gcacaaaaat gttgtatgat    1560
tgtgagagag agagaggggc aaaggagttc gtatgcttat agagaatgtt gtgccaatct    1620
tctttgtaac ttaaaaaaca gaacaataaa aatcacttct ttttat

```

(2) INFORMATION FOR SEQ ID NO:1311:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 443 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..443

(D) OTHER INFORMATION: / Ceres Seq. ID 1569590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311:

```

Met Arg Gly Val Lys Arg Ala Ala Ile Ser Glu Ser Asn Asp Ser Pro
1           5           10           15
Phe Lys Asn Ala Lys Pro Val Gly Gly Ile Phe Phe Gly Thr Gln Lys
20           25           30
Asn Val Ala Pro Met Gln Gln Ser Pro Leu Thr Ser Ala Ser Leu Asp
35           40           45
Lys Gln Arg Ala Glu Leu Ala Arg Lys His Val Arg Ala Leu Asn Asn
50           55           60
Gln Phe Val Ser Trp Val Gln Leu Gln Leu Lys Asn His Pro Asp Glu
65           70           75           80

```

Leu Trp Glu Asp Gly Met Asn Asp Tyr Ile Thr His Ala Ser Asn Ile
85 90 95
Leu Glu Lys Phe Lys Asp Val Val Ser Trp Leu Lys Glu Asn Lys Gly
100 105 110
Lys Gly Glu Asn Leu Ser Pro Glu Ser Arg Gly Ala Glu Lys Lys Leu
115 120 125
Val Ala Glu Val Lys Asn Thr Asn Val Lys Ser Phe Ser Asn Asn Ile
130 135 140
Pro Phe Ala Ser Asn Asn Gln Pro Gly Ile Phe Ser Asn Asn Gln Ser
145 150 155 160
Ser Asp Phe Ser Ser Ser Gln Ser Gly Phe Phe Ser Ser Gln Ser Gly
165 170 175
Ala Phe Ser Ser Ser Pro Ser Gly Leu Ile Ser Asn Ser Gln Thr Gly
180 185 190
Ser Phe Ser Ser Gly Gln Phe Gly Thr Thr Lys Ser Ser Gln Pro Ser
195 200 205
Leu Phe Ser Gly Ser Gln Ala Gly Ala Ile Ser Asn Ser Gln Pro Gly
210 215 220
Thr Phe Ser Ser Ser Pro Ser Gly Ile Thr Ser Asn Ser Gln Thr Gly
225 230 235 240
Ser Phe Ser Ser Gly Gln Phe Gly Gln Thr Lys Ser Ser Gln Pro Ser
245 250 255
Leu Leu Ser Gly Ser Gln Ala Gly Val Ile Ser Ser Ser Gln Pro Ser
260 265 270
Phe Gln Phe Ser Asn Ser Gln Ser Pro Phe Thr Ser Ala Val Pro Pro
275 280 285
Val Ser Ile Pro Ala Lys Gln Asp His Ser Asp Asp Ala Asp Gly Gly
290 295 300
Asp Glu Gln Ser Gln Pro Ser Ser Pro Ser Val Lys Lys Thr Glu Glu
305 310 315 320
Lys Gly Ile Thr Val Val His Glu Val Lys Cys Lys Leu Tyr Val Lys
325 330 335
Ser Ser Asp Pro Ala Asp Lys Gly Trp Lys Asp Lys Gly Thr Gly Asn
340 345 350
Leu Tyr Ile Lys Cys Lys Glu Gly Val Asp Lys Gly Thr Lys Glu Ser
355 360 365
Lys Pro Thr Ile Leu Val Arg Asn Asp Val Gly Lys Leu Leu Asn
370 375 380
Ala Leu Leu Tyr Ala Gly Met Lys Thr Ser Pro Gln Lys Asn Ala Leu
385 390 395 400
Val Ala Ile Phe His Ser Ser Asp Asp Ser Asn Glu Asn Val Thr Pro
405 410 415
Arg Thr Phe Leu Ile Arg Thr Lys Asn Ala Glu Ala Arg Asp Asn Leu
420 425 430
Ala Thr Ala Ile Gln Glu Tyr Ala Pro Ser Ser
435 440

(2) INFORMATION FOR SEQ ID NO:1312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..407
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312:

Met Gln Gln Ser Pro Leu Thr Ser Ala Ser Leu Asp Lys Gln Arg Ala
1 5 10 15
Glu Leu Ala Arg Lys His Val Arg Ala Leu Asn Asn Gln Phe Val Ser

	20		25		30	
Trp Val Gln Leu Gln Leu Lys Asn His Pro Asp Glu Leu Trp Glu Asp						
	35		40		45	
Gly Met Asn Asp Tyr Ile Thr His Ala Ser Asn Ile Leu Glu Lys Phe						
	50		55		60	
Lys Asp Val Val Ser Trp Leu Lys Glu Asn Lys Gly Lys Gly Glu Asn						
	65		70		75	
Leu Ser Pro Glu Ser Arg Gly Ala Glu Lys Lys Leu Val Ala Glu Val						
		85	90		95	
Lys Asn Thr Asn Val Lys Ser Phe Ser Asn Asn Ile Pro Phe Ala Ser						
	100		105		110	
Asn Asn Gln Pro Gly Ile Phe Ser Asn Asn Gln Ser Ser Asp Phe Ser						
	115		120		125	
Ser Ser Gln Ser Gly Phe Phe Ser Ser Gln Ser Gly Ala Phe Ser Ser						
	130		135		140	
Ser Pro Ser Gly Leu Ile Ser Asn Ser Gln Thr Gly Ser Phe Ser Ser						
	145		150		155	
Gly Gln Phe Gly Thr Thr Lys Ser Ser Gln Pro Ser Leu Phe Ser Gly						
		165	170		175	
Ser Gln Ala Gly Ala Ile Ser Asn Ser Gln Pro Gly Thr Phe Ser Ser						
	180		185		190	
Ser Pro Ser Gly Ile Thr Ser Asn Ser Gln Thr Gly Ser Phe Ser Ser						
	195		200		205	
Gly Gln Phe Gly Gln Thr Lys Ser Ser Gln Pro Ser Leu Leu Ser Gly						
	210		215		220	
Ser Gln Ala Gly Val Ile Ser Ser Ser Gln Pro Ser Phe Gln Phe Ser						
	225		230		235	
Asn Ser Gln Ser Pro Phe Thr Ser Ala Val Pro Pro Val Ser Ile Pro						
		245	250		255	
Ala Lys Gln Asp His Ser Asp Asp Ala Asp Gly Gly Asp Glu Gln Ser						
	260		265		270	
Gln Pro Ser Ser Pro Ser Val Lys Lys Thr Glu Glu Lys Gly Ile Thr						
	275		280		285	
Val Val His Glu Val Lys Cys Lys Leu Tyr Val Lys Ser Ser Asp Pro						
	290		295		300	
Ala Asp Lys Gly Trp Lys Asp Lys Gly Thr Gly Asn Leu Tyr Ile Lys						
	305		310		315	
Cys Lys Glu Gly Val Asp Lys Gly Thr Lys Glu Ser Lys Pro Thr Ile						
		325	330		335	
Leu Val Arg Asn Asp Val Gly Lys Leu Leu Leu Asn Ala Leu Leu Tyr						
	340		345		350	
Ala Gly Met Lys Thr Ser Pro Gln Lys Asn Ala Leu Val Ala Ile Phe						
	355		360		365	
His Ser Ser Asp Asp Ser Asn Glu Asn Val Thr Pro Arg Thr Phe Leu						
	370		375		380	
Ile Arg Thr Lys Asn Ala Glu Ala Arg Asp Asn Leu Ala Thr Ala Ile						
	385		390		395	
Gln Glu Tyr Ala Pro Ser Ser					400	
		405				

(2) INFORMATION FOR SEQ ID NO:1313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..358
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313:

Met Asn Asp Tyr Ile Thr His Ala Ser Asn Ile Leu Glu Lys Phe Lys
1 5 10 15
Asp Val Val Ser Trp Leu Lys Glu Asn Lys Gly Lys Gly Glu Asn Leu
20 25 30
Ser Pro Glu Ser Arg Gly Ala Glu Lys Lys Leu Val Ala Glu Val Lys
35 40 45
Asn Thr Asn Val Lys Ser Phe Ser Asn Asn Ile Pro Phe Ala Ser Asn
50 55 60
Asn Gln Pro Gly Ile Phe Ser Asn Asn Gln Ser Ser Asp Phe Ser Ser
65 70 75 80
Ser Gln Ser Gly Phe Phe Ser Ser Gln Ser Gly Ala Phe Ser Ser Ser
85 90 95
Pro Ser Gly Leu Ile Ser Asn Ser Gln Thr Gly Ser Phe Ser Ser Gly
100 105 110
Gln Phe Gly Thr Thr Lys Ser Ser Gln Pro Ser Leu Phe Ser Gly Ser
115 120 125
Gln Ala Gly Ala Ile Ser Asn Ser Gln Pro Gly Thr Phe Ser Ser Ser
130 135 140
Pro Ser Gly Ile Thr Ser Asn Ser Gln Thr Gly Ser Phe Ser Ser Gly
145 150 155 160
Gln Phe Gly Gln Thr Lys Ser Ser Gln Pro Ser Leu Leu Ser Gly Ser
165 170 175
Gln Ala Gly Val Ile Ser Ser Ser Gln Pro Ser Phe Gln Phe Ser Asn
180 185 190
Ser Gln Ser Pro Phe Thr Ser Ala Val Pro Pro Val Ser Ile Pro Ala
195 200 205
Lys Gln Asp His Ser Asp Asp Ala Asp Gly Gly Asp Glu Gln Ser Gln
210 215 220
Pro Ser Ser Pro Ser Val Lys Lys Thr Glu Glu Lys Gly Ile Thr Val
225 230 235 240
Val His Glu Val Lys Cys Lys Leu Tyr Val Lys Ser Ser Asp Pro Ala
245 250 255
Asp Lys Gly Trp Lys Asp Lys Gly Thr Gly Asn Leu Tyr Ile Lys Cys
260 265 270
Lys Glu Gly Val Asp Lys Gly Thr Lys Glu Ser Lys Pro Thr Ile Leu
275 280 285
Val Arg Asn Asp Val Gly Lys Leu Leu Asn Ala Leu Leu Tyr Ala
290 295 300
Gly Met Lys Thr Ser Pro Gln Lys Asn Ala Leu Val Ala Ile Phe His
305 310 315 320
Ser Ser Asp Asp Ser Asn Glu Asn Val Thr Pro Arg Thr Phe Leu Ile
325 330 335
Arg Thr Lys Asn Ala Glu Ala Arg Asp Asn Leu Ala Thr Ala Ile Gln
340 345 350
Glu Tyr Ala Pro Ser Ser
355

(2) INFORMATION FOR SEQ ID NO:1314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1306
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314:

aaccacaag aagaatccaa agacatgaaa cttctcttta ttgtctcat cttctttctt	60
tcctctctcc aagcatcaaa aggattcgat ttgcacgaaa aagaattaga aaccgaagag	120
aacctatgga agctctatga gaggtggaga gggccaccact ctgtatccCa gagcttctca	180

tgaggcaata	aagcgggttca	acgttttttag	acacaatgtc	cttcgatgtcc	acaggactaa	240
caagaagaac	aagcctttaca	aactcaagat	caatagattc	gccgcacaacg	caccacgagt	300
ttagaagctc	ctacgctggc	ttaaatgtta	agcatcaccg	aatgcttctg	ggaccgaagc	360
cgggatctgg	tggtttcatg	tatgagaatg	tgaccagagt	tcgaggttct	gttgattggc	420
gagagaaagg	agctgtcaat	gaagtcaaga	atcaacagg	ttgtggaaat	tgctggcgct	480
tttcgacggt	tgacgacgtg	gaagggataa	acaagatcgg	aacaacaaaa	ctagtttcat	540
tgtctgaaca	agagcttgtg	gattgtgaca	ctgaagagaa	tcaaggttgt	gcaggaggct	600
tcattggaac	tgcgtttgaa	tttataaaga	acaatggtgg	catcaaaaac	gaagagactt	660
atcccttaag	ttccagtgac	gttcaattct	gtagagctaa	gagtatgtgt	ggagaaactg	720
taaccatoga	tggaacagaa	cacgtccctg	agaatgatga	ggaagaactt	ctcaaaagctg	780
ttgctcacca	gcctgtctct	gtagctattg	atgctgggag	ctcagatttc	cagctttact	840
ctgaggggtg	gtttatcgga	gaatcgggga	ctcagttgaa	ccacgggggtg	gtgattgttg	900
ggtatggaga	gaccaaaaat	ggaacaaaat	attggatagt	aaggaaactca	tggggacgtg	960
aatggggaga	agggagctat	gttcggatag	aaagaggaat	atcgagaaat	gaaggacggt	1020
gcggtatagc	catggaggct	tcttatccca	ccaagctctc	ttcgactcct	tctactcatg	1080
agtcagtagt	tcgtgatgat	gttaaagacg	agctctagag	actttaagtc	attgaaaact	1140
gaatttcgaa	ccattctctt	agtgcgctta	cactgagttt	attattttaa	tggtattgag	1200
ttcattgggt	tcaattttaca	catctatcgt	gtattcatct	taagtttgaga	cgatttttat	1260
ctccttgtaa	tattggccag	catttgcctt	gcggaaaaat	ggcggtt		

(2) INFORMATION FOR SEQ ID NO:1315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..300

(D) OTHER INFORMATION: / Ceres Seq. ID 1569604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:

Met	Ser	Phe	Met	Ser	Thr	Gly	Leu	Thr	Arg	Arg	Thr	Ser	Leu	Thr	Asn
1			5					10					15		
Ser	Arg	Ser	Ile	Asp	Ser	Pro	Thr	Thr	His	His	Glu	Phe	Arg	Ser	Ser
			20					25					30		
Tyr	Ala	Gly	Ser	Asn	Val	Lys	His	His	Arg	Met	Leu	Arg	Gly	Pro	Lys
			35				40					45			
Arg	Gly	Ser	Gly	Gly	Phe	Met	Tyr	Glu	Asn	Val	Thr	Arg	Val	Pro	Ser
			50				55					60			
Ser	Val	Asp	Trp	Arg	Glu	Lys	Gly	Ala	Val	Thr	Glu	Val	Lys	Asn	Gln
			65				70				75			80	
Gln	Asp	Cys	Gly	Ser	Cys	Trp	Ala	Phe	Ser	Thr	Val	Ala	Ala	Val	Glu
			85						90				95		
Gly	Ile	Asn	Lys	Ile	Gly	Thr	Asn	Lys	Leu	Val	Ser	Leu	Ser	Glu	Gln
			100				105					110			
Glu	Leu	Val	Asp	Cys	Asp	Thr	Glu	Glu	Asn	Gln	Gly	Cys	Ala	Gly	Gly
			115				120					125			
Leu	Met	Glu	Pro	Ala	Phe	Glu	Phe	Ile	Lys	Asn	Asn	Gly	Gly	Ile	Lys
			130				135					140			
Thr	Glu	Glu	Thr	Tyr	Pro	Tyr	Asp	Ser	Ser	Asp	Val	Gln	Phe	Cys	Arg
			145				150				155			160	
Ala	Lys	Ser	Ile	Gly	Gly	Glu	Thr	Val	Thr	Ile	Asp	Gly	His	Glu	His
			165						170				175		
Val	Pro	Glu	Asn	Asp	Glu	Glu	Glu	Leu	Lys	Ala	Val	Ala	His	Gln	
			180						185				190		
Pro	Val	Ser	Val	Ala	Ile	Asp	Ala	Gly	Ser	Ser	Asp	Phe	Gln	Leu	Tyr
			195				200					205			
Ser	Glu	Gly	Val	Phe	Ile	Gly	Glu	Cys	Gly	Thr	Gln	Leu	Asn	His	Gly
			210				215					220			
Val	Val	Ile	Val	Gly	Tyr	Gly	Glu	Thr	Lys	Asn	Gly	Thr	Lys	Tyr	Trp
			225				230				235				

Ile	Val	Arg	Asn	Ser	Trp	Gly	Pro	Glu	Trp	Gly	Glu	Gly	Gly	Tyr	Val
			245						250					255	
Arg	Ile	Glu	Arg	Gly	Ile	Ser	Glu	Asn	Glu	Gly	Arg	Cys	Gly	Ile	Ala
			260					265					270		
Met	Glu	Ala	Ser	Tyr	Pro	Thr	Lys	Leu	Ser	Ser	Thr	Pro	Ser	Thr	His
			275				280					285			
Glu	Ser	Val	Val	Arg	Asp	Asp	Val	Lys	Asp	Glu	Leu				
			290			295					300				

(2) INFORMATION FOR SEQ ID NO:1316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..297

(D) OTHER INFORMATION: / Ceres Seq. ID 1569605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

Met	Ser	Thr	Gly	Leu	Thr	Arg	Arg	Thr	Ser	Leu	Thr	Asn	Ser	Arg	Ser
1				5				10						15	
Ile	Asp	Ser	Pro	Thr	Thr	His	His	Glu	Phe	Arg	Ser	Ser	Ser	Tyr	Gly
			20					25						30	
Ser	Asn	Val	Lys	His	His	Arg	Met	Leu	Arg	Gly	Pro	Lys	Arg	Gly	Ser
			35				40					45			
Gly	Gly	Phe	Met	Tyr	Glu	Asn	Val	Thr	Arg	Val	Pro	Ser	Ser	Val	Asp
			50			55					60				
Trp	Arg	Glu	Lys	Gly	Ala	Val	Thr	Glu	Val	Lys	Asn	Gln	Gln	Asp	Cys
			65			70				75				80	
Gly	Ser	Cys	Trp	Ala	Phe	Ser	Thr	Val	Ala	Ala	Val	Glu	Gly	Ile	Asn
			85						90					95	
Lys	Ile	Gly	Thr	Asn	Lys	Leu	Val	Ser	Leu	Ser	Glu	Gln	Glu	Leu	Val
			100				105						110		
Asp	Cys	Asp	Thr	Glu	Glu	Asn	Gln	Gly	Cys	Ala	Gly	Gly	Leu	Met	Glu
			115				120					125			
Pro	Ala	Phe	Glu	Phe	Ile	Lys	Asn	Asn	Gly	Gly	Ile	Lys	Thr	Glu	Glu
			130				135					140			
Thr	Tyr	Pro	Tyr	Asp	Ser	Ser	Asp	Val	Gln	Phe	Cys	Arg	Ala	Lys	Ser
			145			150				155				160	
Ile	Gly	Gly	Glu	Thr	Val	Thr	Ile	Asp	Gly	His	Glu	His	Val	Pro	Glu
			165					170						175	
Asn	Asp	Glu	Glu	Glu	Leu	Leu	Lys	Ala	Val	Ala	His	Gln	Pro	Val	Ser
			180				185						190		
Val	Ala	Ile	Asp	Ala	Gly	Ser	Ser	Asp	Phe	Gln	Leu	Tyr	Ser	Glu	Gly
			195				200					205			
Val	Phe	Ile	Gly	Glu	Cys	Gly	Thr	Gln	Leu	Asn	His	Gly	Val	Val	Ile
			210			215					220				
Val	Gly	Tyr	Gly	Glu	Thr	Lys	Asn	Gly	Thr	Lys	Tyr	Trp	Ile	Val	Arg
			225			230				235				240	
Asn	Ser	Trp	Gly	Pro	Glu	Trp	Gly	Glu	Gly	Gly	Tyr	Val	Arg	Ile	Glu
			245				250							255	
Arg	Gly	Ile	Ser	Glu	Asn	Glu	Gly	Arg	Cys	Gly	Ile	Ala	Met	Glu	Ala
			260				265						270		
Ser	Tyr	Pro	Thr	Lys	Leu	Ser	Ser	Thr	Pro	Ser	Thr	His	Glu	Ser	Val
			275				280					285			
Val	Arg	Asp	Asp	Val	Lys	Asp	Glu	Leu							
			290			295									

(2) INFORMATION FOR SEQ ID NO:1317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..258
(D) OTHER INFORMATION: / Ceres Seq. ID 1569606
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

```
Met Leu Arg Gly Pro Lys Arg Gly Ser Gly Phe Met Tyr Glu Asn
1      5      10      15
Val Thr Arg Val Pro Ser Ser Val Asp Trp Arg Glu Lys Gly Ala Val
20      25      30
Thr Glu Val Lys Asn Gln Gln Asp Cys Gly Ser Cys Trp Ala Phe Ser
35      40      45
Thr Val Ala Ala Val Glu Gly Ile Asn Lys Ile Gly Thr Asn Lys Leu
50      55      60
Val Ser Leu Ser Glu Gln Glu Leu Val Asp Cys Asp Thr Glu Glu Asn
65      70      75      80
Gln Gly Cys Ala Gly Gly Leu Met Glu Pro Ala Phe Glu Phe Ile Lys
85      90      95
Asn Asn Gly Gly Ile Lys Thr Glu Glu Thr Tyr Pro Tyr Asp Ser Ser
100      105      110
Asp Val Gln Phe Cys Arg Ala Lys Ser Ile Gly Gly Glu Thr Val Thr
115      120      125
Ile Asp Gly His Glu His Val Pro Glu Asn Asp Glu Glu Leu Leu
130      135      140
Lys Ala Val Ala His Gln Pro Val Ser Val Ala Ile Asp Ala Gly Ser
145      150      155      160
Ser Asp Phe Gln Leu Tyr Ser Glu Gly Val Phe Ile Gly Glu Cys Gly
165      170      175
Thr Gln Leu Asn His Gly Val Val Ile Val Gly Tyr Gly Glu Thr Lys
180      185      190
Asn Gly Thr Lys Tyr Trp Ile Val Arg Asn Ser Trp Gly Pro Glu Trp
195      200      205
Gly Glu Gly Gly Tyr Val Arg Ile Glu Arg Gly Ile Ser Glu Asn Glu
210      215      220
Gly Arg Cys Gly Ile Ala Met Glu Ala Ser Tyr Pro Thr Lys Leu Ser
225      230      235      240
Ser Thr Pro Ser Thr His Glu Ser Val Val Arg Asp Asp Val Lys Asp
245      250      255
Glu Leu
```

(2) INFORMATION FOR SEQ ID NO:1318:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2081 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..2081
(D) OTHER INFORMATION: / Ceres Seq. ID 1569611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:

```
aaaagcttct tcacatcagg agaagcaagg atgtgagatc gaagctttgag atattgatta      60
caacatcttt gtaaggaaga ttaatgttaa tccctttgga ctcttttaggc ggaaccgcg      120
gcgggaagct gaccagccgg taaagacaga ggaagagtca ttgaagctag aggatgaaac      180
cggttaacaaa gtcaagcatg tactaaaagg agtgacttgc agagcccaac catgggaagat      240
tcttgctatt gttggcccaa gtggtgcagg gaagtctgtc ttgcttgaaa ttctagtctg      300
tagactcatc cctcaaaccc ggtcgggtta tgtcaacaag agccccggtg atagagccaa      360
```

```

tttcaagaaa atctctgtgtt atgtcactca gaaggatact ctgtttccct tgcttacggg 420
ggaggaaacc ctctctgttca gtgctaagct gcgtttaaag ctccctcgag atgaactcgag 480
atocacgggtt aagtcttttg tccatgagct tgggcttgaa gctgttgcca cggctcgtgt 540
tgggcgtgat agtgcagag gtatatcggt tgagagagaga cgtcgtgtct ccatgaggat 600
tgaagtattt cagcaccccta aagtcttgat ccttgatgag ccaacctctg gtcttgatag 660
tacttcgggt ctgctgatca tagacatgct caaacacatg gctgaaacac gaggcaggac 720
cataattctt actatccacc aaccgggatt tcggtatgct aaacagtcca atctctgttt 780
cttgttggtt aatggctcga ccttgaagca ggggtcggtg gatcagcttg ggtttactt 840
aaggtcaaat gggttgaccc ctctcttcca tgaataacatc gttgaatttg ccatggaatc 900
aatcgaaatc atcacaataac agcaacgggt acaggaaagc agaagagcag ctcagtctct 960
aacacacaaa acaacattac aagagaagag atcagaagat atcgaagggg agagcaaaag 1020
tgggcaatac acactacaac agctgtttca acaacaaggt gtgcgtgatg taggaacagt 1080
gaacatagca acagagtcca caagagattt tgcaaatcca agattagaag aaactatgat 1140
actcacacat aggtttctcca agaacatttt cagaaccaag gagctttttg cgtgcaggac 1200
ggttcagatg tttaggttcag gaattgtctt agtctgtatt ttcataatct caaagacgat 1260
ttaaaagggt cgcgagaaaag agtcggcctc ttgtcattca tattgacctt tctgctaact 1320
tcgacaatag aggcactccc tataattctg caagaaagag agattctgat gaaggagacc 1380
tctagtggaa gctacagagt gtctctatct gcgcgtcgta atggactagt ttacttgcca 1440
tttctgtcca tcttagctat tctattctca accccagtg actggctggt gggactgaac 1500
cccagtttca tggcgtttct acacttttct ctctcattt ggttaactct ctacacagca 1560
aactcgggtg ttgtgtgctt tagtgcactg gttcctaatt tcatagttg aaactcagtg 1620
atctccgggt tgatgggttg ctctttttgt ttctccgggt actcattatc gaacctatgt 1680
atccctgggt actggatttt catgcactac atctcctgt tcaagtaccg gttcgaagga 1740
tttctgatta acgagttctt aaaatcaaac aagtgttttg agtatggatt cggaaaatgt 1800
ttgtgtgacg agaggagatt actcaagaa gaaaggtacg gaaggaaag tagatgaga 1860
aatgttgtga tcatgctatg ttttgtctg ctctacaggt tcatttccca tgtgattctg 1920
aggtgtagat gtccccaacg aagtttcaaa accactctgc ctaataaat gtggtagcaa 1980
taagtctctt ttgtgaaaaac attgggttac aggtttgttc atgtgtttaa ttatttactT 2040
cgtacagcaa ccgaagatgt gaaagaaaat gttgtttctg c

```

(2) INFORMATION FOR SEQ ID NO:1319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..411
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:

```

Lys Ala Ser Ser Ser Met Glu Lys Gln Gly Cys Glu Ile Glu Ala Leu
1      5      10      15
Asp Ile Asp Tyr Asn Ile Phe Val Arg Lys Ile Asn Val Asn Pro Phe
20     25     30
Gly Ile Phe Arg Arg Lys Pro Arg Pro Glu Ala Asp Gln Pro Val Lys
35     40     45
Thr Glu Glu Glu Ser Leu Lys Leu Glu Asp Glu Thr Gly Asn Lys Val
50     55     60
Lys His Val Leu Lys Gly Val Thr Cys Arg Ala Lys Pro Trp Glu Ile
65     70     75     80
Leu Ala Ile Val Gly Pro Ser Gly Ala Gly Lys Ser Ser Leu Leu Glu
85     90     95
Ile Leu Ala Ala Arg Leu Ile Pro Gln Thr Gly Ser Val Tyr Val Asn
100    105    110
Lys Ser Pro Val Asp Arg Ala Asn Phe Lys Lys Ile Ser Gly Tyr Val
115    120    125
Thr Gln Lys Asp Thr Leu Phe Pro Leu Leu Thr Val Glu Glu Thr Leu
130    135    140
Leu Phe Ser Ala Lys Leu Arg Leu Lys Leu Pro Ala Asp Glu Leu Arg
145    150    155    160

```

Ser Arg Val Lys Ser Leu Val His Glu Leu Gly Leu Glu Ala Val Ala
165 170 175
Thr Ala Arg Val Gly Asp Asp Ser Val Arg Gly Ile Ser Gly Gly Glu
180 185 190
Arg Arg Arg Val Ser Ile Gly Val Glu Val Ile His Asp Pro Lys Val
195 200 205
Leu Ile Leu Asp Glu Pro Thr Ser Gly Leu Asp Ser Thr Ser Ala Leu
210 215 220
Leu Ile Ile Asp Met Leu Lys His Met Ala Glu Thr Arg Gly Arg Thr
225 230 235
Ile Ile Leu Thr Ile His Gln Pro Gly Phe Arg Ile Val Lys Gln Phe
245 250 255
Asn Ser Val Leu Leu Leu Ala Asn Gly Ser Thr Leu Lys Gln Gly Ser
260 265 270
Val Asp Gln Leu Gly Val Tyr Leu Arg Ser Asn Gly Leu His Pro Pro
275 280 285
Leu His Glu Asn Ile Val Glu Phe Ala Ile Glu Ser Ile Glu Ser Ile
290 295 300
Thr Lys Gln Gln Arg Leu Gln Glu Ser Arg Arg Ala Ala His Val Leu
305 310 315
Thr Pro Gln Thr Thr Leu Gln Glu Lys Arg Ser Glu Asp Ser Gln Gly
325 330 335
Glu Ser Lys Ser Gly Lys Phe Thr Leu Gln Gln Leu Phe Gln Gln Thr
340 345 350
Arg Val Ala Asp Val Gly Thr Met Asn Ile Ala Thr Glu Phe Thr Arg
355 360 365
Asp Phe Ala Asn Ser Arg Leu Glu Glu Thr Met Ile Leu Thr His Arg
370 375 380
Phe Ser Lys Asn Ile Phe Arg Thr Lys Glu Leu Phe Ala Cys Arg Thr
385 390 395
Val Gln Met Leu Gly Ser Gly Ile Val Leu Val
405 410

(2) INFORMATION FOR SEQ ID NO:1320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 406 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..406

(D) OTHER INFORMATION: / Ceres Seq. ID 1569613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:

Met Glu Lys Gln Gly Cys Glu Ile Glu Ala Leu Asp Ile Asp Tyr Asn
1 5 10 15
Ile Phe Val Arg Lys Ile Asn Val Asn Pro Phe Gly Ile Phe Arg Arg
20 25 30
Lys Pro Arg Pro Glu Ala Asp Gln Pro Val Lys Thr Glu Glu Ser
35 40 45
Leu Lys Leu Glu Asp Glu Thr Gly Asn Lys Val Lys His Val Leu Lys
50 55 60
Gly Val Thr Cys Arg Ala Lys Pro Trp Glu Ile Leu Ala Ile Val Gly
65 70 75 80
Pro Ser Gly Ala Gly Lys Ser Ser Leu Leu Glu Ile Leu Ala Ala Arg
85 90 95
Leu Ile Pro Gln Thr Gly Ser Val Tyr Val Asn Lys Ser Pro Val Asp
100 105 110
Arg Ala Asn Phe Lys Lys Ile Ser Gly Tyr Val Thr Gln Lys Asp Thr
115 120 125
Leu Phe Pro Leu Leu Thr Val Glu Glu Thr Leu Leu Phe Ser Ala Lys

130	135	140
Leu Arg Leu Lys Leu	Pro Ala Asp Glu Leu Arg Ser Arg Val Lys Ser	
145	150	155
Leu Val His Glu Leu Gly Leu Glu Ala Val Ala Thr Ala Arg Val Gly		160
165	170	175
Asp Asp Ser Val Arg Gly Ile Ser Gly Gly Glu Arg Arg Arg Val Ser		180
180	185	190
Ile Gly Val Glu Glu Val Ile His Asp Pro Lys Val Leu Ile Leu Asp Glu		200
195	200	205
Pro Thr Ser Gly Leu Asp Ser Thr Ser Ala Leu Leu Ile Ile Asp Met		210
210	215	220
Leu Lys His Met Ala Glu Thr Arg Gly Arg Thr Ile Ile Leu Thr Ile		225
225	230	235
His Gln Pro Gly Phe Arg Ile Val Lys Gln Phe Asn Ser Val Leu Leu		240
245	250	255
Leu Ala Asn Gly Ser Thr Leu Lys Gln Gly Ser Val Asp Gln Leu Gly		260
260	265	270
Val Tyr Leu Arg Ser Asn Gly Leu His Pro Pro Leu His Glu Asn Ile		275
275	280	285
Val Glu Phe Ala Ile Glu Ser Ile Glu Ser Ile Thr Lys Gln Gln Arg		290
290	295	300
Leu Gln Glu Ser Arg Arg Ala Ala His Val Leu Thr Pro Gln Thr Thr		305
305	310	315
Leu Gln Glu Lys Arg Ser Glu Asp Ser Gln Gly Glu Ser Lys Ser Gly		320
325	330	335
Lys Phe Thr Leu Gln Gln Leu Phe Gln Gln Thr Arg Val Ala Asp Val		340
340	345	350
Gly Thr Met Asn Ile Ala Thr Glu Phe Thr Arg Asp Phe Ala Asn Ser		355
355	360	365
Arg Leu Glu Glu Thr Met Ile Leu Thr His Arg Phe Ser Lys Asn Ile		370
370	375	380
Phe Arg Thr Lys Glu Leu Phe Ala Cys Arg Thr Val Gln Met Leu Gly		385
385	390	395
Ser Gly Ile Val Leu Val		400
405		

(2) INFORMATION FOR SEQ ID NO:1321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..470
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:

acgatctggt gctggataag ctttttgctt cattctcact tcttctctca tccaaaaaag	60
ctctctccatt tcaatggcga cagCatcatc tctctcatca ctctcttcac tctcaactcca	120
caccogaacc tcttctctca tctctcttct ctcacacaaa tccatcgctct ctttctctct	180
cttctctcaac cgcgcgtctct catctctcac tctcgtcaaa gcctcatcga ccgataaccga	240
aaccatcttc ttctgaagacg aaacaccaga aataaccgca aatgtcgtct tcgacccacc	300
aattgtctccc gaagatttcg tctctctctcc gtatttcgac gaagggaagcg acgagacaga	360
ggaagagatc gCtaaccgtt ttgaagagct ctatggacct gcgtatagtg gtgagagtat	420
gctttgagtc catcacataa atatctttcc caagcatact ctcaccagtc	

(2) INFORMATION FOR SEQ ID NO:1322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..127
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569615
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:

Thr	Ile	Trp	Cys	Trp	Ile	Ser	Leu	Leu	Leu	His	Ser	His	Phe	Leu	Pro
1			5						10					15	
His	Pro	Lys	Lys	Leu	Leu	His	Phe	Asn	Gly	Asp	Ser	Ile	Ile	Ser	Leu
			20					25					30		
Ile	Thr	Leu	Phe	Thr	Leu	Thr	Pro	His	Pro	Asn	Leu	Phe	Ser	His	Leu
		35					40					45			
Leu	Phe	Leu	His	Lys	Ile	His	Arg	Leu	Phe	Leu	Leu	Pro	Gln	Pro	
		50				55				60					
Pro	Leu	Leu	Ile	Ser	His	Ser	Arg	Gln	Ser	Leu	Ile	Asp	Arg	Tyr	Arg
				70					75				80		
Asn	His	Leu	Leu	Arg	Arg	Arg	Asn	Thr	Arg	Asn	Asn	Arg	Lys	Cys	Arg
				85				90					95		
Leu	Arg	Pro	Thr	Asn	Cys	Ser	Arg	Arg	Ile	Arg	Leu	Ser	Ser	Val	Phe
			100					105					110		
Arg	Arg	Arg	Lys	Arg	Arg	Asp	Arg	Gly	Arg	Asp	Arg	Tyr	Arg	Phe	
			115				120						125		

(2) INFORMATION FOR SEQ ID NO:1323:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..90
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569616
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:

Asp	Leu	Val	Leu	Asp	Lys	Pro	Phe	Ala	Ser	Phe	Ser	Leu	Pro	Ser	Ser
1					5					10				15	
Ser	Lys	Lys	Ala	Pro	Pro	Phe	Gln	Trp	Arg	Gln	His	His	Leu	Ser	His
			20					25					30		
His	Ser	Leu	His	Ser	His	Ser	Thr	Pro	Glu	Pro	Leu	Leu	Ser	Ser	Pro
		35					40					45			
Leu	Pro	Pro	Gln	Asn	Pro	Ser	Ser	Leu	Ser	Pro	Pro	Ser	Ser	Thr	Ala
		50				55				60					
Ala	Ser	His	Leu	Ser	Leu	Ser	Ser	Lys	Pro	His	Arg	Pro	Ile	Pro	Lys
				70					75					80	
Pro	Ser	Ser	Ser	Lys	Thr	Lys	His	Gln	Lys						
				85				90							

(2) INFORMATION FOR SEQ ID NO:1324:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..117
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569617
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324:

Met	Ala	Thr	Ala	Ser	Ser	Leu	Ser	Ser	Leu	Ser	Ser	Leu	Ser	Leu	His
1						5				10				15	
Thr	Arg	Thr	Ser	Ser	Leu	Ile	Ser	Ser	Ser	Thr	Lys	Ser	Ile	Val	

	20		25		30	
Ser Phe Ser Ser Phe Leu Asn Arg Arg Phe Ser Ser Leu Thr Leu Val						
	35		40		45	
Lys Ala Ser Ser Thr Asp Thr Glu Thr Ile Phe Phe Glu Asp Glu Thr						
	50		55		60	
Pro Glu Ile Thr Ala Asn Val Val Phe Asp Pro Pro Ile Ala Pro Glu						
	65		70		75	
Gly Phe Val Ser Pro Pro Tyr Phe Asp Glu Gly Ser Asp Glu Thr Glu						
	85		90		95	
Glu Glu Ile Ala Thr Ala Phe Glu Glu Leu Tyr Gly Pro Ala Tyr Ser						
	100		105		110	
Gly Glu Ser Met Leu						
	115					

(2) INFORMATION FOR SEQ ID NO:1325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1356
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:

aaacccaaac	atttttcgat	tttcccgcac	tttctccgac	gatgcgatgg	cgatagCgat	60
gggtattccc	gtgacttatg	ctccgacgat	tgacacgatc	atttgaggca	gtctcccttg	120
tccagatttt	ctttttcaac	ctctttctct	tgcttaccga	ccaaattcat	catctttgaa	180
actgcttcac	cccttttcgt	ttgggtatcc	tgaagactcc	gcctttatacc	cattttgatc	240
tggagaagga	tatagatgaa	gtgctacagt	cgcatactgt	ttattcaaat	gtttcgaagg	300
gagttctctg	aaaatcgaaa	gacttgatga	agtcggttgg	atcagatgat	catcacgaaa	360
tatgcacatga	tatttttgag	aaagagagac	ttcaagtggc	tggaaaaaaa	agagaatcac	420
agttctcaag	ccagttttcg	gatatacgaa	cgattgttat	cgagaaaact	atcaacctgt	480
aaacacaacg	acctttatacc	atcagcatgg	tagagcgctc	aatgcataaa	attcattttg	540
ctgttgatcc	tcatagtaat	tccaagaagc	aggcacttga	tgtcatccgt	gagctgcata	600
agcacttccc	tataaagcgt	tttccaatga	gactgcgtct	tactgttctc	gttcaaaatt	660
tcccctcgct	tctggagaag	ctaaaagaat	gggatggtag	tgtgtgtctc	aaagacgaat	720
ctggaaacac	gatgtccact	gtctgcgaga	tggaaacggg	ccatttccga	gagtgatgat	780
cccatgtgag	gagtatccag	ggaagactag	aaataactgc	tgtatcagtt	catcgagaag	840
gtgacacaag	catgatgatc	tacgatgagc	atgatgatat	ggcattcgaa	acccacaagg	900
cgttgttacc	tgctgagact	gagactaagg	atttgaccga	tccctgcgtt	gaactatgca	960
agaaaactga	gaagcaagag	ataagtacta	cgatatacat	aaagcaagaa	gggtgagaag	1020
aaaagaaggg	gaccaagtgc	agcacttgca	acacgttctg	tgagagagct	aagcataaca	1080
gagagcactg	taagagtatg	tggcacaac	acacacttaa	cggttaagct	cggaactctc	1140
ctctctattag	tgtctgcaga	tgcattgtct	agattgacat	ggacagactc	agagcagatt	1200
tgaagacta	ctctttctga	aactacaatt	ttctctcttt	gtgcttttaa	ttttgtcaat	1260
gtgttaaatc	tctgtatcat	atgtgagtat	gaatacaca	aacttgtgga	atgaaatttt	1320
gcgaagaact	taagagtaaa	aacttgtgtt	taagag			

(2) INFORMATION FOR SEQ ID NO:1326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..297
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:

Met Lys Ser Phe Gly Ser Asp Asp His Thr Lys Ile Cys Ile Asp Ile

Met	Gln	Lys	Thr	Ile	Asn	Pro	Glu	Thr	Gln	Arg	Pro	Tyr	Thr	Ile	Ser
1				5					10					15	
Met	Val	Glu	Arg	Leu	Met	His	Glu	Ile	His	Phe	Ala	Val	Asp	Pro	His
			20					25					30		
Ser	Asn	Ser	Lys	Lys	Gln	Ala	Leu	Asp	Val	Ile	Arg	Glu	Leu	Gln	Lys
		35					40					45			
His	Phe	Pro	Ile	Lys	Arg	Ser	Pro	Met	Arg	Leu	Arg	Leu	Thr	Val	Pro
	50					55					60				
Val	Gln	Asn	Phe	Pro	Ser	Leu	Leu	Glu	Lys	Leu	Lys	Glu	Trp	Asp	Gly
65					70					75				80	
Ser	Val	Val	Ser	Lys	Asp	Glu	Ser	Gly	Thr	Gln	Met	Ser	Thr	Val	Cys
			85						90					95	

Glu	Met	Glu	Pro	Gly	Leu	Phe	Arg	Glu	Cys	Asp	Ser	His	Val	Arg	Ser
			100					105					110		
Ile	Gln	Gly	Arg	Leu	Glu	Ile	Leu	Ala	Val	Ser	Val	His	Ala	Glu	Gly
		115					120					125			
Asp	Thr	Ser	Met	Asp	His	Tyr	Asp	Glu	His	Asp	Asp	Met	Ala	Leu	Gln
		130				135					140				
Thr	His	Lys	Pro	Leu	Leu	Pro	Ala	Glu	Thr	Thr	Lys	Asp	Leu	Thr	
		145			150					155			160		
Asp	Pro	Val	Val	Glu	Leu	Ser	Lys	Lys	Leu	Gln	Lys	Gln	Glu	Ile	Ser
				165					170				175		
Thr	Thr	Asp	Asn	Ile	Lys	Gln	Glu	Gly	Gly	Glu	Glu	Lys	Lys	Gly	Thr
			180					185					190		
Lys	Cys	Ser	Thr	Cys	Asn	Thr	Phe	Val	Gly	Glu	Ala	Lys	Gln	Tyr	Arg
			195				200					205			
Glu	His	Cys	Lys	Ser	Asp	Trp	His	Lys	His	Asn	Leu	Lys	Arg	Lys	Thr
						215					220				
Arg	Lys	Leu	Pro	Pro	Ile	Ser	Ala	Asp	Glu	Cys	Met	Ser	Glu	Ile	Asp
					230					235				240	
Met	Asp	Asp	Ser	Arg	Ala	Asp	Leu	Lys	Asp	Tyr	Ser	Phe			
				245					250						

(2) INFORMATION FOR SEQ ID NO:1328:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..237

(D) OTHER INFORMATION: / Ceres Seq. ID 1569621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:

Met	Val	Glu	Arg	Leu	Met	His	Glu	Ile	His	Phe	Ala	Val	Asp	Pro	His
1			5					10					15		
Ser	Asn	Ser	Lys	Lys	Gln	Ala	Leu	Asp	Val	Ile	Arg	Glu	Leu	Gln	Lys
			20					25					30		
His	Phe	Pro	Ile	Lys	Arg	Ser	Pro	Met	Arg	Leu	Arg	Leu	Thr	Val	Pro
		35					40				45				
Val	Gln	Asn	Phe	Pro	Ser	Leu	Leu	Glu	Lys	Leu	Lys	Glu	Trp	Asp	Gly
		50			55						60				
Ser	Val	Val	Ser	Lys	Asp	Glu	Ser	Gly	Thr	Gln	Met	Ser	Thr	Val	Cys
				70					75					80	
Glu	Met	Glu	Pro	Gly	Leu	Phe	Arg	Glu	Cys	Asp	Ser	His	Val	Arg	Ser
				85					90				95		
Ile	Gln	Gly	Arg	Leu	Glu	Ile	Leu	Ala	Val	Ser	Val	His	Ala	Glu	Gly
		100					105						110		
Asp	Thr	Ser	Met	Asp	His	Tyr	Asp	Glu	His	Asp	Asp	Met	Ala	Leu	Gln
		115				120						125			
Thr	His	Lys	Pro	Leu	Leu	Pro	Ala	Glu	Thr	Glu	Thr	Lys	Asp	Leu	Thr
		130				135					140				
Asp	Pro	Val	Val	Glu	Leu	Ser	Lys	Lys	Leu	Gln	Lys	Gln	Glu	Ile	Ser
				145		150				155				160	
Thr	Thr	Asp	Asn	Ile	Lys	Gln	Glu	Gly	Gly	Glu	Glu	Lys	Lys	Gly	Thr
				165					170					175	
Lys	Cys	Ser	Thr	Cys	Asn	Thr	Phe	Val	Gly	Glu	Ala	Lys	Gln	Tyr	Arg
				180				185					190		
Glu	His	Cys	Lys	Ser	Asp	Trp	His	Lys	His	Asn	Leu	Lys	Arg	Lys	Thr
				195			200					205			
Arg	Lys	Leu	Pro	Pro	Ile	Ser	Ala	Asp	Glu	Cys	Met	Ser	Glu	Ile	Asp
		210				215					220				
Met	Asp	Asp	Ser	Arg	Ala	Asp	Leu	Lys	Asp	Tyr	Ser	Phe			

225

230

235

(2) INFORMATION FOR SEQ ID NO:1329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1511 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1511

(D) OTHER INFORMATION: / Ceres Seq. ID 1569652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329:

```
aaattcaaaa ttttaacacac aaacacaaac acacacacca aaaaaaaaca cagaccttaa      60
aaaaataaaa atggttgata tggattggaa gaggaagatg gtatcatcag atttaccaaa      120
ctcacctaaag cttttcttcaa agcttcacgt aactattcca tcaccgttca aaatcgtccc      180
tgtttcattct cggatctcat gttcagcacc tgctctttgc tctgcttacg agctttacct      240
tcgtctccctt gagctaagaa agctcttggtc atctcgtgat ttctctcaat ggacatcaga      300
gcgcattcttc aaaccagctc ttcaagcttt ggagatcagt ttctgcgcgt ttttcgcgtt      360
ttgttctgat actagaccgt acatcaacca ccgtgaatgg aaccggaggg tagattctct      420
catcacgaag cagatccagc ttgtagcagc gatctgcgaa gatgaagaag aagaaggtat      480
atacagcggag cgtccggtcg gcggtggagc gagttcgttg agttgttac cgcagctagc      540
tacgtggagg agatcaaggc ctttggggaa gaagatctta tatacgatcg ataacagatg      600
gagtcggtgtt aagtacacgc tcggactcgg tgaacaaaac atcgccggaa aaccaaatct      660
cgggtacgat gcgatttgcg gaccaaaacg gatctatagc ctcaaggata atccatacgc      720
agatacatatc gataatcacg agaatcaaac tctctatatac attcaccaga tctctgaatc      780
gtggatctac gcactctgaa atctcttgaa tcgaatcgct tcaagtatcg aagaagagaa      840
attcgaaaaa cgttcaaacg atgtttactt gctggagaag attcggaaaa ttttagcgga      900
gattgaagat ctctcatagt tgatggatcc ggaagatttt ttgaattga agaaacagtt      960
acagatcaaaa tcgacgggta aaaaacgatgc gttttgtttc agatctaaa gattagtga      1020
gatgatgaag atgtcgaagg atctgagaca gaaagtaccg gcggtcttgg cgttgtaggt      1080
agatccaacg ggaggaccga gattAcaaga ggcggcgatg aagctttacg cgcgaagagc      1140
agagtcgcat aaagattcat tgcttcaggc gatgcaagcg gtggaagcgg cgcggaagag      1200
tttctctttt gggatataggc agttagtggc ggctatgatg ggaagtgcgg agatgaacgc      1260
gacggcgagt caagagtcgt gtgactcact gactcagata ttatggagc gcacgtattt      1320
cccgagcctt gacgcggcaa agacgtttct gggagagttt tggagtcatt tgggagatt      1380
aaattttaat tctgcgtggt ataattattt aatataaatt taaatttggt gtttggttta      1440
atttactttg taagatagtg aaatttttgg aacatttgac gatccatatt tgaatacaaa      1500
ttcattttta c
```

(2) INFORMATION FOR SEQ ID NO:1330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..458

(D) OTHER INFORMATION: / Ceres Seq. ID 1569653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:

```
Asn Ser Lys Phe Asn Thr Gln Thr Gln Thr His Thr Pro Lys Lys Asn
1      5      10      15
Thr Asp Leu Lys Lys Ile Lys Met Val Asp Met Asp Trp Lys Arg Lys
20      25      30
Met Val Ser Ser Asp Leu Pro Asn Ser Pro Lys Leu Ser Ser Lys Leu
35      40      45
His Val Thr Ile Pro Ser Pro Phe Lys Ile Val Pro Val Ser Ser Pro
50      55      60
Ile Ser Cys Ser Ala Pro Ala Leu Cys Ser Ala Tyr Glu Leu Tyr Leu
65      70      75      80
```

Arg Leu Pro Glu Leu Arg Lys Leu Trp Ser Ser Arg Asp Phe Pro Gln
85 90 95
Trp Thr Ser Glu Pro Ile Leu Lys Pro Ala Leu Gln Ala Leu Glu Ile
100 105 110
Ser Phe Arg Leu Val Phe Ala Val Cys Ser Asp Thr Arg Pro Tyr Ile
115 120 125
Asn His Arg Glu Trp Asn Arg Arg Leu Asp Ser Leu Ile Thr Lys Gln
130 135 140
Ile Gln Leu Val Ala Ala Ile Cys Glu Asp Glu Glu Glu Gly Ile
145 150 155 160
Ser Ala Glu Ala Pro Val Gly Gly Gly Arg Ser Ser Leu Ser Leu Leu
165 170 175
Pro Gln Leu Ala Thr Trp Arg Arg Ser Glu Ala Leu Gly Lys Lys Ile
180 185 190
Leu Tyr Thr Ile Asp Asn Glu Met Ser Arg Cys Lys Tyr Thr Leu Gly
195 200 205
Leu Gly Glu Gln Asn Ile Ala Gly Lys Pro Asn Leu Arg Tyr Asp Ala
210 215 220
Ile Cys Arg Pro Asn Glu Ile Tyr Ser Leu Lys Asp Asn Pro Tyr Ala
225 230 235 240
Asp His Ile Asp Asn His Glu Asn Gln Thr Leu Tyr Ile Ile His Gln
245 250 255
Ile Leu Glu Ser Trp Ile Tyr Ala Ser Gly Asn Leu Leu Asn Arg Ile
260 265 270
Val Ser Ser Ile Glu Glu Glu Lys Phe Glu Lys Ala Ser Asn Asp Val
275 280 285
Tyr Leu Leu Glu Lys Ile Trp Lys Ile Leu Ala Glu Ile Glu Asp Leu
290 295 300
His Met Leu Met Asp Pro Glu Asp Phe Leu Lys Leu Lys Lys Gln Leu
305 310 315 320
Gln Ile Lys Ser Thr Gly Lys Asn Asp Ala Phe Cys Phe Arg Ser Lys
325 330 335
Gly Leu Val Glu Met Met Lys Met Ser Lys Asp Leu Arg Gln Lys Val
340 345 350
Pro Ala Val Leu Ala Val Glu Val Asp Pro Thr Gly Gly Pro Arg Leu
355 360 365
Gln Glu Ala Ala Met Lys Leu Tyr Ala Arg Lys Thr Glu Cys Asp Lys
370 375 380
Ile His Leu Leu Gln Gly Met Gln Ala Val Glu Ala Ala Ala Lys Ser
385 390 395 400
Phe Phe Phe Gly Tyr Arg Gln Leu Val Ala Met Met Gly Ser Ala
405 410 415
Glu Met Asn Ala Thr Ala Ser Gln Glu Ser Cys Asp Ser Leu Ser Gln
420 425 430
Ile Phe Met Glu Pro Thr Tyr Phe Pro Ser Leu Asp Ala Ala Lys Thr
435 440 445
Phe Leu Gly Glu Phe Trp Ser His Leu Gly
450 455

(2) INFORMATION FOR SEQ ID NO:1331:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 435 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..435

(D) OTHER INFORMATION: / Ceres Seq. ID 1569654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:

Met Val Asp Met Asp Trp Lys Arg Lys Met Val Ser Ser Asp Leu Pro

1	5	10	15
Asn Ser Pro Lys Leu Ser Ser Lys Leu His Val Thr Ile Pro Ser Pro	20	25	30
Phe Lys Ile Val Pro Val Ser Ser Pro Ile Ser Cys Ser Ala Pro Ala	35	40	45
Leu Cys Ser Ser Ala Tyr Glu Leu Tyr Leu Arg Leu Pro Glu Leu Arg Lys	50	55	60
Leu Trp Ser Ser Arg Asp Phe Pro Gln Trp Thr Ser Glu Pro Ile Leu	65	70	75
Lys Pro Ala Leu Gln Ala Leu Glu Ile Ser Phe Arg Leu Val Phe Ala	85	90	95
Val Cys Ser Asp Thr Arg Pro Tyr Ile Asn His Arg Glu Trp Asn Arg	100	105	110
Arg Leu Asp Ser Leu Ile Thr Lys Gln Ile Gln Leu Val Ala Ala Ile	115	120	125
Cys Glu Asp Glu Glu Glu Glu Gly Ile Ser Ala Glu Ala Pro Val Gly	130	135	140
Gly Gly Arg Ser Ser Leu Ser Leu Leu Pro Gln Leu Ala Thr Trp Arg	145	150	155
Arg Ser Glu Ala Leu Gly Lys Lys Ile Leu Tyr Thr Ile Asp Asn Glu	165	170	175
Met Ser Arg Cys Lys Tyr Thr Leu Gly Leu Gly Glu Gln Asn Ile Ala	180	185	190
Gly Lys Pro Asn Leu Arg Tyr Asp Ala Ile Cys Arg Pro Asn Glu Ile	195	200	205
Tyr Ser Leu Lys Asp Asn Pro Tyr Ala Asp His Ile Asp Asn His Glu	210	215	220
Asn Gln Thr Leu Tyr Ile Ile His Gln Ile Leu Glu Ser Trp Ile Tyr	225	230	235
Ala Ser Gly Asn Leu Leu Asn Arg Ile Val Ser Ser Ile Glu Glu Glu	245	250	255
Lys Phe Glu Lys Ala Ser Asn Asp Val Tyr Leu Leu Glu Lys Ile Trp	260	265	270
Lys Ile Leu Ala Glu Ile Glu Asp Leu His Met Leu Met Asp Pro Glu	275	280	285
Asp Phe Leu Lys Leu Lys Lys Gln Leu Gln Ile Lys Ser Thr Gly Lys	290	295	300
Asn Asp Ala Phe Cys Phe Arg Ser Lys Gly Leu Val Glu Met Met Lys	305	310	315
Met Ser Lys Asp Leu Arg Gln Lys Val Pro Ala Val Leu Ala Val Glu	325	330	335
Val Asp Pro Thr Gly Gly Pro Arg Leu Gln Glu Ala Ala Met Lys Leu	340	345	350
Tyr Ala Arg Lys Thr Glu Cys Asp Lys Ile His Leu Leu Gln Gly Met	355	360	365
Gln Ala Val Glu Ala Ala Ala Lys Ser Phe Phe Phe Gly Tyr Arg Gln	370	375	380
Leu Val Ala Ala Met Met Gly Ser Ala Glu Met Asn Ala Thr Ala Ser	385	390	395
Gln Glu Ser Cys Asp Ser Leu Ser Gln Ile Phe Met Glu Pro Thr Tyr	405	410	415
Phe Pro Ser Leu Asp Ala Ala Lys Thr Phe Leu Gly Glu Phe Trp Ser	420	425	430
His Leu Gly	435		

(2) INFORMATION FOR SEQ ID NO:1332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Met	Asp	Trp	Lys	Arg	Lys	Met	Val	Ser	Ser	Asp	Leu	Pro	Asn	Ser	Pro
1			5					10					15		
Lys	Leu	Ser	Ser	Lys	Leu	His	Val	Thr	Ile	Pro	Ser	Pro	Phe	Lys	Ile
			20					25					30		
Val	Pro	Val	Ser	Ser	Pro	Ile	Ser	Cys	Ser	Ala	Pro	Ala	Leu	Cys	Ser
		35					40					45			
Ala	Tyr	Glu	Leu	Tyr	Leu	Arg	Leu	Pro	Glu	Leu	Arg	Lys	Leu	Trp	Ser
	50					55					60				
Ser	Arg	Asp	Phe	Pro	Gln	Trp	Thr	Ser	Glu	Pro	Ile	Leu	Lys	Pro	Ala
65					70					75					80
Leu	Gln	Ala	Leu	Glu	Ile	Ser	Phe	Arg	Leu	Val	Phe	Ala	Val	Cys	Ser
				85					90					95	
Asp	Thr	Arg	Pro	Tyr	Ile	Asn	His	Arg	Glu	Trp	Asn	Arg	Arg	Leu	Asp
			100					105					110		
Ser	Leu	Ile	Thr	Lys	Gln	Ile	Gln	Leu	Val	Ala	Ala	Ile	Cys	Glu	Asp
		115						120				125			
Glu	Glu	Glu	Glu	Gly	Ile	Ser	Ala	Glu	Ala	Pro	Val	Gly	Gly	Gly	Arg
	130					135					140				
Ser	Ser	Leu	Ser	Leu	Leu	Pro	Gln	Leu	Ala	Thr	Trp	Arg	Arg	Ser	Glu
145					150					155					160
Ala	Leu	Gly	Lys	Lys	Ile	Leu	Tyr	Thr	Ile	Asp	Asn	Glu	Met	Ser	Arg
				165						170				175	
Cys	Lys	Tyr	Thr	Leu	Gly	Leu	Gly	Glu	Gln	Asn	Ile	Ala	Gly	Lys	Pro
			180					185						190	
Asn	Leu	Arg	Tyr	Asp	Ala	Ile	Cys	Arg	Pro	Asn	Glu	Ile	Tyr	Ser	Leu
			195				200					205			
Lys	Asp	Asn	Pro	Tyr	Ala	Asp	His	Ile	Asp	Asn	His	Glu	Asn	Gln	Thr
					215						220				
Leu	Tyr	Ile	Ile	His	Gln	Ile	Leu	Glu	Ser	Trp	Ile	Tyr	Ala	Ser	Gly
225					230					235					240
Asn	Leu	Leu	Asn	Arg	Ile	Val	Ser	Ser	Ile	Glu	Glu	Glu	Lys	Phe	Glu
				245					250					255	
Lys	Ala	Ser	Asn	Asp	Val	Tyr	Leu	Leu	Glu	Lys	Ile	Trp	Lys	Ile	Leu
			260					265					270		
Ala	Glu	Ile	Glu	Asp	Leu	His	Met	Leu	Met	Asp	Pro	Glu	Asp	Phe	Leu
	275						280					285			
Lys	Leu	Lys	Lys	Gln	Leu	Gln	Ile	Lys	Ser	Thr	Gly	Lys	Asn	Asp	Ala
	290					295					300				
Phe	Cys	Phe	Arg	Ser	Lys	Gly	Leu	Val	Glu	Met	Met	Lys	Met	Ser	Lys
305					310					315					320
Asp	Leu	Arg	Gln	Lys	Val	Pro	Ala	Val	Leu	Ala	Val	Glu	Val	Asp	Pro
				325					330					335	
Thr	Gly	Gly	Pro	Arg	Leu	Gln	Glu	Ala	Ala	Met	Lys	Leu	Tyr	Ala	Arg
			340					345					350		
Lys	Thr	Glu	Cys	Asp											

(2) INFORMATION FOR SEQ ID NO:1333:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1276

(D) OTHER INFORMATION: / Ceres Seq. ID 1569656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333:

acttaaaagcc	ctcaaaaatct	cagagaacgc	tcgctgatca	aatccgctcgt	ccctcaaccg	60
tcgcctcctc	cgctcatgaca	attgagtgcg	ttaataccga	aggtctctcga	ttcaaccacaa	120
tgaaaagctc	ctctcatcaa	accctagaaa	cgaggatgag	gccgattttg	atgaagggac	180
atgaacgctc	attgacgttc	ctgaggtaca	acagaaatgg	tgatctgctt	ttctcctcgc	240
ccaagagacc	cactcccaca	gtctgggttg	ccgataacgg	cgagcgtctt	ggcacttacc	300
gtggccacag	tgggtcgtgt	tgggtcgtgt	atatctccag	agactcgtct	agattgatca	360
ctggtagtcg	tgatcagact	gcaaaagctg	gggagtgtga	atctggcaca	gaattgttca	420
ctttcaagtt	tgggtccctc	gcaaGgtctg	tggatttctc	tgttggtgat	catcttgcag	480
tgattaccac	tgatcacttc	gtgggaactt	cctctgctat	tcatgtcaaa	cgatttgag	540
aagatcccca	agaccagggt	ggtgattctg	tgcttctcct	tcaaaagtct	gatgaaaaga	600
agaagatcaa	tagagctgtt	tggggctccc	tgaaccaaac	cattgttagt	gggtgtgaag	660
atgctgctat	cagaactctg	gatgcagaga	ctagaaaatt	gcttaagcaa	tcagatgagg	720
aagtgggtca	caaggaggcc	attacatccc	tctgcaaaag	agctgatgac	tctcacttCc	780
ttacaaagtc	acatgacaaa	actgcaaaag	tttgggacat	gagaaacgtg	actcttatta	840
agacttacac	cactgtgggtg	cctgtaaaatG	ctgtcgccat	gtctccactt	ctcaaccatg	900
ttgtgctagg	agggtgttcaa	gatgcacatc	ctgtgactac	cactgatcat	cgtgctggga	960
agtttgaaac	taagtgtttac	gacacagatt	tgcaagagga	aattgggtgg	gtgaagagtc	1020
attttggacc	tattaatgct	ttggcatttca	gtccctgatg	gaagagtctt	tctagtggag	1080
gtgaagagcg	ctacgtgaga	ctgcactcatt	ttgactccaa	ttacttcaac	atcaagattt	1140
agattctttg	aacatgtctt	tccatttttt	catcattcca	cataatattt	ttctcttttt	1200
taacattttc	agaattgatg	tactaccaaa	ttaccaatat	actaacttga	tgataaagct	1260
tggtgttgtt	cttttc					

(2) INFORMATION FOR SEQ ID NO:1334:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..379

(D) OTHER INFORMATION: / Ceres Seq. ID 1569657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334:

Leu	Lys	Pro	Ser	Lys	Ser	Gln	Arg	Thr	Leu	Ala	Asp	Gln	Ile	Arg	Arg	
1				5				10					15			
Pro	Ser	Thr	Val	Ala	Ser	Ser	Val	Met	Thr	Ile	Glu	Cys	Val	Asn	Pro	
			20					25					30			
Glu	Gly	Leu	Arg	Phe	Asn	Gln	Met	Lys	Ser	Ser	Ser	His	Gln	Thr	Leu	
			35				40					45				
Glu	Thr	Arg	Met	Arg	Pro	Ile	Leu	Met	Lys	Gly	His	Glu	Arg	Pro	Leu	
			50				55					60				
Thr	Phe	Leu	Arg	Tyr	Asn	Arg	Asn	Gly	Asp	Leu	Phe	Ser	Cys	Ala		
			65				70			75				80		
Lys	Asp	His	Thr	Pro	Thr	Val	Trp	Phe	Ala	Asp	Asn	Gly	Glu	Arg	Leu	
			85				90						95			
Gly	Thr	Tyr	Arg	Gly	His	Ser	Gly	Ala	Val	Trp	Cys	Cys	Asp	Ile	Ser	
			100				105						110			

Arg Asp Ser Ser Arg Leu Ile Thr Gly Ser Ala Asp Gln Thr Ala Lys
115 120 125
Leu Trp Asp Val Lys Ser Gly Lys Glu Leu Phe Thr Phe Lys Phe Gly
130 135 140
Ala Pro Ala Arg Ser Val Asp Phe Ser Val Gly Asp His Leu Ala Val
145 150 155 160
Ile Thr Thr Asp His Phe Val Gly Thr Ser Ala Ile His Val Lys
165 170 175
Arg Ile Ala Glu Asp Pro Glu Asp Gln Val Gly Asp Ser Val Leu Val
180 185 190
Leu Gln Ser Pro Asp Gly Lys Lys Lys Ile Asn Arg Ala Val Trp Gly
195 200 205
Pro Leu Asn Gln Thr Ile Val Ser Gly Gly Glu Asp Ala Ala Ile Arg
210 215 220
Ile Trp Asp Ala Glu Thr Arg Lys Leu Leu Lys Gln Ser Asp Glu Glu
225 230 235 240
Val Gly His Lys Glu Ala Ile Thr Ser Leu Cys Lys Ala Ala Asp Asp
245 250 255
Ser His Phe Leu Thr Gly Ser His Asp Lys Thr Ala Lys Leu Trp Asp
260 265 270
Met Arg Thr Leu Thr Leu Ile Lys Thr Tyr Thr Thr Val Val Pro Val
275 280 285
Asn Ala Val Ala Met Ser Pro Leu Leu Asn His Val Val Leu Gly Gly
290 295 300
Gly Gln Asp Ala Ser Ala Val Thr Thr Thr Asp His Arg Ala Gly Lys
305 310 315 320
Phe Glu Ala Lys Phe Tyr Asp Thr Ile Leu Gln Glu Glu Ile Gly Gly
325 330 335
Val Lys Gly His Phe Gly Pro Ile Asn Ala Leu Ala Phe Ser Pro Asp
340 345 350
Gly Lys Ser Phe Ser Ser Gly Gly Glu Asp Gly Tyr Val Arg Leu His
355 360 365
His Phe Asp Ser Asn Tyr Phe Asn Ile Lys Ile
370 375

(2) INFORMATION FOR SEQ ID NO:1335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..355
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:

Met Thr Ile Glu Cys Val Asn Pro Glu Gly Leu Arg Phe Asn Gln Met
1 5 10 15
Lys Ser Ser Ser His Gln Thr Leu Glu Thr Arg Met Arg Pro Ile Leu
20 25 30
Met Lys Gly His Glu Arg Pro Leu Thr Phe Leu Arg Tyr Asn Arg Asn
35 40 45
Gly Asp Leu Leu Phe Ser Cys Ala Lys Asp His Thr Pro Thr Val Trp
50 55 60
Phe Ala Asp Asn Gly Glu Arg Leu Gly Thr Tyr Arg Gly His Ser Gly
65 70 75 80
Ala Val Trp Cys Cys Asp Ile Ser Arg Asp Ser Ser Arg Leu Ile Thr
85 90 95
Gly Ser Ala Asp Gln Thr Ala Lys Leu Trp Asp Val Lys Ser Gly Lys
100 105 110
Glu Leu Phe Thr Phe Lys Phe Gly Ala Pro Ala Arg Ser Val Asp Phe

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..340

(D) OTHER INFORMATION: / Ceres Seq. ID 1569659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:

Met	Lys	Ser	Ser	5	His	Gln	Thr	Leu	Glu	Thr	Arg	Met	Arg	Pro	Ile
1									10					15	
Leu	Met	Lys	Gly	His	Glu	Arg	Pro	Leu	Thr	Phe	Leu	Arg	Tyr	Asn	Arg
			20					25					30		
Asn	Gly	Asp	Leu	Leu	Phe	Ser	Cys	Ala	Lys	Asp	His	Thr	Pro	Thr	Val
		35					40					45			
Trp	Phe	Ala	Asp	Asn	Gly	Glu	Arg	Leu	Gly	Thr	Tyr	Arg	Gly	His	Ser
	50					55					60				
Gly	Ala	Val	Trp	Cys	Cys	Asp	Ile	Ser	Arg	Asp	Ser	Ser	Arg	Leu	Ile
65					70					75				80	
Thr	Gly	Ser	Ala	Asp	Gln	Thr	Ala	Lys	Leu	Trp	Asp	Val	Lys	Ser	Gly
			85						90					95	
Lys	Glu	Leu	Phe	Thr	Phe	Lys	Phe	Gly	Ala	Pro	Ala	Arg	Ser	Val	Asp
		100						105					110		
Phe	Ser	Val	Gly	Asp	His	Leu	Ala	Val	Ile	Thr	Thr	Asp	His	Phe	Val
		115					120					125			
Gly	Thr	Ser	Ser	Ala	Ile	His	Val	Lys	Arg	Ile	Ala	Glu	Asp	Pro	Glu
	130					135					140				

Asp Gln Val Gly Asp Ser Val Leu Val Leu Gln Ser Pro Asp Gly Lys
145 150 155 160
Lys Lys Ile Asn Arg Ala Val Trp Gly Pro Leu Asn Gln Thr Ile Val
165 170 175
Ser Gly Gly Glu Asp Ala Ala Ile Arg Ile Trp Asp Ala Glu Thr Arg
180 185 190
Lys Leu Leu Lys Gln Ser Asp Glu Glu Val Gly His Lys Lys Glu Ala Ile
195 200 205
Thr Ser Leu Cys Lys Ala Ala Asp Asp Ser His Phe Leu Thr Gly Ser
210 215 220
His Asp Lys Thr Ala Lys Leu Trp Asp Met Arg Thr Leu Thr Leu Ile
225 230 235 240
Lys Thr Tyr Thr Thr Val Val Pro Val Asn Ala Val Ala Met Ser Pro
245 250 255
Leu Leu Asn His Val Val Leu Gly Gly Gly Gln Asp Ala Ser Ala Val
260 265 270
Thr Thr Thr Asp His Arg Ala Gly Lys Phe Glu Ala Lys Phe Tyr Asp
275 280 285
Thr Ile Leu Gln Glu Glu Ile Gly Gly Val Lys Gly His Phe Gly Pro
290 295 300
Ile Asn Ala Leu Ala Phe Ser Pro Asp Gly Lys Ser Phe Ser Ser Gly
305 310 315 320
Gly Glu Asp Gly Tyr Val Arg Leu His His Phe Asp Ser Asn Tyr Phe
325 330 335
Asn Ile Lys Ile
340

(2) INFORMATION FOR SEQ ID NO:1337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:

atctctctct	ctctaaacct	ctctctcaat	ggccgtcgat	gctcaccatc	tctttctttc	60
tcctctctca	ctctctctcca	acagagaatt	aacgatgaat	aataaacacta	tggaaaccaac	120
tagtgccggt	tctgtcaata	acaatcaaac	cggttacggc	gtcgtttcac	ctttctccgt	180
tccaacaact	acatcaacaa	caacaacagc	aacgcctcct	cttcttcaata	tgtacgcggg	240
ctctgatact	attcccacca	cgcgcgggta	ctacgcgcga	ggtgctacta	atctcgactg	300
tgaatttttc	cttttaccaa	cgagaaaaac	ctcaagagat	tcttcaagat	caaatattca	360
tcactctctt	cttcagaaac	cgagatcatc	atcatgtgtt	aacgctgcta	ctacaacaac	420
tacaacaact	ccgttctcgt	ttcttggcca	agacattgat	atctctcttc	acatgaattc	480
acaacaacac	gaatatagat	gattcgtctc	cttccactta	tatcagatgg	agagatgtga	540
atatgagata	gaagagaaga	ggaaaaagca	agcgagaaac	ataatggagg	cgatagagca	600
aggactgggt	aaaagggttc	gtgtcaaaag	agaagaaaga	gagaggatcg	gcaagggtta	660
ccacgcgctt	gaggagcgag	tgaagtcaat	tcttatagag	aaccaaatct	ggagagacct	720
tgctcagacg	aacgaagcca	cggctaacca	cctccgaacc	aacctcgagc	atgttctggc	780
gcagggttaag	gacgtatcac	gcgcgcgagg	attagagaaa	aacatgaacg	aagaggagca	840
tgcggagtcg	tgctgcggaa	cgagctgtgg	tgtgtgtgtg	gaagaaacgg	taaggcgcag	900
ggtaggatta	gaaaggaggg	gcagagataa	ggcggagagg	aggaggagga	ggaatgtgtg	960
aaactgtggg	gaggaggaa	cgtgtgtgtt	gctgttaccg	tcgacagact	tgtgtgtgtg	1020
tggagtagtc	gggtccagtg	tgcacacgtg	tccatctgt	acatctctca	aaaacgctag	1080
cgttcatgtc	aacatgtcat	cttgaccocg	tcccggttat	ggaatactcc	tcttctctct	1140
tttttWttt	tttttttgtt	ctttagaaaa	tttgaagga	tatttttagt	gaatattatt	1200
attattttta	gct					

(2) INFORMATION FOR SEQ ID NO:1338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..358
(D) OTHER INFORMATION: / Ceres Seq. ID 1569668
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:

```

Met Ala Val Asp Ala His His Leu Phe Leu Ser Pro Pro Gln Leu Phe
1      5      10      15
Ser Asn Arg Glu Leu Thr Met Asn Asn Asn Thr Met Glu Pro Thr Ser
20      25      30
Gly Gly Phe Cys Asn Asn Asn Gln Thr Gly Tyr Gly Val Val Ser Pro
35      40      45
Phe Ser Val Pro Asn His Thr Ser Thr Thr Thr Thr Ala Thr Pro Pro
50      55      60
Leu Leu His Met Tyr Gly Gly Ser Asp Thr Ile Pro Thr Thr Ala Gly
65      70      75      80
Tyr Tyr Ala Asp Gly Ala Thr Asn Leu Asp Cys Glu Phe Phe Pro Leu
85      90      95
Pro Thr Arg Lys Arg Ser Arg Asp Ser Ser Arg Ser Asn Tyr His His
100      105      110
Leu Leu Leu Gln Asn Pro Arg Ser Ser Cys Val Asn Ala Ala Thr
115      120      125
Thr Thr Thr Thr Thr Thr Phe Ser Phe Leu Gly Gln Asp Ile Asp
130      135      140
Ile Ser Ser His Met Asn Gln Gln Gln His Glu Ile Asp Arg Phe Val
145      150      155      160
Ser Leu His Leu Tyr Gln Met Glu Arg Val Lys Tyr Glu Ile Glu Glu
165      170      175
Lys Arg Lys Arg Gln Ala Arg Thr Ile Met Glu Ala Ile Glu Gln Gly
180      185      190
Leu Val Lys Arg Leu Arg Val Lys Glu Glu Glu Arg Glu Arg Ile Gly
195      200      205
Lys Val Asn His Ala Leu Glu Glu Arg Val Lys Ser Leu Ser Ile Glu
210      215      220
Asn Gln Ile Trp Arg Asp Leu Ala Gln Thr Asn Glu Ala Thr Ala Asn
225      230      235
His Leu Arg Thr Asn Leu Glu His Val Leu Ala Gln Val Lys Asp Val
245      250      255
Ser Arg Gly Ala Gly Leu Glu Lys Asn Met Asn Glu Glu Asp Asp Ala
260      265      270
Glu Ser Cys Cys Gly Ser Ser Cys Gly Gly Gly Glu Thr Val
275      280      285
Arg Arg Arg Val Gly Leu Glu Arg Glu Ala Gln Asp Lys Ala Glu Arg
290      295      300
Arg Arg Arg Arg Met Cys Arg Asn Cys Gly Glu Glu Glu Ser Cys Val
305      310      315
Leu Leu Leu Pro Cys Arg His Leu Cys Leu Cys Gly Val Cys Gly Ser
325      330      335
Ser Val His Thr Cys Pro Ile Cys Thr Ser Pro Lys Asn Ala Ser Val
340      345      350
His Val Asn Met Ser Ser
355

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(2) INFORMATION FOR SEQ ID NO:1339:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..336
(D) OTHER INFORMATION: / Ceres Seq. ID 1569669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339:

Met	Asn	Asn	Asn	Thr	Met	Glu	Pro	Thr	Ser	Gly	Gly	Phe	Cys	Asn	Asn
1				5					10					15	
Asn	Gln	Thr	Gly	Tyr	Gly	Val	Val	Ser	Pro	Phe	Ser	Val	Pro	Asn	His
			20					25					30		
Thr	Ser	Thr	Thr	Thr	Thr	Ala	Thr	Pro	Leu	Leu	His	Met	Tyr	Gly	
		35				40					45				
Gly	Ser	Asp	Thr	Ile	Pro	Thr	Thr	Ala	Gly	Tyr	Tyr	Ala	Asp	Gly	Ala
		50				55					60				
Thr	Asn	Leu	Asp	Cys	Glu	Phe	Phe	Pro	Leu	Pro	Thr	Arg	Lys	Arg	Ser
		65			70					75				80	
Arg	Asp	Ser	Ser	Arg	Ser	Asn	Tyr	His	His	Leu	Leu	Leu	Gln	Asn	Pro
			85					90					95		
Arg	Ser	Ser	Ser	Cys	Val	Asn	Ala	Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr
			100					105					110		
Pro	Phe	Ser	Phe	Leu	Gly	Gln	Asp	Ile	Asp	Ile	Ser	Ser	His	Met	Asn
			115				120					125			
Gln	Gln	Gln	His	Glu	Ile	Asp	Arg	Phe	Val	Ser	Leu	His	Leu	Tyr	Gln
		130				135					140				
Met	Glu	Arg	Val	Lys	Tyr	Glu	Ile	Glu	Glu	Lys	Arg	Lys	Arg	Gln	Ala
		145			150					155					
Arg	Thr	Ile	Met	Glu	Ala	Ile	Glu	Gln	Gly	Leu	Val	Lys	Arg	Leu	Arg
			165					170					175		
Val	Lys	Glu	Glu	Glu	Arg	Glu	Arg	Ile	Gly	Lys	Val	Asn	His	Ala	Leu
			180					185					190		
Glu	Glu	Arg	Val	Lys	Ser	Leu	Ser	Ile	Glu	Asn	Gln	Ile	Trp	Arg	Asp
		195				200						205			
Leu	Ala	Gln	Thr	Asn	Glu	Ala	Thr	Ala	Asn	His	Leu	Arg	Thr	Asn	Leu
		210				215					220				
Glu	His	Val	Leu	Ala	Gln	Val	Lys	Asp	Val	Ser	Arg	Gly	Ala	Gly	Leu
		225			230				235					240	
Glu	Lys	Asn	Met	Asn	Glu	Glu	Asp	Asp	Ala	Glu	Ser	Cys	Cys	Gly	Ser
			245					250					255		
Ser	Cys	Gly	Gly	Gly	Gly	Glu	Glu	Thr	Val	Arg	Arg	Arg	Val	Gly	Leu
			260					265					270		
Glu	Arg	Glu	Ala	Gln	Asp	Lys	Ala	Glu	Arg	Arg	Arg	Arg	Arg	Met	Cys
		275				280						285			
Arg	Asn	Cys	Gly	Glu	Glu	Glu	Ser	Cys	Val	Leu	Leu	Leu	Pro	Cys	Arg
		290				295					300				
His	Leu	Cys	Leu	Cys	Gly	Val	Cys	Gly	Ser	Ser	Val	His	Thr	Cys	Pro
		305			310					315				320	
Ile	Cys	Thr	Ser	Pro	Lys	Asn	Ala	Ser	Val	His	Val	Asn	Met	Ser	Ser
			325					330					335		

(2) INFORMATION FOR SEQ ID NO:1340:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..331

(D) OTHER INFORMATION: / Ceres Seq. ID 1569670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:

Met	Glu	Pro	Thr	Ser	Gly	Gly	Phe	Cys	Asn	Asn	Asn	Gln	Thr	Gly	Tyr
1				5				10						15	
Gly	Val	Val	Ser	Pro	Phe	Ser	Val	Pro	Asn	His	Thr	Ser	Thr	Thr	
				20				25					30		
Thr	Ala	Thr	Pro	Pro	Leu	Leu	His	Met	Tyr	Gly	Gly	Ser	Asp	Thr	Ile
				35			40					45			
Pro	Thr	Thr	Ala	Gly	Tyr	Tyr	Ala	Asp	Gly	Ala	Thr	Asn	Leu	Asp	Cys
				50		55					60				
Glu	Phe	Phe	Pro	Leu	Pro	Thr	Arg	Lys	Arg	Ser	Arg	Asp	Ser	Ser	Arg
65				70					75					80	
Ser	Asn	Tyr	His	His	Leu	Leu	Leu	Gln	Asn	Pro	Arg	Ser	Ser	Ser	Cys
				85					90					95	
Val	Asn	Ala	Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Pro	Phe	Ser	Phe	Leu
				100				105					110		
Gly	Gln	Asp	Ile	Asp	Ile	Ser	Ser	His	Met	Asn	Gln	Gln	Gln	His	Glu
				115			120					125			
Ile	Asp	Arg	Phe	Val	Ser	Leu	His	Leu	Tyr	Gln	Met	Glu	Arg	Val	Lys
				130			135				140				
Tyr	Glu	Ile	Glu	Glu	Lys	Arg	Lys	Arg	Gln	Ala	Arg	Thr	Ile	Met	Glu
145					150					155				160	
Ala	Ile	Glu	Gln	Gly	Leu	Val	Lys	Arg	Leu	Arg	Val	Lys	Glu	Glu	Glu
				165				170						175	
Arg	Glu	Arg	Ile	Gly	Lys	Val	Asn	His	Ala	Leu	Glu	Glu	Arg	Val	Lys
				180				185					190		
Ser	Leu	Ser	Ile	Glu	Asn	Gln	Ile	Trp	Arg	Asp	Leu	Ala	Gln	Thr	Asn
				195			200					205			
Glu	Ala	Thr	Ala	Asn	His	Leu	Arg	Thr	Asn	Leu	Glu	His	Val	Leu	Ala
				210			215				220				
Gln	Val	Lys	Asp	Val	Ser	Arg	Gly	Ala	Gly	Leu	Glu	Lys	Asn	Met	Asn
225					230					235				240	
Glu	Glu	Asp	Asp	Ala	Glu	Ser	Cys	Cys	Gly	Ser	Ser	Cys	Gly	Gly	Gly
				245					250					255	
Gly	Glu	Glu	Thr	Val	Arg	Arg	Arg	Val	Gly	Leu	Glu	Arg	Glu	Ala	Gln
				260				265					270		
Asp	Lys	Ala	Glu	Arg	Arg	Arg	Arg	Met	Cys	Arg	Asn	Cys	Gly	Glu	
				275				280				285			
Glu	Glu	Ser	Cys	Val	Leu	Leu	Leu	Pro	Cys	Arg	His	Leu	Cys	Leu	Cys
				290			295				300				
Gly	Val	Cys	Gly	Ser	Ser	Val	His	Thr	Cys	Pro	Ile	Cys	Thr	Ser	Pro
305					310					315					320
Lys	Asn	Ala	Ser	Val	His	Val	Asn	Met	Ser	Ser					
				325					330						

(2) INFORMATION FOR SEQ ID NO:1341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1169
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:

acacccaaac	acgcgacgcg	agcgaaAgaa	gacgatgacg	aacaaggaga	aagctcgaga	60
gagaaggagg	aaaaaaatgc	aggagatctc	tctccttcga	actattcctt	actctgacca	120
ccataggttgG	tggtcttggt	aaaatgtagc	agtagtgact	gtttcaaacc	gcgggattgg	180
attcgagatt	gcaagacagc	ttcggtttca	cggattgacg	gttggtctta	cagctagaaa	240
cgtgaatgct	ggtcttgaag	cagttaaatc	tttgaggcac	caagaagaag	gtctcaaggt	300

ttattttcat	caacttgatg	tcacagactc	tctctcgatt	agagagtttg	gtgtctggct	360
taagcaaaaca	tttggagggt	tagatattct	cgtgaataat	Ygcaggtggt	aactacaatc	420
tcggctcaga	taatacgggt	gaatttgcgt	aaacagttat	atctactaac	taccacaggaa	480
ccaaaaacat	gacaaaaagct	atgataaccCt	tgatgagacc	atctctcat	ggcgctcgtg	540
tagtcaatgt	tagttctcgg	ctaggttagag	taaatggaag	acgtaataga	ctggcaaatg	600
tagagttgag	agatcagcta	agcagtcacg	atttgcgtac	cgaggaaactt	atagacagaa	660
ctgtctctaa	attcatcaac	caagtaaaag	acggaaacttg	ggaatcagcg	gggtggcctc	720
agacattcac	tgactactcc	atgtctaagc	ttgcagttca	tgcttacacg	agactaatgg	780
caaaagaact	tgagagacga	ggagaggaag	agaagattta	tgttaacagc	ttttccocgt	840
gttgggtgaa	gactcgcgatg	aNctgGctac	gccggaaata	tgcacacctga	agatgcagct	900
gatactggag	tttggcttag	ccgtgctctt	tccgaagagt	cagtaaccgg	aaaattcttc	960
gcagagagac	gtgagatcaa	cttctgaggg	ttgttgaatg	tttgtaaacg	ttggaataga	1020
ttgtgtcgtc	ttcgtttagt	gccatagttt	tagtcaaaag	tttcaaaaat	caattgtaat	1080
tggttaagtga	atggtttagt	tcagtatcag	cgtcagattt	gccacaaaaa	taggagttta	1140
taatttaaat	atgaattaatt	tttaattgc				

(2) INFORMATION FOR SEQ ID NO:1342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1569672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:

His	Pro	Asn	Thr	Arg	Arg	Glu	Arg	Lys	Lys	Thr	Met	Thr	Asn	Lys	Glu
1				5						10				15	
Lys	Ala	Arg	Glu	Arg	Arg	Glu	Lys	Lys	Met	Gln	Glu	Ile	Ser	Leu	Leu
			20					25					30		
Arg	Thr	Ile	Pro	Tyr	Ser	Asp	His	His	Arg	Trp	Trp	Ser	Cys	Glu	Asn
			35					40					45		
Val	Ala	Val	Val	Thr	Gly	Ser	Asn	Arg	Gly	Ile	Gly	Phe	Glu	Ile	Ala
			50				55				60				
Arg	Gln	Leu	Ala	Val	His	Gly	Leu	Thr	Val	Val	Leu	Thr	Ala	Arg	Asn
			65				70				75			80	
Val	Asn	Ala	Gly	Leu	Glu	Ala	Val	Lys	Ser	Leu	Arg	His	Gln	Glu	Glu
				85					90				95		
Gly	Leu	Lys	Val	Tyr	Phe	His	Gln	Leu	Asp	Val	Thr	Asp	Ser	Ser	Ser
			100					105					110		
Ile	Arg	Glu	Phe	Gly	Cys	Trp	Leu	Lys	Gln	Thr	Phe	Gly	Gly	Leu	Asp
			115					120					125		
Ile	Leu	Val	Asn	Asn	Xaa	Arg	Cys								
			130				135								

(2) INFORMATION FOR SEQ ID NO:1343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1569673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:

Met	Thr	Lys	Ala	Met	Ile	Pro	Leu	Met	Arg	Pro	Ser	Pro	His	Gly	Ala
1				5						10				15	
Arg	Val	Val	Asn	Val	Ser	Ser	Arg	Leu	Gly	Arg	Val	Asn	Gly	Arg	Arg
			20						25				30		

Asn Arg Leu Ala Asn Val Glu Leu Arg Asp Gln Leu Ser Ser Pro Asp
35 40 45
Leu Leu Thr Glu Glu Leu Ile Asp Arg Thr Val Ser Lys Phe Ile Asn
50 55 60
Gln Val Lys Asp Gly Thr Trp Glu Ser Gly Gly Trp Pro Gln Thr Phe
65 70 75 80
Thr Asp.Tyr Ser Met Ser Lys Leu Ala Val Asn Ala Tyr Thr Arg Leu
85 90 95
Met Ala Lys Glu Leu Glu Arg Arg Gly Glu Glu Glu Lys Ile Tyr Val
100 105 110
Asn Ser Phe Cys Pro Gly Trp Val Lys Thr Ala Met Xaa Trp Leu Arg
115 120 125
Arg Lys Tyr Ala Thr
130

(2) INFORMATION FOR SEQ ID NO:1344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1569674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344:

Met Ile Pro Leu Met Arg Pro Ser Pro His Gly Ala Arg Val Val Asn
1 5 10 15
Val Ser Ser Arg Leu Gly Arg Val Asn Gly Arg Arg Asn Arg Leu Ala
20 25 30
Asn Val Glu Leu Arg Asp Gln Leu Ser Ser Pro Asp Leu Leu Thr Glu
35 40 45
Glu Leu Ile Asp Arg Thr Val Ser Lys Phe Ile Asn Gln Val Lys Asp
50 55 60
Gly Thr Trp Glu Ser Gly Gly Trp Pro Gln Thr Phe Thr Asp Tyr Ser
65 70 75 80
Met Ser Lys Leu Ala Val Asn Ala Tyr Thr Arg Leu Met Ala Lys Glu
85 90 95
Leu Glu Arg Arg Gly Glu Glu Glu Lys Ile Tyr Val Asn Ser Phe Cys
100 105 110
Pro Gly Trp Val Lys Thr Ala Met Xaa Trp Leu Arg Arg Lys Tyr Ala
115 120 125
Thr

(2) INFORMATION FOR SEQ ID NO:1345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1214 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1214

(D) OTHER INFORMATION: / Ceres Seq. ID 1569685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:

aatcaaaaag gcaaaaagca aagagagaga gagagagaag aagaagtggg acctgtgttc	60
ttacgggtgtt tatagcttct ttgtttttgtc ttttaggttc ttgccttttt cogatcaatc	120
agaccaatcc ctccctcaact tttagcatct tattctcttt cgttctcttt atatttctgg	180
gaattttctt caatcgattc ctctttgttg taatctcaaca attAgagaga gagatrtgtg	240
Gtaatcagtt ggcgatatct tgcgtcttct catcttsttc gtactatgaa tctttgaagg	300

ttttggaagc	tgtatgttcaa	cacgctaatt	ctttggcaga	agcaattcca	atggggaaga	360
acaatgtgcg	gcttcagatg	aaactgggtc	atagtaactt	tgcttCatta	ttactcttct	420
tgcttgggtg	gattgatctt	tcttctcat	gtcttattcc	tcgtactacta	aaactcttct	480
atgtttctgt	ctacaaggtc	cagtcgtatg	gacaacctaa	gcttaccacg	cacggaagga	540
aagcaacgat	tagtgagttc	tatggtgtga	tactaccatc	actgcagcta	ttacacagca	600
acttagatga	gttggaiaac	acagacatcg	ggtttgacct	taaaagactc	agtaagaaga	660
taacaaaaga	ggctcgtagt	agtagattca	gcaatgccgg	tttagagcgt	gaagaagaat	720
gcgggtatct	tttagaaaact	tgacccaaaa	tggtgttgcc	taattgttgc	cattctatgt	780
gcatcaaatG	ctatcgcaat	tggaacttga	agtctcagtc	atgcccggtt	tgctgaggca	840
gcatgaagag	agtgaaactca	gaggacttgt	gggtgcttgc	gggtgataac	gatgtgggtg	900
atacaaggac	ggcttcaagg	gaagatttgt	tcagatttcta	ttctctacat	aatagccttc	960
ccaagattta	cccaagaagct	ctctttgtgg	ttactatga	gtactcaaat	ctgctataga	1020
atctggacaa	acaaaacttt	gtacagattt	ttagatggta	aatgtattgt	atagaatgta	1080
aaactgtgtt	aaggcttttg	gatgatatga	tgcaaatgcc	aaagctctca	gtttttacat	1140
acttaataat	tgtcaaatg	cgagaaaaaa	aaaaagcttg	aatgcagcaa	agaataaaga	1200
ttctatttca	tctc					

(2) INFORMATION FOR SEQ ID NO:1346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..338
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:

Ser	Lys	Arg	Gln	Lys	Ala	Lys	Arg	Glu	Arg	Glu	Arg	Arg	Arg	Ser	Glu
1			5					10					15		
Thr	Cys	Val	Leu	Thr	Val	Phe	Ile	Ala	Ser	Leu	Phe	Cys	Leu	Leu	Gly
			20					25					30		
Ser	Cys	Leu	Phe	Pro	Ile	Asn	Gln	Thr	Asn	Pro	Ser	Phe	Thr	Phe	Ser
			35					40					45		
Ile	Leu	Phe	Ser	Phe	Val	Leu	Leu	Ile	Phe	Leu	Gly	Ile	Phe	Phe	Asn
			50					55							
Arg	Phe	Leu	Phe	Val	Val	Ile	Ser	Gln	Leu	Glu	Arg	Glu	Xaa	Cys	Ser
			65					70					75		80
Asn	Gln	Leu	Ala	Ile	Ser	Ser	Ser	Ser	Ser	Xaa	Ser	Tyr	Tyr	Glu	
			85					90					95		
Ser	Leu	Lys	Val	Leu	Glu	Ala	Asp	Val	Gln	His	Ala	Asn	Ser	Leu	Ala
			100					105					110		
Glu	Ala	Ile	Pro	Met	Gly	Lys	Asn	Asn	Val	Arg	Leu	Gln	Met	Lys	Leu
			115					120					125		
Val	His	Ser	Asn	Phe	Ala	Ser	Leu	Leu	Phe	Leu	Leu	Arg	Trp	Ile	
			130					135					140		
Asp	Leu	Ser	Ser	Ser	Cys	Leu	Ile	Pro	Arg	Tyr	Leu	Asn	Leu	Phe	His
					150					155					160
Val	Leu	Val	Tyr	Lys	Val	Gln	Ser	Asp	Gly	Gln	Pro	Lys	Leu	Thr	Thr
					165					170					175
His	Gly	Arg	Lys	Ala	Thr	Ile	Ser	Glu	Phe	Tyr	Gly	Val	Ile	Leu	Pro
					180					185				190	
Ser	Leu	Gln	Leu	Leu	His	Ser	Asn	Leu	Asp	Glu	Leu	Glu	Thr	Thr	Asp
					195					200				205	
Ile	Gly	Phe	Asp	Leu	Lys	Arg	Leu	Ser	Lys	Lys	Ile	Thr	Lys	Glu	Ala
					210					215				220	
Arg	Ser	Ser	Arg	Phe	Ser	Asn	Ala	Gly	Leu	Glu	Arg	Glu	Glu	Glu	Cys
					225					230					240
Gly	Ile	Cys	Leu	Glu	Thr	Cys	Thr	Lys	Met	Val	Leu	Pro	Asn	Cys	Cys
					245					250				255	
His	Ser	Met	Cys	Ile	Lys	Cys	Tyr	Arg	Asn	Trp	Asn	Leu	Lys	Ser	Gln

2025 RELEASE UNDER E.O. 14176

(2) INFORMATION FOR SEQ ID NO:1347:

(A) LENGTH: 222 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..222

(D) OTHER INFORMATION: / Ceres Seq. ID 1569687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:

Met	Gly	Lys	Asn	Asn	Val	Arg	Leu	Gln	Met	Lys	Leu	Val	His	Ser	Asn
1			5					10						15	
Phe	Ala	Ser	Leu	Leu	Leu	Phe	Leu	Leu	Arg	Trp	Ile	Asp	Leu	Ser	Ser
			20					25					30		
Ser	Cys	Leu	Ile	Pro	Arg	Tyr	Leu	Asn	Leu	Phe	His	Val	Leu	Val	Tyr
		35					40					45			
Lys	Val	Gln	Ser	Asp	Gly	Gln	Pro	Lys	Leu	Thr	Thr	His	Gly	Arg	Lys
		50				55					60				
Ala	Thr	Ile	Ser	Glu	Phe	Tyr	Gly	Val	Ile	Leu	Pro	Ser	Leu	Gln	Leu
65					70					75					80
Leu	His	Ser	Asn	Leu	Asp	Glu	Leu	Glu	Thr	Thr	Asp	Ile	Gly	Phe	Asp
				85					90					95	
Leu	Lys	Arg	Leu	Ser	Lys	Lys	Ile	Thr	Lys	Glu	Ala	Arg	Ser	Ser	Arg
			100					105					110		
Phe	Ser	Asn	Ala	Gly	Leu	Glu	Arg	Glu	Glu	Glu	Cys	Gly	Ile	Cys	Leu
		115					120					125			
Glu	Thr	Cys	Thr	Lys	Met	Val	Leu	Pro	Asn	Cys	Cys	His	Ser	Met	Cys
		130				135					140				
Ile	Lys	Cys	Tyr	Arg	Asn	Trp	Asn	Leu	Lys	Ser	Gln	Ser	Cys	Pro	Phe
145					150					155					160
Cys	Arg	Gly	Ser	Met	Lys	Arg	Val	Asn	Ser	Glu	Asp	Leu	Trp	Val	Leu
				165					170					175	
Ala	Gly	Asp	Asn	Asp	Val	Val	Asp	Thr	Arg	Thr	Ala	Ser	Arg	Glu	Asp
			180					185					190		
Leu	Phe	Arg	Phe	Tyr	Leu	Tyr	Ile	Asn	Ser	Leu	Pro	Lys	Asp	Tyr	Pro
		195					200					205			
Glu	Ala	Leu	Phe	Val	Val	Tyr	Tyr	Glu	Tyr	Ser	Asn	Leu	Leu		
		210				215					220				

(2) INFORMATION FOR SEQ ID NO:1348:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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(A) NAME/KEY: peptide

(B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:

(2) INFORMATION FOR SEQ ID NO:1349:

(A) LENGTH: 792 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
```

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..792

(D) OTHER INFORMATION: / Ceres Seq. ID 1569697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:

(2) INFORMATION FOR SEQ ID NO:1350:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..107
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569698
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350:
Ile Gln Ser Leu Ser Ala Arg Glu Thr Lys Lys Glu Arg Glu Glu Arg
1 5 10 15
Trp Lys Met Ile Lys Ala Val Met Met Met Asn Thr Gln Gly Lys Pro
 20 25 30
Arg Leu Ala Lys Phe Tyr Asp Tyr Met Pro Val Glu Lys Gln Gln Glu
 35 40 45
Leu Ile Arg Gly Val Phe Ser Val Leu Cys Ser Arg Pro Glu Asn Val
 50 55 60
Ser Asn Phe Leu Glu Ile Glu Ser Leu Phe Gly Pro Asp Ser Arg Leu
65 70 75 80
Val Tyr Lys His Tyr Ala Thr Leu Tyr Phe Val Leu Val Phe Asp Gly
 85 90 95
Ser Glu Asn Glu Leu Ala Met Leu Asp Leu Ile
 100 105
(2) INFORMATION FOR SEQ ID NO:1351:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..89
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569699
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351:
Met Ile Lys Ala Val Met Met Met Asn Thr Gln Gly Lys Pro Arg Leu
1 5 10 15
Ala Lys Phe Tyr Asp Tyr Met Pro Val Glu Lys Gln Gln Glu Leu Ile
 20 25 30
Arg Gly Val Phe Ser Val Leu Cys Ser Arg Pro Glu Asn Val Ser Asn
 35 40 45
Phe Leu Glu Ile Glu Ser Leu Phe Gly Pro Asp Ser Arg Leu Val Tyr
 50 55 60
Lys His Tyr Ala Thr Leu Tyr Phe Val Leu Val Phe Asp Gly Ser Glu
65 70 75 80
Asn Glu Leu Ala Met Leu Asp Leu Ile
 85
(2) INFORMATION FOR SEQ ID NO:1352:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..84
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569700
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352:
Met Met Met Asn Thr Gln Gly Lys Pro Arg Leu Ala Lys Phe Tyr Asp
1 5 10 15
Tyr Met Pro Val Glu Lys Gln Gln Glu Leu Ile Arg Gly Val Phe Ser
 20 25 30

Val Leu Cys Ser Arg Pro Glu Asn Val Ser Asn Phe Leu Glu Ile Glu
35 40 45
Ser Leu Phe Gly Pro Asp Ser Arg Leu Val Tyr Lys His Tyr Ala Thr
50 55 60
Leu Tyr Phe Val Leu Val Phe Asp Gly Ser Glu Asn Glu Leu Ala Met
65 70 75 80
Leu Asp Leu Ile

(2) INFORMATION FOR SEQ ID NO:1353:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1377 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1377

(D) OTHER INFORMATION: / Ceres Seq. ID 1569717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353:

aaaccaAgt	cCAagtTCct	gtTaaatggc	gaaaaaagaa	gggtcaaaaga	tgaacatcgc	60
cattatacat	ccagatctgtt	gaatagcgcg	aGcagagaga	ttgattgttg	atgcggccgt	120
tgagcttgcc	tgcacgcttg	ataaagtcca	tatcttcacc	tctcaccacg	acaaatccag	180
atgcttccag	gaactctttt	cgggtatctt	tcaagttacg	gtgatgtgat	ctttctctgc	240
acggcatatt	ttctacccag	tacacgcagt	KgtGgcata	ttgcgggtgc	tggtttgtgc	300
tctctgtgtt	cttttggggt	gggtcttcatt	cgatgttgtta	ctagcagacc	aagtttcagt	360
cgtagtccca	ttgctgaacc	tcaaaaggct	acttaagbtt	gttttctact	gccatttccc	420
ggatctctgt	ctagctaaagc	atacaacaac	acttagacgg	atgtatcggg	aaccattgga	480
tttcattgaa	gaacaaacaa	cagggatggc	tgatgatgat	cttgtaacaa	gtaaactcac	540
ggcatcaaca	tttgccaata	cattttaaag	gctaaatgca	caaggggagt	gccccagctg	600
actttacccc	cgagtcata	ttgatcagtt	cattgaaccc	cacacttata	agttgaattt	660
ctctccata	aaacgctttt	agaggaaaaa	gaacatcgat	ctagctgttt	cagcttttgc	720
tatctctatg	aaacataagc	aaaatctgag	tgatgttacc	cttaccgctg	caggtggata	780
tgacgacgca	ttgaaggaga	atgttgagta	cttgaggagg	ctcagaagtt	tagccagaaa	840
agaaggagtt	tctgatcgag	ttaaactttat	cacatcttgt	tcaaccgcgt	aaagaaatga	900
actttctcca	agctgcttgt	gcgttctcta	caccccacag	gatgaacatt	ttggtattgt	960
tccattagaa	gcaatggctg	catacaaaac	ogtगतagcc	tgcaacagtg	gtggcccccgt	1020
ggagacggta	aagaatggag	taacaggcta	tcttttgtga	ccaactccag	aagatttcag	1080
ttcggcgatg	gctagattca	tgcgaaatcc	tgagttggcg	aatagaatgg	gagctgaagc	1140
caggaaacct	gtcgttgaat	cattctctgt	gaagacgttt	ggacagagat	tgaatcagta	1200
tctcgttgat	gtcgtatcaa	gtcctaaga	agattgagat	tctctgttgt	agtaatacata	1260
gatcgttgtg	gaacacagct	actttaggct	tagttctgaa	actacagagg	ctttattctc	1320
ggatacctca	tcttgacogt	gaagatttgt	taaatctagg	tgaacagttt	tttgtttt	

(2) INFORMATION FOR SEQ ID NO:1354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 403 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..403

(D) OTHER INFORMATION: / Ceres Seq. ID 1569718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:

Met	Ala	Lys	Lys	Glu	Gly	Ser	Lys	Met	Asn	Ile	Ala	Ile	Ile	His	Pro
1				5					10					15	
Asp	Leu	Gly	Ile	Gly	Gly	Ala	Glu	Arg	Leu	Ile	Val	Asp	Ala	Ala	Val
			20				25				30				
Glu	Leu	Ala	Ser	His	Gly	His	Lys	Val	His	Ile	Phe	Thr	Ser	His	His
			35				40				45				

```

Asp Lys Ser Arg Cys Phe Glu Glu Thr Leu Ser Gly Ile Phe Gln Val
50      55      60
Thr Val Tyr Gly Ser Phe Leu Pro Arg His Ile Phe Tyr Arg Leu His
65      70      75      80
Ala Xaa Val Ala Tyr Leu Arg Cys Leu Phe Val Ala Leu Cys Val Leu
85      90      95
Leu Gly Trp Ser Ser Phe Asp Val Val Leu Ala Asp Gln Val Ser Val
100     105     110
Val Val Pro Leu Leu Lys Leu Lys Arg Ser Ser Lys Val Val Phe Tyr
115     120     125
Cys His Phe Pro Asp Leu Leu Leu Ala Lys His Thr Thr Thr Leu Arg
130     135     140
Arg Met Tyr Arg Lys Pro Ile Asp Phe Ile Glu Glu Gln Thr Thr Gly
145     150     155     160
Met Ala Asp Met Ile Leu Val Asn Ser Asn Phe Thr Ala Ser Thr Phe
165     170     175
Ala Asn Thr Phe Lys Arg Leu Asn Ala Gln Gly Ser Arg Pro Ala Val
180     185     190
Leu Tyr Pro Ala Val Asn Ile Asp Gln Phe Ile Glu Pro His Thr Tyr
195     200     205
Lys Leu Asn Phe Leu Ser Ile Asn Arg Phe Glu Arg Lys Lys Asn Ile
210     215     220
Asp Leu Ala Val Ser Ala Phe Ala Ile Leu Cys Lys His Lys Gln Asn
225     230     235     240
Leu Ser Asp Val Thr Leu Thr Val Ala Gly Tyr Asp Glu Arg Leu
245     250     255
Lys Glu Asn Val Glu Tyr Leu Glu Glu Leu Arg Ser Leu Ala Glu Lys
260     265     270
Glu Gly Val Ser Asp Arg Val Asn Phe Ile Thr Ser Cys Ser Thr Ala
275     280     285
Glu Arg Asn Glu Leu Leu Ser Ser Cys Leu Cys Val Leu Tyr Thr Pro
290     295     300
Thr Asp Glu His Phe Gly Ile Val Pro Leu Glu Ala Met Ala Ala Tyr
305     310     315     320
Lys Pro Val Ile Ala Cys Asn Ser Gly Gly Pro Val Glu Thr Val Lys
325     330     335
Asn Gly Val Thr Gly Tyr Leu Cys Glu Pro Thr Pro Glu Asp Phe Ser
340     345     350
Ser Ala Met Ala Arg Phe Ile Glu Asn Pro Glu Leu Ala Asn Arg Met
355     360     365
Gly Ala Glu Ala Arg Asn His Val Val Glu Ser Phe Ser Val Lys Thr
370     375     380
Phe Gly Gln Lys Leu Asn Gln Tyr Leu Val Asp Val Val Ser Ser Pro
385     390     395     400
Lys Glu Asp

```

(2) INFORMATION FOR SEQ ID NO:1355:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 395 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..395

(D) OTHER INFORMATION: / Ceres Seq. ID 1569719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:

```

Met Asn Ile Ala Ile Ile His Pro Asp Leu Gly Ile Gly Gly Ala Glu
1      5      10      15
Arg Leu Ile Val Asp Ala Ala Val Glu Leu Ala Ser His Gly His Lys

```

(2) INFORMATION FOR SEQ ID NO:1356:

(A) LENGTH: 258 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

```

FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..258
(D) OTHER INFORMATION

```

Met Tyr Arg Lys Pro Ile Asp Phe Ile Glu Glu Gln Thr Thr Gly Met
1 5 10 15

Ala Asp Met Ile Leu Val Asn Ser Asn Phe Thr Ala Ser Thr Phe Ala
20 25 30
Asn Thr Phe Lys Arg Leu Asn Ala Gln Gly Ser Arg Pro Ala Val Leu
35 40 45
Tyr Pro Ala Val Asn Ile Asp Gln Phe Ile Glu Pro His Thr Tyr Lys
50 55 60
Leu Asn Phe Leu Ser Ile Asn Arg Phe Glu Arg Lys Lys Asn Ile Asp
65 70 75 80
Leu Ala Val Ser Ala Phe Ala Ile Leu Cys Lys His Lys Gln Asn Leu
85 90 95
Ser Asp Val Thr Leu Thr Val Ala Gly Gly Tyr Asp Glu Arg Leu Lys
100 105 110
Glu Asn Val Glu Tyr Leu Glu Glu Leu Arg Ser Leu Ala Glu Lys Glu
115 120 125
Gly Val Ser Asp Arg Val Asn Phe Ile Thr Ser Cys Ser Thr Ala Glu
130 135 140
Arg Asn Glu Leu Leu Ser Ser Cys Leu Cys Val Leu Tyr Thr Pro Thr
145 150 155 160
Asp Glu His Phe Gly Ile Val Pro Leu Glu Ala Met Ala Tyr Lys
165 170 175
Pro Val Ile Ala Cys Asn Ser Gly Gly Pro Val Glu Thr Val Lys Asn
180 185 190
Gly Val Thr Gly Tyr Leu Cys Glu Pro Thr Pro Glu Asp Phe Ser Ser
195 200 205
Ala Met Ala Arg Phe Ile Glu Asn Pro Glu Leu Ala Asn Arg Met Gly
210 215 220
Ala Glu Ala Arg Asn His Val Val Glu Ser Phe Ser Val Lys Thr Phe
225 230 235 240
Gly Gln Lys Leu Asn Gln Tyr Leu Val Asp Val Val Ser Ser Pro Lys
245 250 255
Glu Asp

(2) INFORMATION FOR SEQ ID NO:1357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..662
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:

actcgatcat	agaataaaaa	acaaaaaccc	ttgaagtcac	taagttgatt	caaaatggtt	60
gcgagaagt	aggaagtga	gatagtggaa	gatacggcg	cgaaatgatt	gatgttgta	120
tcaagagttg	gagaaggcgg	cggaggagga	gagaaacgag	ttttccgatg	caagacttgt	180
cttaaaagat	tttctcgatt	tcaagctttg	ggaggtcac	gtgcaagcca	caacaaactc	240
attaacagta	gcgatccatc	actctctgga	tctctgtcta	acaagaaaaa	taaaacggcg	300
acgtctcatc	cttgtccgat	atgtggcggt	gagtttccga	tggggcaagc	tcttggtggt	360
cacatgagga	gacataggag	tgagaaagcc	tcaccaggca	cgttggttta	acagttcttt	420
tttaccggag	acgacgacgg	tgacgacttt	gaagaaatcg	agtagtgga	agagagtggc	480
ttgtttgac	ttagatccga	tgagaggttt	agtcaattgg	aagtgtgagt	tggaagaagc	540
gatttcttga	tctgttttat	tcttctatat	tcgttatagg	gttttaacat	attttcatat	600
agtttcatt	tgtaaatctt	gtagatccat	ttatcttaac	gatcgatgty	aatattattt	660

(2) INFORMATION FOR SEQ ID NO:1358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..136
(D) OTHER INFORMATION: / Ceres Seq. ID 1569722

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:

```
Met Val Ala Arg Ser Glu Glu Val Glu Ile Val Glu Asp Thr Ala Ala
1      5      10      15
Lys Cys Leu Met Leu Leu Ser Arg Val Gly Glu Gly Gly Gly Gly
20      25      30
Glu Lys Arg Val Phe Arg Cys Lys Thr Cys Leu Lys Glu Phe Ser Ser
35      40      45
Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Asn Lys Leu Ile Asn
50      55      60
Ser Ser Asp Pro Ser Leu Leu Gly Ser Leu Ser Asn Lys Lys Thr Lys
65      70      75      80
Thr Ala Thr Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met
85      90      95
Gly Gln Ala Leu Gly Gly His Met Arg Arg His Arg Ser Glu Lys Ala
100      105      110
Ser Pro Gly Thr Leu Gly Tyr Thr Phe Phe Phe Thr Gly Asp Asp Asp
115      120      125
Gly Asp Asp Phe Glu Glu Ile Glu
130      135
```

- (2) INFORMATION FOR SEQ ID NO:1359:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..117
(D) OTHER INFORMATION: / Ceres Seq. ID 1569723

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359:

```
Met Leu Leu Ser Arg Val Gly Glu Gly Gly Gly Gly Glu Lys Arg
1      5      10      15
Val Phe Arg Cys Lys Thr Cys Leu Lys Glu Phe Ser Ser Phe Gln Ala
20      25      30
Leu Gly Gly His Arg Ala Ser His Asn Lys Leu Ile Asn Ser Ser Asp
35      40      45
Pro Ser Leu Leu Gly Ser Leu Ser Asn Lys Lys Thr Lys Thr Ala Thr
50      55      60
Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met Gly Gln Ala
65      70      75      80
Leu Gly Gly His Met Arg Arg His Arg Ser Glu Lys Ala Ser Pro Gly
85      90      95
Thr Leu Gly Tyr Thr Phe Phe Phe Thr Gly Asp Asp Asp Gly Asp Asp
100      105      110
Phe Glu Glu Ile Glu
115
```

- (2) INFORMATION FOR SEQ ID NO:1360:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1488 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1.1488
(D) OTHER INFORMATION: / Ceres Seq. ID 1569724

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360:

cttagcagat	gcttttttgc	aaaaaaaata	tacaaaaaaa	aaaaaatctg	catctgcctt	60
cgtctctctc	cttgccctcta	aaatttaatta	cccatttttt	ccgataaaat	tttgttgagg	120
aagaaatttt	gttgtaaaaga	gagtttaatt	aaattatgcc	ttcaatagaa	gatgagctgt	180
ttccgtcaac	gcggggtaaa	ttcaaaattg	accggtcaaa	ccgtcagctc	caccgttgtt	240
tgcgtctcat	gagcaccatg	tttctttggg	ctctcttctc	catcgctctc	accgctttct	300
acttgagttt	ccaaagcttt	gtcgattccg	gtagccgtta	tctaaccgct	ttttggggcg	360
gcattccaat	ggagaaacag	gttcgtacct	ccgctcagat	ccatcgctcc	ggcggtatct	420
ccgtccttgt	taccggcgct	accggattcg	tcggtagcaa	cggtcgaact	ccgttgagga	480
aaacgcggca	tggtgtctgt	ggacttgata	atttcaacaa	ttactacgat	ccgtctttga	540
aaactgctcg	tagatctctg	ttgtctgcga	gagggatctt	cgctgttgaa	ggagatctaa	600
acgacggcaa	gctgttagca	aaacttttgc	atgtggttgc	tttactcac	gtgatgcac	660
tcgtctgcta	agctgtgtgt	agatacgttt	tgagaaatcc	tcaatcgtat	gttcatagca	720
acatgcgcgg	acttgtgaat	cttctcgaga	tttgcaaaag	ggcgaatcct	cagccggcga	780
ttgtttgggc	ttcatcgagc	tccgtttatg	gactcaacga	gaaagtctca	ttctctgaat	840
ctgacgggac	ggatcaacgc	gcgagttctc	acgcccgaac	gaaaaaagcc	ggcggaagaa	900
tcaccacac	ttataaccat	atttagcggt	ttgccattac	cggtttaaga	ttcttcaagg	960
tttacggacc	atgggggtaga	ccgatatagg	cttaactctc	cttcaccaga	aacatcctac	1020
aaggtaaacc	gcatacaatc	taccggggca	aaaacggggt	cgatttagcc	cgggatttca	1080
catatcagca	cgatatagtg	aaaggatgtt	taggatctct	ggaattcctg	ggtaaaagta	1140
ccgggtcggg	gtaaaaaacg	tgagcagcga	cCgtaccgga	tatttaacct	gggaaacaca	1200
ttctcgggtta	cagtaccgat	tctgtgtggt	atatgtggag	agcattttaa	ggtgaaagcg	1260
aagagggaact	tcgtggagat	gccaggaac	ggcgacgtac	cgttcacaca	tgccaatatt	1320
agctcagccc	gaatatgaat	cggtgtataa	ccgacaacgc	atttggaac	cggtgtgaag	1380
aagtctgcta	gatgttatct	tctttattac	ggatacaata	ctaaagccaa	gctgtgtacat	1440
taaccgtgac	tattattatt	atttttaagt	aaattatttt	ttctctcc		

(2) INFORMATION FOR SEQ ID NO:1361:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1.332
(D) OTHER INFORMATION: / Ceres Seq. ID 1569725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361:

Met	Pro	Ser	Ile	Glu	Asp	Glu	Leu	Phe	Pro	Ser	Thr	Pro	Gly	Lys	Phe
1			5				10						15		
Lys	Ile	Asp	Arg	Ser	Asn	Arg	Gln	Leu	His	Arg	Cys	Phe	Ala	Ser	Thr
			20				25						30		
Ser	Thr	Met	Phe	Leu	Trp	Ala	Leu	Phe	Leu	Ile	Ala	Leu	Thr	Ala	Ser
			35				40						45		
Tyr	Leu	Ser	Phe	Gln	Ser	Phe	Val	Asp	Ser	Gly	Ser	Arg	Tyr	Leu	Thr
			50				55						60		
Ala	Ser	Trp	Gly	Gly	Ile	Gln	Trp	Glu	Lys	Gln	Val	Arg	Thr	Ser	Ala
			65				70						75		
Gln	Ile	His	Arg	Ser	Gly	Gly	Ile	Ser	Val	Leu	Val	Thr	Gly	Ala	Thr
			85				90						95		
Gly	Val	Val	Gly	Ser	His	Val	Ser	Leu	Ala	Leu	Arg	Lys	Arg	Gly	Asp
			100				105						110		
Gly	Val	Val	Gly	Leu	Asp	Asn	Phe	Asn	Asn	Tyr	Tyr	Asp	Pro	Ser	Leu
			115				120						125		
Lys	Arg	Ala	Arg	Arg	Ser	Leu	Leu	Ser	Ser	Arg	Gly	Ile	Phe	Val	Val
			130				135						140		
Glu	Gly	Asp	Leu	Asn	Asp	Ala	Lys	Leu	Leu	Ala	Lys	Leu	Phe	Asp	Val
			145				150						155		

Val Ala Phe Thr His Val Met His Leu Ala Ala Gln Ala Gly Val Arg
165 170 175
Tyr Ala Leu Glu Asn Pro Gln Ser Tyr Val His Ser Asn Ile Ala Gly
180 185 190
Leu Val Asn Leu Leu Glu Ile Cys Lys Ala Ala Asn Pro Gln Pro Ala
195 200 205
Ile Val Trp Ala Ser Ser Ser Val Tyr Gly Leu Asn Glu Lys Val
210 215 220
Pro Phe Ser Glu Ser Asp Arg Thr Asp Gln Pro Ala Ser Leu Tyr Ala
225 230 235 240
Ala Thr Lys Lys Ala Gly Glu Glu Ile Thr His Thr Tyr Asn His Ile
245 250 255
Tyr Gly Leu Ala Ile Thr Gly Leu Arg Phe Phe Thr Val Tyr Gly Pro
260 265 270
Trp Gly Arg Pro Asp Met Ala Tyr Phe Ser Phe Thr Arg Asn Ile Leu
275 280 285
Gln Gly Lys Pro Ile Thr Ile Tyr Arg Gly Lys Asn Arg Val Asp Leu
290 295 300
Ala Arg Asp Phe Thr Tyr Ile Asp Asp Ile Val Lys Gly Cys Leu Gly
305 310 315 320
Ser Leu Asp Ser Ser Gly Lys Ser Thr Gly Ser Gly
325 330

(2) INFORMATION FOR SEQ ID NO:1362:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..298

(D) OTHER INFORMATION: / Ceres Seq. ID 1569726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362:

Met Phe Leu Trp Ala Leu Phe Leu Ile Ala Leu Thr Ala Ser Tyr Leu
1 5 10 15
Ser Phe Gln Ser Phe Val Asp Ser Gly Ser Arg Tyr Leu Thr Ala Ser
20 25 30
Trp Gly Gly Ile Gln Trp Glu Lys Gln Val Arg Thr Ser Ala Gln Ile
35 40 45
His Arg Ser Gly Gly Ile Ser Val Leu Val Thr Gly Ala Thr Gly Phe
50 55 60
Val Gly Ser His Val Ser Leu Ala Leu Arg Lys Arg Gly Asp Gly Val
65 70 75 80
Val Gly Leu Asp Asn Phe Asn Asn Tyr Tyr Asp Pro Ser Leu Lys Arg
85 90 95
Ala Arg Arg Ser Leu Leu Ser Ser Arg Gly Ile Phe Val Val Glu Gly
100 105 110
Asp Leu Asn Asp Ala Lys Leu Leu Ala Lys Leu Phe Asp Val Val Ala
115 120 125
Phe Thr His Val Met His Leu Ala Ala Gln Ala Gly Val Arg Tyr Ala
130 135 140
Leu Glu Asn Pro Gln Ser Tyr Val His Ser Asn Ile Ala Gly Leu Val
145 150 155 160
Asn Leu Leu Glu Ile Cys Lys Ala Ala Asn Pro Gln Pro Ala Ile Val
165 170 175
Trp Ala Ser Ser Ser Ser Val Tyr Gly Leu Asn Glu Lys Val Pro Phe
180 185 190
Ser Glu Ser Asp Arg Thr Asp Gln Pro Ala Ser Leu Tyr Ala Ala Thr
195 200 205
Lys Lys Ala Gly Glu Glu Ile Thr His Thr Tyr Asn His Ile Tyr Gly

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210	215	220
Leu Ala Ile Thr Gly	Leu Arg Phe Phe Thr Val Tyr Gly	Pro Trp Gly
225	230	235
Arg Pro Asp Met Ala Tyr Phe Ser Phe Thr Arg Asn Ile Leu Gln Gly		240
	245	250
Lys Pro Ile Thr Ile Tyr Arg Gly Lys Asn Arg Val Asp Leu Ala Arg		255
	260	265
Asp Phe Thr Tyr Ile Asp Asp Ile Val Lys Gly Cys Leu Gly Ser Leu		270
	275	280
Asp Ser Ser Gly Lys Ser Thr Gly Ser Gly		285
290	295	

(2) INFORMATION FOR SEQ ID NO:1363:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1569727

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:

Met His Leu Ala Ala Gln Ala Gly Val Arg Tyr Ala Leu Glu Asn Pro	
1	5
Gln Ser Tyr Val His Ser Asn Ile Ala Gly Leu Val Asn Leu Leu Glu	
	20
Ile Cys Lys Ala Ala Asn Pro Gln Pro Ala Ile Val Trp Ala Ser Ser	
	35
Ser Ser Val Tyr Gly Leu Asn Glu Lys Val Pro Phe Ser Glu Ser Asp	
	50
Arg Thr Asp Gln Pro Ala Ser Leu Tyr Ala Ala Thr Lys Lys Ala Gly	
	65
Glu Glu Ile Thr His Thr Tyr Asn His Ile Tyr Gly Leu Ala Ile Thr	
	85
Gly Leu Arg Phe Phe Thr Val Tyr Gly Pro Trp Gly Arg Pro Asp Met	
	100
Ala Tyr Phe Ser Phe Thr Arg Asn Ile Leu Gln Gly Lys Pro Ile Thr	
	115
Ile Tyr Arg Gly Lys Asn Arg Val Asp Leu Ala Arg Asp Phe Thr Tyr	
	130
Ile Asp Asp Ile Val Lys Gly Cys Leu Gly Ser Leu Asp Ser Ser Gly	
	145
Lys Ser Thr Gly Ser Gly	
	165

(2) INFORMATION FOR SEQ ID NO:1364:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1142 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1142

(D) OTHER INFORMATION: / Ceres Seq. ID 1569732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364:

aagtcatctt	ctctctcTtt	tttttagtgt	gtgcaaagtc	atcttctctt	ttaatattta	60
cctaaaaattc	caaacaaaag	agaacgttat	gaacccaaag	agcaaaagttg	cagaatctac	120
agctgcacaa	tgttttctcg	tcatgagctt	gttatgcagc	tgcatatttg	gtgacccaaat	180
ggagactaat	aatgaaggct	tgtctttacag	ttactacgag	aaaacttgtc	ccaaagtgcga	240

agagatagtg	agatcttcac	tttcatcaat	gtttatactt	gatactactt	ctcctgcagc	300
cttgctaagg	cttatgtttc	atgactgcca	agttcaggga	tgtagacgat	ctatctactt	360
cgagccaatt	agagaccaac	agttcaccca	gcttgattca	gccaagaact	tcggatcag	420
aaagagggac	ctggttggct	ctatcaaaac	ctcactagag	cttgagtgtc	ccaagcaagt	480
ctcatgtctt	gaagtcata	tcctcgccgc	cagagacgcc	gtggctctca	cgggagcccc	540
actcatctcc	gtgccattag	gacgaaaaga	ctccctctcc	actccaagca	aacacgtggc	600
agactctgag	cttctctcct	ccactgctga	cgttgacact	accttaagcc	tattcgctaa	660
caaaggcatg	accatcgaag	agtcctgtgc	catcatgggt	gcacatacga	taggagtcac	720
acattgcaac	aacgtattat	cgcgttttca	taacgcaaac	gcgacaagcg	agaacatgga	780
tcacgttttt	caaacgtttc	tgcggtttgc	ttgtccagag	ttttctccaa	cttctcaagc	840
tgccgaagcg	acattttgtc	ccaacgatca	aacttcgggt	atcttcgata	cagcttatta	900
cgatgatgcc	atcgccggac	gtggcaatct	taggattgac	tcggagattg	gagctgatcc	960
acgtacacgt	ccattttgtg	aagcgtttgc	agctgatcaa	gaccgtttct	tcaacgcott	1020
ctctctccgc	tttgtaaaat	tgctgtctta	caaagtgtaa	accgggaatg	aaggagtaat	1080
tagaagcggt	tgtgacaaag	ttgattgatg	tatatattata	attatcaaat	gttaaaaaata	1140
tt						

(2) INFORMATION FOR SEQ ID NO:1365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..368
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569733

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365:

Ser	His	Leu	Leu	Ser	Leu	Phe	Phe	Ser	Val	Cys	Lys	Val	Ile	Phe	Ser
1			5						10				15		
Phe	Asn	Ile	Tyr	Leu	Lys	Phe	Gln	Thr	Lys	Glu	Asn	Val	Met	Lys	Pro
			20					25					30		
Lys	Ser	Lys	Val	Ala	Glu	Ser	Thr	Ala	Ala	Ser	Cys	Phe	Leu	Val	Met
		35					40					45			
Ser	Leu	Leu	Cys	Ser	Cys	Ile	Ile	Gly	Asp	Gln	Met	Glu	Thr	Asn	Asn
		50				55					60				
Glu	Gly	Leu	Ser	Tyr	Ser	Tyr	Tyr	Glu	Lys	Thr	Cys	Pro	Lys	Val	Glu
		65		70					75				80		
Glu	Ile	Val	Arg	Ser	Ser	Leu	Ser	Ser	Met	Phe	Ile	Leu	Asp	Pro	Thr
		85						90					95		
Ser	Pro	Ala	Ala	Leu	Leu	Arg	Leu	Met	Phe	His	Asp	Cys	Gln	Val	Gln
		100					105						110		
Gly	Cys	Asp	Ala	Ser	Ile	Leu	Leu	Glu	Pro	Ile	Arg	Asp	Gln	Gln	Phe
		115				120					125				
Thr	Glu	Leu	Asp	Ser	Ala	Lys	Asn	Phe	Gly	Ile	Arg	Lys	Arg	Asp	Leu
		130				135					140				
Val	Gly	Ser	Ile	Lys	Thr	Ser	Leu	Glu	Leu	Glu	Cys	Pro	Lys	Gln	Val
		145			150					155				160	
Ser	Cys	Ser	Asp	Val	Ile	Ile	Leu	Ala	Ala	Arg	Asp	Ala	Val	Ala	Leu
			165					170					175		
Thr	Gly	Gly	Pro	Leu	Ile	Ser	Val	Pro	Leu	Gly	Arg	Lys	Asp	Ser	Leu
		180					185						190		
Ser	Thr	Pro	Ser	Lys	His	Val	Ala	Asp	Ser	Glu	Leu	Pro	Pro	Ser	Thr
		195					200					205			
Ala	Asp	Val	Asp	Thr	Thr	Leu	Ser	Leu	Phe	Ala	Asn	Lys	Gly	Met	Thr
		210				215						220			
Ile	Glu	Glu	Ser	Val	Ala	Ile	Met	Gly	Ala	His	Thr	Ile	Gly	Val	Thr
		225				230				235					240
His	Cys	Asn	Asn	Val	Leu	Ser	Arg	Phe	Asp	Asn	Ala	Asn	Ala	Thr	Ser
			245					250					255		
Glu	Asn	Met	Asp	Pro	Arg	Phe	Gln	Thr	Phe	Leu	Arg	Val	Ala	Cys	Pro

										260											265											270
Glu	Phe	Ser	Pro	Thr	Ser	Gln	Ala	Ala	Glu	Ala	Thr	Phe	Val	Pro	Asn																	
										275											280											285
Asp	Gln	Thr	Ser	Val	Ile	Phe	Asp	Thr	Ala	Tyr	Tyr	Asp	Asp	Ala	Ile																	
										290											295											300
Ala	Gly	Arg	Gly	Asn	Leu	Arg	Ile	Asp	Ser	Glu	Ile	Gly	Ala	Asp	Pro																	
										305											310											315
Arg	Thr	Arg	Pro	Phe	Val	Glu	Ala	Phe	Ala	Ala	Asp	Gln	Asp	Arg	Phe																	
										325											330											335
Phe	Asn	Ala	Phe	Ser	Ser	Ala	Phe	Val	Lys	Leu	Ser	Ser	Tyr	Lys	Val																	
										340											345											350
Leu	Thr	Gly	Asn	Glu	Gly	Val	Ile	Arg	Ser	Val	Cys	Asp	Lys	Val	Asp																	
										355											360											365

(2) INFORMATION FOR SEQ ID NO:1366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..339

(D) OTHER INFORMATION: / Ceres Seq. ID 1569734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366:

Met	Lys	Pro	Lys	Ser	Lys	Val	Ala	Glu	Ser	Thr	Ala	Ala	Ser	Cys	Phe
1			5					10						15	
Leu	Val	Met	Ser	Leu	Leu	Cys	Ser	Cys	Ile	Ile	Gly	Asp	Gln	Met	Glu
			20					25					30		
Thr	Asn	Asn	Glu	Gly	Leu	Ser	Tyr	Ser	Tyr	Tyr	Glu	Lys	Thr	Cys	Pro
			35				40					45			
Lys	Val	Glu	Glu	Ile	Val	Arg	Ser	Ser	Leu	Ser	Ser	Met	Phe	Ile	Leu
			50				55					60			
Asp	Pro	Thr	Ser	Pro	Ala	Ala	Leu	Leu	Arg	Leu	Met	Phe	His	Asp	Cys
			65				70					75			80
Gln	Val	Gln	Gly	Cys	Asp	Ala	Ser	Ile	Leu	Leu	Glu	Pro	Ile	Arg	Asp
			85					90						95	
Gln	Gln	Phe	Thr	Glu	Leu	Asp	Ser	Ala	Lys	Asn	Phe	Gly	Ile	Arg	Lys
			100					105					110		
Arg	Asp	Leu	Val	Gly	Ser	Ile	Lys	Thr	Ser	Leu	Glu	Leu	Glu	Cys	Pro
			115				120						125		
Lys	Gln	Val	Ser	Cys	Ser	Asp	Val	Ile	Ile	Leu	Ala	Ala	Arg	Asp	Ala
			130				135					140			
Val	Ala	Leu	Thr	Gly	Gly	Pro	Leu	Ile	Ser	Val	Pro	Leu	Gly	Arg	Lys
			145				150					155			160
Asp	Ser	Leu	Ser	Thr	Pro	Ser	Lys	His	Val	Ala	Asp	Ser	Glu	Leu	Pro
			165					170						175	
Pro	Ser	Thr	Ala	Asp	Val	Asp	Thr	Thr	Leu	Ser	Leu	Phe	Ala	Asn	Lys
			180				185						190		
Gly	Met	Thr	Ile	Glu	Glu	Ser	Val	Ala	Ile	Met	Gly	Ala	His	Thr	Ile
			195				200					205			
Gly	Val	Thr	His	Cys	Asn	Asn	Val	Leu	Ser	Arg	Phe	Asp	Asn	Ala	Asn
			210				215					220			
Ala	Thr	Ser	Glu	Asn	Met	Asp	Pro	Arg	Phe	Gln	Thr	Phe	Leu	Arg	Val
			225				230					235			240
Ala	Cys	Pro	Glu	Phe	Ser	Pro	Thr	Ser	Gln	Ala	Ala	Glu	Ala	Thr	Phe
			245					250						255	
Val	Pro	Asn	Asp	Gln	Thr	Ser	Val	Ile	Phe	Asp	Thr	Ala	Tyr	Tyr	Asp
			260					265					270		

Asp Ala Ile Ala Gly Arg Gly Asn Leu Arg Ile Asp Ser Glu Ile Gly
275 280 285
Ala Asp Pro Arg Thr Arg Pro Phe Val Glu Ala Phe Ala Ala Asp Gln
290 295 300
Asp Arg Phe Phe Asn Ala Phe Ser Ser Ala Phe Val Lys Leu Ser Ser
305 310 315 320
Tyr Lys Val Leu Thr Gly Asn Glu Gly Val Ile Arg Ser Val Cys Asp
325 330 335
Lys Val Asp

(2) INFORMATION FOR SEQ ID NO:1367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..321

(D) OTHER INFORMATION: / Ceres Seq. ID 1569735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367:

Met Ser Leu Leu Cys Ser Cys Ile Ile Gly Asp Gln Met Glu Thr Asn
1 5 10 15
Asn Glu Gly Leu Ser Tyr Ser Tyr Tyr Glu Lys Thr Cys Pro Lys Val
20 25 30
Glu Glu Ile Val Arg Ser Ser Leu Ser Ser Met Phe Ile Leu Asp Pro
35 40 45
Thr Ser Pro Ala Ala Leu Leu Arg Leu Met Phe His Asp Cys Gln Val
50 55 60
Gln Gly Cys Asp Ala Ser Ile Leu Leu Glu Pro Ile Arg Asp Gln Gln
65 70 75 80
Phe Thr Glu Leu Asp Ser Ala Lys Asn Phe Gly Ile Arg Lys Arg Asp
85 90 95
Leu Val Gly Ser Ile Lys Thr Ser Leu Glu Leu Glu Cys Pro Lys Gln
100 105 110
Val Ser Cys Ser Asp Val Ile Ile Leu Ala Ala Arg Asp Ala Val Ala
115 120 125
Leu Thr Gly Gly Pro Leu Ile Ser Val Pro Leu Gly Arg Lys Asp Ser
130 135 140
Leu Ser Thr Pro Ser Lys His Val Ala Asp Ser Glu Leu Pro Pro Ser
145 150 155 160
Thr Ala Asp Val Asp Thr Thr Leu Ser Leu Phe Ala Asn Lys Gly Met
165 170 175
Thr Ile Glu Glu Ser Val Ala Ile Met Gly Ala His Thr Ile Gly Val
180 185 190
Thr His Cys Asn Asn Val Leu Ser Arg Phe Asp Asn Ala Asn Ala Thr
195 200 205
Ser Glu Asn Met Asp Pro Arg Phe Gln Thr Phe Leu Arg Val Ala Cys
210 215 220
Pro Glu Phe Ser Pro Thr Ser Gln Ala Ala Glu Ala Thr Phe Val Pro
225 230 235 240
Asn Asp Gln Thr Ser Val Ile Phe Asp Thr Ala Tyr Tyr Asp Asp Ala
245 250 255
Ile Ala Gly Arg Gly Asn Leu Arg Ile Asp Ser Glu Ile Gly Ala Asp
260 265 270
Pro Arg Thr Arg Pro Phe Val Glu Ala Phe Ala Ala Asp Gln Asp Arg
275 280 285
Phe Phe Asn Ala Phe Ser Ser Ala Phe Val Lys Leu Ser Ser Tyr Lys
290 295 300
Val Leu Thr Gly Asn Glu Gly Val Ile Arg Ser Val Cys Asp Lys Val

305 310 315 320
Asp

(2) INFORMATION FOR SEQ ID NO:1368:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1672 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1672

(D) OTHER INFORMATION: / Ceres Seq. ID 1569744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:

```
tacgaagcag aagacagaac ccaaaaacog acaaaagctcc cctattctct cgaaaattca 60
ttactcttaa agatggatgt tgtagggtggc tgatgactct tcttccctag catgaccttt 120
attgatacca agatgtgtat gagaagaacac aacatcaatt taacaacagt catagattct 180
aacgaagcca ttggtatgga acatgaatta gattctgcta gacatcaata ttcttcagtg 240
ctcactgcaa ttccattctt ctccgctaca ttgtttatct ctctctcttt gaaaatacat 300
atacgtgacg gggttcacga aagtcctttaa taacatttcc atacacaaaa cacaaatagt 360
ttagagattt gtctctaggg agatttagct atctctctgt tcaaaagatt ggctctaaag 420
tgcaagcttt tgctttaagt gggaagaaaa ggattgtgaa tcacggcatg tgtttttcca 480
aaggaatctt tgatctcggt tcacgcctgt ctgagaattt tatggatgat cctttgatcc 540
cgggattgct tgaatgtgtc ctgaagcagt gtctagcgct tgttcccggt gctaggttcc 600
catccatggg aagtgtatgc aagaaatgga ggtttgttgt ccagagcaaa gagtttatta 660
ctgtgagaag actcgtcggt atgcttgagg agtggcttta tgccttaacg atgaatgctg 720
gtgggaaaaga taaccgatgg gaggtgatgg actgtttggg acagaagcta tcatctcttc 780
caccgatgcc ttgtctcgca aaaaacaggtt ttaaggttgt tgtggttgat gggaaacttc 840
ttgtcattgt ttgtgttgtt atgatcaacg gttcgttgtt tgatctgct gatgtttatc 900
agtatgatac atgcctcaat agctggagta gactagcaga cctggaagta gctcggatgt 960
atttctgttg ttgtgaggtg aacggcgatg ttatgttgtt ggagggtgat ggggttagtg 1020
gtgagagctt gtcaagtgca gaggtgTatG aTCTgatctt gagacgtgta catggaactt 1080
catagagctc ttaaggcgct cgagggtggg ttgtttcGct agcgcttca acgggaagct 1140
atatgtgatg ggtgggaagt ccaacttcac tattgaaac tcaaaaattc ttgatgtgta 1200
caacactcaa tgtggctctt ggcattgtag caaaaaaggt ttaacgatgg tcaacagctca 1260
tgttgaagta gggaaaaagc tgttctgtat cgaactggaag aaccaccgga agatgtcggt 1320
gttcaatgcg gaagacgaac cctgggaagt ggtggctctt ccgctatcag gaagctcgag 1380
ggcggggttt cagtttggtta agctgagttg gaagcttttg ctattctcgt ttcaggaaga 1440
aaccggtcaa tgtactttac tgtatgaccg ggaatgttca ccaggcacac agtggaaaaa 1500
gtctgagatc aaactctctg ttcttctcgt atgcagtgtc acaatcacag cctgattgat 1560
accatttgtt tgtttacatt tctttttatg atccaaatcc aaagagagca ttgtcgtctc 1620
ttttaagttg atgataacac tgattttaa aagtggagag tgttttgttt gg
```

(2) INFORMATION FOR SEQ ID NO:1369:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..221

(D) OTHER INFORMATION: / Ceres Seq. ID 1569745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:

```
Met Gln Ala Phe Ala Leu Ser Gly Lys Lys Arg Ile Val Asn His Gly
1 5 10 15
Met Cys Phe Ser Lys Gly Asn Leu Asp Leu Gly Ser Arg Leu Ser Glu
20 25 30
Asn Phe Met Asp Asp Pro Leu Ile Pro Gly Leu Pro Asp Asp Val Ala
35 40 45
```

```

Lys Gln Cys Leu Ala Leu Val Pro Arg Ala Arg Phe Pro Ser Met Gly
50 55 60
Ser Val Cys Lys Lys Trp Arg Phe Val Val Gln Ser Lys Glu Phe Ile
65 70 75 80
Thr Val Arg Arg Leu Ala Gly Met Leu Glu Glu Trp Leu Tyr Val Leu
85 90 95
Thr Met Asn Ala Gly Gly Lys Asp Asn Arg Trp Glu Val Met Asp Cys
100 105 110
Leu Gly Gln Lys Leu Ser Ser Leu Pro Pro Met Pro Gly Pro Ala Lys
115 120 125
Thr Gly Phe Lys Val Val Val Val Asp Gly Lys Leu Leu Val Ile Ala
130 135 140
Gly Cys Cys Met Ile Asn Gly Ser Leu Val Ala Ser Ala Asp Val Tyr
145 150 155 160
Gln Tyr Asp Thr Cys Leu Asn Ser Trp Ser Arg Leu Ala Asp Leu Glu
165 170 175
Val Ala Arg Tyr Asp Phe Ala Cys Ala Glu Val Asn Gly His Val Tyr
180 185 190
Val Val Gly Gly His Gly Val Asp Gly Glu Ser Leu Ser Ser Ala Glu
195 200 205
Val Tyr Asp Leu Ile Leu Arg Arg Val His Gly Leu Ser
210 215 220

```

(2) INFORMATION FOR SEQ ID NO:1370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..205

(D) OTHER INFORMATION: / Ceres Seq. ID 1569746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370:

```

Met Cys Phe Ser Lys Gly Asn Leu Asp Leu Gly Ser Arg Leu Ser Glu
1 5 10 15
Asn Phe Met Asp Asp Pro Leu Ile Pro Gly Leu Pro Asp Asp Val Ala
20 25 30
Lys Gln Cys Leu Ala Leu Val Pro Arg Ala Arg Phe Pro Ser Met Gly
35 40 45
Ser Val Cys Lys Lys Trp Arg Phe Val Val Gln Ser Lys Glu Phe Ile
50 55 60
Thr Val Arg Arg Leu Ala Gly Met Leu Glu Glu Trp Leu Tyr Val Leu
65 70 75 80
Thr Met Asn Ala Gly Gly Lys Asp Asn Arg Trp Glu Val Met Asp Cys
85 90 95
Leu Gly Gln Lys Leu Ser Ser Leu Pro Pro Met Pro Gly Pro Ala Lys
100 105 110
Thr Gly Phe Lys Val Val Val Val Asp Gly Lys Leu Leu Val Ile Ala
115 120 125
Gly Cys Cys Met Ile Asn Gly Ser Leu Val Ala Ser Ala Asp Val Tyr
130 135 140
Gln Tyr Asp Thr Cys Leu Asn Ser Trp Ser Arg Leu Ala Asp Leu Glu
145 150 155 160
Val Ala Arg Tyr Asp Phe Ala Cys Ala Glu Val Asn Gly His Val Tyr
165 170 175
Val Val Gly Gly His Gly Val Asp Gly Glu Ser Leu Ser Ser Ala Glu
180 185 190
Val Tyr Asp Leu Ile Leu Arg Arg Val His Gly Leu Ser
195 200 205

```

(2) INFORMATION FOR SEQ ID NO:1371:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..187
(D) OTHER INFORMATION: / Ceres Seq. ID 1569747
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371:

Met	Asp	Asp	Pro	Leu	Ile	Pro	Gly	Leu	Pro	Asp	Asp	Val	Ala	Lys	Gln
1			5				10					15			
Cys	Leu	Ala	Leu	Val	Pro	Arg	Ala	Arg	Phe	Pro	Ser	Met	Gly	Ser	Val
			20				25					30			
Cys	Lys	Lys	Trp	Arg	Phe	Val	Val	Gln	Ser	Lys	Glu	Phe	Ile	Thr	Val
			35				40				45				
Arg	Arg	Leu	Ala	Gly	Met	Leu	Glu	Glu	Trp	Leu	Tyr	Val	Leu	Thr	Met
			50			55					60				
Asn	Ala	Gly	Gly	Lys	Asp	Asn	Arg	Trp	Glu	Val	Met	Asp	Cys	Leu	Gly
65				70					75					80	
Gln	Lys	Leu	Ser	Ser	Leu	Pro	Pro	Met	Pro	Gly	Pro	Ala	Lys	Thr	Gly
			85						90				95		
Phe	Lys	Val	Val	Val	Val	Asp	Gly	Lys	Leu	Leu	Val	Ile	Ala	Gly	Cys
			100				105					110			
Cys	Met	Ile	Asn	Gly	Ser	Leu	Val	Ala	Ser	Ala	Asp	Val	Tyr	Gln	Tyr
			115			120					125				
Asp	Thr	Cys	Leu	Asn	Ser	Trp	Ser	Arg	Leu	Ala	Asp	Leu	Glu	Val	Ala
			130			135					140				
Arg	Tyr	Asp	Phe	Ala	Cys	Ala	Glu	Val	Asn	Gly	His	Val	Tyr	Val	Val
			145			150				155				160	
Gly	Gly	His	Gly	Val	Asp	Gly	Glu	Ser	Leu	Ser	Ser	Ala	Glu	Val	Tyr
			165				170						175		
Asp	Leu	Ile	Leu	Arg	Arg	Val	His	Gly	Leu	Ser					
			180				185								

(2) INFORMATION FOR SEQ ID NO:1372:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1412
(D) OTHER INFORMATION: / Ceres Seq. ID 1569748
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372:

actcaatcgt	cattctctcg	gtatctctctc	ctcgaaagaa	gaatgcctgg	aattagaggt	60
ccttcggaat	actgcagga	accactctct	cacctctctc	tcaaggtcaa	cgccaaggaa	120
ccttccaaag	ccgagcctcc	ccgctcgccc	ttagtctctc	cttatgtcac	tcccgctcac	180
ctttctotaca	agcgaatca	tggtcccatc	cccattgttg	atcaccttca	aagctactcc	240
gtcacccctta	ctggattgat	ccagaaccgc	agaaaagctc	ttatcaaga	catcaggctcc	300
ctcccaaagt	acaattgttac	tgctactctt	cttggtccgg	taacagaagg	actgccaatga	360
gcaaaagttag	gaatgttaga	ggtgttggt	gggatgtttc	tgctattggc	aacgctgtct	420
gggggtggggc	gaaactggcc	gatgttcttg	agcttctggg	gataccaaag	ctgactgott	480
ctaccaattt	aggagccaga	catgttgagt	tcgttagtgt	tgatcgctgt	aaggaggaaa	540
atggggggccc	ttataaggcg	ctaatcactc	taagtcaagc	cacaaatctc	gaagcgggat	600
ttctacccct	tatgatagta	atggagagac	cctgaacagg	gatcacggat	ttccgttaag	660
gggtgtgtgtc	cctggtgtga	ttggtgctcg	tatcagwcaa	atggcttgat	tcacatcaat	720
tcatcgctga	agaaagccag	ggattcttca	tgcaaaaaga	ttacaaaatg	tttccaccc	780
ctgtcaattg	ggataaatc	aactgggtcc	ctaggagacc	gcaaatggat	ttccctgttc	840

agagtgc	atgctctgtg	gaggatgtgc	aaatggtgaa	gcctggaaa	gtaagtatca	900
aaggatatgc	gggttcagga	ggtggacgcg	ggatagaaa	agtgagacata	tccttggtg	960
gagggaaaaa	ctgggtggaa	gcttctagaa	cgaggaacc	aggaagcag	tacatctcag	1020
aaacacagctc	cagtgacaaa	tgggcatggg	tgtgtttga	agccaccatt	gatgtttcac	1080
agactacaga	ggtcatgcc	aaagcggttg	attcggcggc	gaatgttcaa	ccggaaaatg	1140
tggagtcggt	gtggaaacct	agaggagttc	tcaaCacttc	gtggcacctg	gtccttctcc	1200
ggcttggcca	ctctaaactg	tagaccaagt	taccactatg	ctgtctggtc	ctctttatct	1260
tttctttaag	aactaaaaa	tccttgaata	tgcttgcct	tgtgagctg	ttagagacaa	1320
atactgttta	tagttaaata	aaatgggaaa	accatctgt	tgtcatgtgg	tggattataa	1380
attattttatt	tatatgatag	aactgtttatt	cg			

(2) INFORMATION FOR SEQ ID NO:1373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1569749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:

Met	Gln	Lys	Asp	Tyr	Lys	Met	Phe	Pro	Pro	Ser	Val	Asn	Trp	Asp	Asn
1				5						10				15	
Ile	Asn	Trp	Ser	Ser	Arg	Arg	Pro	Gln	Met	Asp	Phe	Pro	Val	Gln	Ser
			20					25					30		
Ala	Ile	Cys	Ser	Val	Glu	Asp	Val	Gln	Met	Val	Lys	Pro	Gly	Lys	Val
			35				40				45				
Ser	Ile	Lys	Gly	Tyr	Ala	Val	Ser	Gly	Gly	Gly	Arg	Gly	Ile	Glu	Arg
			50			55				60					
Val	Asp	Ile	Ser	Leu	Asp	Gly	Gly	Lys	Asn	Trp	Val	Glu	Ala	Ser	Arg
			65		70				75				80		
Thr	Gln	Glu	Pro	Gly	Lys	Gln	Tyr	Ile	Ser	Glu	His	Ser	Ser	Ser	Asp
				85					90				95		
Lys	Trp	Ala	Trp	Val	Leu	Phe	Glu	Ala	Thr	Ile	Asp	Val	Ser	Gln	Thr
			100					105					110		
Thr	Glu	Val	Ile	Ala	Lys	Ala	Val	Asp	Ser	Ala	Ala	Asn	Val	Gln	Pro
			115				120					125			
Glu	Asn	Val	Glu	Ser	Val	Trp	Asn	Leu	Arg	Gly	Val	Leu	Asn	Thr	Ser
			130			135					140				
Trp	His	Arg	Val	Leu	Leu	Arg	Leu	Gly	His	Ser	Asn	Leu			
			145		150			155							

(2) INFORMATION FOR SEQ ID NO:1374:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1569750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:

Met	Phe	Pro	Pro	Ser	Val	Asn	Trp	Asp	Asn	Ile	Asn	Trp	Ser	Ser	Arg
1				5					10				15		
Arg	Pro	Gln	Met	Asp	Phe	Pro	Val	Gln	Ser	Ala	Ile	Cys	Ser	Val	Glu
			20					25					30		
Asp	Val	Gln	Met	Val	Lys	Pro	Gly	Lys	Val	Ser	Ile	Lys	Gly	Tyr	Ala
			35				40					45			
Val	Ser	Gly	Gly	Gly	Arg	Gly	Ile	Glu	Arg	Val	Asp	Ile	Ser	Leu	Asp

50	55	60
Gly Gly Lys Asn Trp Val Glu Ala Ser Arg Thr Gln Glu Pro Gly Lys		
65	70	75
Gln Tyr Ile Ser Glu His Ser Ser Ser Asp Lys Trp Ala Trp Val Leu		80
	85	90
Phe Glu Ala Thr Ile Asp Val Ser Gln Thr Thr Glu Val Ile Ala Lys		95
	100	105
Ala Val Asp Ser Ala Ala Asn Val Gln Pro Glu Asn Val Glu Ser Val		110
	115	120
Trp Asn Leu Arg Gly Val Leu Asn Thr Ser Trp His Arg Val Leu Leu		125
	130	135
Arg Leu Gly His Ser Asn Leu		140
	145	150

(2) INFORMATION FOR SEQ ID NO:1375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1569751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:

Met Asp Phe Pro Val Gln Ser Ala Ile Cys Ser Val Glu Asp Val Gln	
1	5
Met Val Lys Pro Gly Lys Val Ser Ile Lys Gly Tyr Ala Val Ser Gly	
	20
Gly Gly Arg Gly Ile Glu Arg Val Asp Ile Ser Leu Asp Gly Gly Lys	
	35
Asn Trp Val Glu Ala Ser Arg Thr Gln Glu Pro Gly Lys Gln Tyr Ile	
	50
Ser Glu His Ser Ser Ser Asp Lys Trp Ala Trp Val Leu Phe Glu Ala	
	65
Thr Ile Asp Val Ser Gln Thr Thr Glu Val Ile Ala Lys Ala Val Asp	
	85
Ser Ala Ala Asn Val Gln Pro Glu Asn Val Glu Ser Val Trp Asn Leu	
	100
Arg Gly Val Leu Asn Thr Ser Trp His Arg Val Leu Leu Arg Leu Gly	
	115
His Ser Asn Leu	
	130

(2) INFORMATION FOR SEQ ID NO:1376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1221

(D) OTHER INFORMATION: / Ceres Seq. ID 1569760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:

aattctataat catttttgta ctcttgagc actctctctt ctttgtctct gtgactcaca	60
ttcatccaat ccaggaggca tgcgcacatc tgaggataaa ccggaataca tcagtagagt	120
agttcatcag gaggttgacg tggaaaAtcg tcgatagaag tcagaaggat aagmcgagg	180
aaaaagaaga aggraaaagg ggattctctg ataaggtgaa agatttcatt catgcacattg	240
gtgagaaact cgagggaacc attggctttg ggaagccaac tgctgatgtc tctgcgattc	300
atatccctaa gatcaattct gagaggcgag atattgttgt ggatgtgctt gtcaagaacc	360

cgaatccagt	tccatccct	ctcatcgatg	tcaactacct	ggtcgagagc	gatgggagga	420
aactgggttc	tgggtttgatc	cgggatgctg	gaacactcaa	ggctcatgga	gaagaaactg	480
tgaagatacc	attgaagcttg	atNcTatgat	gacatcaaga	gcacttacaa	cgatatacaac	540
cccgggatga	tcatacctta	cagaatcaa	gttgatctga	ttgtggatgt	gccagattatg	600
ggaagactga	cattgccgct	ggagaaatgt	ggagagatcc	caattccaaa	gaaacctgat	660
gttgatatacg	agaagattaa	gttccagaag	ttctcttttg	aggaaacctg	ggcgattctc	720
catgtgaggg	ttcagaacat	gaatgatctc	gactttgggg	tcaatgactt	ggactgtgaa	780
gtttggctct	gtgatgttaag	cattgggaaa	gcagagatcg	cggactcgat	caagcttgac	840
aaaaacggaa	gcggattgat	taatgtgccg	atgacattcc	gaccaaaagg	ctttggttct	900
gcgctttggg	atatgattcc	tggttaaagg	acagggtaca	caatcaaagg	taattattgat	960
gttgatacac	catttgagac	tatgaagctt	cttattatca	aggaaggtgg	agagaccctg	1020
ctgaagaagg	aagatgatga	tgacgacgat	gagtaataag	gaaacaaagt	gctgcagaga	1080
cagaatggtc	atagtacta	aatctccgat	cttgaaatgt	ctatttaaaa	ttaaaaaaa	1140
aaagaaaagac	ttgtttttgt	tgcttttga	taactgatgg	atcagacttt	tgaatagagc	1200
cgctcttttta	ttggactctt	t				

(2) INFORMATION FOR SEQ ID NO:1377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1569761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377:

Met	Ile	Ile	Pro	Tyr	Arg	Ile	Lys	Val	Asp	Leu	Ile	Val	Asp	Val	Pro
1			5					10						15	
Val	Leu	Gly	Arg	Leu	Thr	Leu	Pro	Leu	Glu	Lys	Cys	Gly	Glu	Ile	Pro
			20					25					30		
Ile	Pro	Lys	Lys	Pro	Asp	Val	Asp	Ile	Glu	Lys	Ile	Lys	Phe	Gln	Lys
			35				40					45			
Phe	Ser	Leu	Glu	Glu	Thr	Val	Ala	Ile	Leu	His	Val	Arg	Leu	Gln	Asn
			50				55				60				
Met	Asn	Asp	Phe	Asp	Leu	Gly	Leu	Asn	Asp	Leu	Asp	Cys	Glu	Val	Trp
			65			70			75					80	
Leu	Cys	Asp	Val	Ser	Ile	Gly	Lys	Ala	Glu	Ile	Ala	Asp	Ser	Ile	Lys
			85						90					95	
Leu	Asp	Lys	Asn	Gly	Ser	Gly	Leu	Ile	Asn	Val	Pro	Met	Thr	Phe	Arg
			100					105					110		
Pro	Lys	Asp	Phe	Gly	Ser	Ala	Leu	Trp	Asp	Met	Ile	Arg	Gly	Lys	Gly
			115				120					125			
Thr	Gly	Tyr	Thr	Ile	Lys	Gly	Asn	Ile	Asp	Val	Asp	Thr	Pro	Phe	Gly
			130				135					140			
Ala	Met	Lys	Leu	Pro	Ile	Ile	Lys	Glu	Gly	Gly	Glu	Thr	Arg	Leu	Lys
			145				150			155				160	
Lys	Glu	Asp	Asp	Asp	Asp	Asp	Asp	Glu							
															165

(2) INFORMATION FOR SEQ ID NO:1378:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1569762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378:

Met Asn Asp Phe Asp Leu Gly Leu Asn Asp Leu Asp Cys Glu Val Trp
1 5 10 15
Leu Cys Asp Val Ser Ile Gly Lys Ala Glu Ile Ala Asp Ser Ile Lys
20 25 30
Leu Asp Lys Asn Gly Ser Gly Leu Ile Asn Val Pro Met Thr Phe Arg
35 40 45
Pro Lys Asp Phe Gly Ser Ala Leu Trp Asp Met Ile Arg Gly Lys Gly
50 55 60
Thr Gly Tyr Thr Ile Lys Gly Asn Ile Asp Val Asp Thr Pro Phe Gly
65 70 75 80
Ala Met Lys Leu Pro Ile Ile Lys Glu Gly Glu Thr Arg Leu Lys
85 90 95
Lys Glu Asp Asp Asp Asp Asp Asp Glu
100 105

(2) INFORMATION FOR SEQ ID NO:1379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1355
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379:

aactctcttc	tcttctctag	tcttctcttc	tattatgcaa	aaggtctctt	tggccatgga	60
tacttctgct	ctagtaaatcc	atcagttctct	gtctcgcctc	aaactttctc	ctcccaaatc	120
tcttctcttc	tcttctcttc	ctgcttcttc	ccctgaatcc	ttaccgatca	gacggatcca	180
gtctgttttc	cgaggagcta	tatgtgcgcc	cgtacaaaga	aactacgaag	aaacgacctc	240
ctccgtgtaa	gaggcagagg	aagatgatga	gtcatcatca	tcgtacggag	aagtgaacaa	300
gatacttgga	agccgaacgg	cgBgggaagg	agccatggag	tacctatcgc	agtggaagca	360
cgccattctc	ccgtcgtggg	ttccatcgag	ctacatcgca	gcagacgtaG	tgtcggagta	420
cgagacaccc	tgtgtggacgg	cagctagaaa	agccgacgag	caggccctgt	cacagctcct	480
ggaggaccga	gacgtcgatg	ccgtggacga	aagcggccgg	acggctctgc	ttttcgtggc	540
aggtctgggg	tccggacaagt	gcgtaaggct	tctggcggag	gctggagcgc	atctcgacca	600
ccgagacatg	aggggaggct	tgacggcgct	gcacatggcg	gctgtgtaacg	tgaggccgga	660
ggtgtgtggg	gcgctgtggg	agctggggag	tgatattgaa	gtggaagacg	agagaggggt	720
aacggcgctt	gaactagcga	gggagattct	gaagacgacg	ccgaagggga	atccgatcca	780
gttcggggag	agaatttggt	tagagaaagt	gatcaatgtc	ctggaaggac	aagtggtcca	840
gtaccccgag	gtggatgaga	ctgtagagaa	acgagggaaa	ggcaagacgc	ttgaatatct	900
ggtcagatgt	aaggacgggt	gagattgcga	gtgggtgaaa	ggtgtacacg	tggcggaaga	960
tgtggctaag	gactacgagg	atgggctgga	gtacgctgta	gcggagagtg	tgtatcgggaa	1020
gagggtggga	gacgatggga	agaccatcga	gtatcttctc	aatggactgc	atatgtctga	1080
tgcacttggg	gaagctcagg	acaatgtcga	ctctactctt	gttctactct	accaacaaca	1140
acaaccaata	aatgaatgat	tgattttgat	gattacattc	ttctcaattt	gctttctttt	1200
catatgtgtt	ggttcatctg	accggttcgg	ttggtaacga	coggtacatt	ttcattttct	1260
tttaagatgt	gactcttgat	gtttttggcc	ttttggggag	actatttgat	ttatatccga	1320
tgctttgaat	ttgtcttccc	tttttgggga	gattc			

(2) INFORMATION FOR SEQ ID NO:1380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..385
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380:

Thr Leu Phe Ser Ser Leu Val Leu Ser Ser Ile Met Gln Lys Val Phe
1 5 10 15
Leu Ala Met Asp Thr Cys Ala Leu Val Ile His Gln Ser Leu Ser Arg
20 25 30
Ile Lys Leu Ser Pro Pro Lys Ser Ser Ser Ser Ser Ser Ala
35 40 45
Phe Ser Pro Glu Ser Leu Pro Ile Arg Arg Ile Glu Leu Cys Phe Arg
50 55 60
Gly Ala Ile Cys Ala Ala Val Gln Arg Asn Tyr Glu Glu Thr Thr Ser
65 70 75 80
Ser Val Glu Glu Ala Glu Glu Asp Asp Glu Ser Ser Ser Ser Tyr Gly
85 90 95
Glu Val Asn Lys Ile Ile Gly Ser Arg Thr Ala Xaa Glu Gly Ala Met
100 105 110
Glu Tyr Leu Ile Glu Trp Lys Asp Gly His Ser Pro Ser Trp Val Pro
115 120 125
Ser Ser Tyr Ile Ala Ala Asp Val Val Ser Glu Tyr Glu Thr Pro Trp
130 135 140
Trp Thr Ala Ala Arg Lys Ala Asp Glu Gln Ala Leu Ser Gln Leu Leu
145 150 155 160
Glu Asp Arg Asp Val Asp Ala Val Asp Glu Ser Gly Arg Thr Ala Leu
165 170 175
Leu Phe Val Ala Gly Leu Gly Ser Asp Lys Cys Val Arg Leu Leu Ala
180 185 190
Glu Ala Gly Ala Asp Leu Asp His Arg Asp Met Arg Gly Gly Leu Thr
195 200 205
Ala Leu His Met Ala Ala Gly Tyr Val Arg Pro Glu Val Val Glu Ala
210 215 220
Leu Val Glu Leu Gly Ala Asp Ile Glu Val Glu Asp Glu Arg Gly Leu
225 230 235 240
Thr Ala Leu Glu Leu Ala Arg Glu Ile Leu Lys Thr Thr Pro Lys Gly
245 250 255
Asn Pro Met Gln Phe Gly Arg Arg Ile Gly Leu Glu Lys Val Ile Asn
260 265 270
Val Leu Glu Gly Gln Val Phe Glu Tyr Ala Glu Val Asp Glu Ile Val
275 280 285
Glu Lys Arg Gly Lys Gly Lys Asp Val Glu Tyr Leu Val Arg Trp Lys
290 295 300
Asp Gly Gly Asp Cys Glu Trp Val Lys Gly Val His Val Ala Glu Asp
305 310 315 320
Val Ala Lys Asp Tyr Glu Asp Gly Leu Glu Tyr Ala Val Ala Glu Ser
325 330 335
Val Ile Gly Lys Arg Val Gly Asp Asp Gly Lys Thr Ile Glu Tyr Leu
340 345 350
Val Lys Trp Thr Asp Met Ser Asp Ala Thr Trp Glu Pro Gln Asp Asn
355 360 365
Val Asp Ser Thr Leu Val Leu Leu Tyr Gln Gln Gln Pro Ile Asn
370 375 380
Glu
385

(2) INFORMATION FOR SEQ ID NO:1381:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 374 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..374
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569777

SEQUENCE INFORMATION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381:

Met	Gln	Lys	Val	Phe	Leu	Ala	Met	Asp	Thr	Cys	Ala	Leu	Val	Ile	His
1			5					10					15		
Gln	Ser	Leu	Ser	Arg	Ile	Lys	Leu	Ser	Pro	Pro	Lys	Ser	Ser	Ser	
			20					25					30		
Ser	Ser	Ser	Ser	Ala	Phe	Ser	Pro	Glu	Ser	Leu	Pro	Ile	Arg	Arg	Ile
			35				40					45			
Glu	Leu	Cys	Phe	Arg	Gly	Ala	Ile	Cys	Ala	Ala	Val	Gln	Arg	Asn	Tyr
			50			55					60				
Glu	Glu	Thr	Thr	Ser	Ser	Val	Glu	Glu	Ala	Glu	Glu	Asp	Asp	Glu	Ser
						70				75				80	
Ser	Ser	Ser	Tyr	Gly	Glu	Val	Asn	Lys	Ile	Ile	Gly	Ser	Arg	Thr	Ala
				85					90					95	
Xaa	Glu	Gly	Ala	Met	Glu	Tyr	Leu	Ile	Glu	Trp	Lys	Asp	Gly	His	Ser
			100					105					110		
Pro	Ser	Thr	Val	Pro	Ser	Ser	Tyr	Ile	Ala	Ala	Asp	Val	Val	Ser	Glu
			115				120					125			
Tyr	Glu	Thr	Pro	Trp	Trp	Thr	Ala	Ala	Arg	Lys	Ala	Asp	Glu	Gln	Ala
			130			135					140				
Leu	Ser	Gln	Leu	Leu	Glu	Asp	Arg	Asp	Val	Asp	Ala	Val	Asp	Glu	Ser
			145			150				155				160	
Gly	Arg	Thr	Ala	Leu	Leu	Phe	Val	Ala	Gly	Leu	Gly	Ser	Asp	Lys	Cys
				165				170						175	
Val	Arg	Leu	Leu	Ala	Glu	Ala	Gly	Ala	Asp	Leu	Asp	His	Arg	Asp	Met
			180					185						190	
Arg	Gly	Gly	Leu	Thr	Ala	Leu	His	Met	Ala	Ala	Gly	Tyr	Val	Arg	Pro
			195				200					205			
Glu	Val	Val	Glu	Ala	Leu	Val	Glu	Leu	Gly	Ala	Asp	Ile	Glu	Val	Glu
			210			215					220				
Asp	Glu	Arg	Gly	Leu	Thr	Ala	Leu	Glu	Leu	Ala	Arg	Glu	Ile	Leu	Lys
				230						235				240	
Thr	Thr	Pro	Lys	Gly	Asn	Pro	Met	Gln	Phe	Gly	Arg	Arg	Ile	Gly	Leu
				245					250					255	
Glu	Lys	Val	Ile	Asn	Val	Leu	Glu	Gly	Gln	Val	Phe	Glu	Tyr	Ala	Glu
			260					265					270		
Val	Asp	Glu	Ile	Val	Glu	Lys	Arg	Gly	Lys	Gly	Lys	Asp	Val	Glu	Tyr
			275				280					285			
Leu	Val	Arg	Trp	Lys	Asp	Gly	Gly	Asp	Cys	Glu	Trp	Val	Lys	Gly	Val
			290			295					300				
His	Val	Ala	Glu	Asp	Val	Ala	Lys	Asp	Tyr	Glu	Asp	Gly	Leu	Glu	Tyr
				310						315				320	
Ala	Val	Ala	Glu	Ser	Val	Ile	Gly	Lys	Arg	Val	Gly	Asp	Asp	Gly	Lys
				325					330					335	
Thr	Ile	Glu	Tyr	Leu	Val	Lys	Trp	Thr	Asp	Met	Ser	Asp	Ala	Thr	Trp
			340					345					350		
Glu	Pro	Gln	Asp	Asn	Val	Asp	Ser	Thr	Leu	Val	Leu	Leu	Tyr	Gln	Gln
			355				360						365		
Gln	Gln	Pro	Ile	Asn	Glu										
			370												

(2) INFORMATION FOR SEQ ID NO:1382:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..367

(D) OTHER INFORMATION: / Ceres Seq. ID 1569778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382:

Met Asp Thr Cys Ala Leu Val Ile His Gln Ser Leu Ser Arg Ile Lys
1 5 10 15
Leu Ser Pro Pro Lys Ser Ser Ser Ser Ser Ser Ser Ala Phe Ser
20 25 30
Pro Glu Ser Leu Pro Ile Arg Arg Ile Glu Leu Cys Phe Arg Gly Ala
35 40 45
Ile Cys Ala Ala Val Gln Arg Asn Tyr Glu Glu Thr Thr Ser Ser Val
50 55 60
Glu Glu Ala Glu Glu Asp Asp Glu Ser Ser Ser Ser Tyr Gly Glu Val
65 70 75 80
Asn Lys Ile Ile Gly Ser Arg Thr Ala Xaa Glu Gly Ala Met Glu Tyr
85 90 95
Leu Ile Glu Trp Lys Asp Gly His Ser Pro Ser Trp Val Pro Ser Ser
100 105 110
Tyr Ile Ala Ala Asp Val Val Ser Glu Tyr Glu Thr Pro Trp Trp Thr
115 120 125
Ala Ala Arg Lys Ala Asp Glu Gln Ala Leu Ser Gln Leu Leu Glu Asp
130 135 140
Arg Asp Val Asp Ala Val Asp Glu Ser Gly Arg Thr Ala Leu Leu Phe
145 150 155 160
Val Ala Gly Leu Gly Ser Asp Lys Cys Val Arg Leu Leu Ala Glu Ala
165 170 175
Gly Ala Asp Leu Asp His Arg Asp Met Arg Gly Gly Leu Thr Ala Leu
180 185 190
His Met Ala Ala Gly Tyr Val Arg Pro Glu Val Val Glu Ala Leu Val
195 200 205
Glu Leu Gly Ala Asp Ile Glu Val Glu Asp Glu Arg Gly Leu Thr Ala
210 215 220
Leu Glu Leu Ala Arg Glu Ile Leu Lys Thr Thr Pro Lys Gly Asn Pro
225 230 235 240
Met Gln Phe Gly Arg Arg Ile Gly Leu Glu Lys Val Ile Asn Val Leu
245 250 255
Glu Gly Gln Val Phe Glu Tyr Ala Glu Val Asp Glu Ile Val Glu Lys
260 265 270
Arg Gly Lys Gly Lys Asp Val Glu Tyr Leu Val Arg Trp Lys Asp Gly
275 280 285
Gly Asp Cys Glu Trp Val Lys Gly Val His Val Ala Glu Asp Val Ala
290 295 300
Lys Asp Tyr Glu Asp Gly Leu Glu Tyr Ala Val Ala Glu Ser Val Ile
305 310 315 320
Gly Lys Arg Val Gly Asp Asp Gly Lys Thr Ile Glu Tyr Leu Val Lys
325 330 335
Trp Thr Asp Met Ser Asp Ala Thr Trp Glu Pro Gln Asp Asn Val Asp
340 345 350
Ser Thr Leu Val Leu Leu Tyr Gln Gln Gln Pro Ile Asn Glu
355 360 365

(2) INFORMATION FOR SEQ ID NO:1383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1287
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383:

acactttctt tagccattta taaacgcttc attttctatat aaacatctct tatcttgttg	60
aaaatctctc gcagcttttg aaaaacatga cttttctaaa aatgaaaagc cttttctttc	120
tcttcacat cctctctct cctctcgacc tcttcacat ctccaacga cggaagtta	180

atgtcggagg	cagtgccgcg	tgggttacaa	acccacctga	aaactacgaa	tcttggtctg	240
gcataaaccc	tttctctgtt	caogacactc	tctatttttag	ctatgctaa	ggagctga	300
cgggtcctaga	gggtgaacaag	gctgattacg	acgcttgtaa	tacaaagaat	ccgatcaaaa	360
gagtgagcaga	tggagattct	gagatctctc	ttgatcgtaa	tggtccggtt	tacttcatca	420
gtggcaatga	agataactgt	aagaagggtc	aaaagcttaa	tgctctgttc	atatctgcta	480
ggattccatc	aacggctcag	tctctctcag	ccgctgcacc	gggaagctct	acgcggggat	540
caatgaactcc	gcggggagga	gcccaactcg	ctaaatcttc	ctccctctgt	tctccgacga	600
cttctctctc	gggatcgact	actccgctg	gaggagctca	ctcgctcaaa	tcttcatcag	660
ctgtctctcc	ggcgacttct	cctccaggat	caatggcgcc	taaactccgc	tcctctgttt	720
ctccgagac	tTcAcGcacc	ggcaccacct	aaatccacgt	ccctgttttc	ccatctctct	780
gctccgatga	cttccaccgc	ggcaccgaat	gcacctaagt	catcttcaac	tattctctcc	840
tcttctgtc	cgatgacttc	accacctgga	tcaatggcac	ctaaatcttc	gtccctctgt	900
tcaaaactcac	ccacccgttc	tccatcgttg	gctccgggag	gctctacttc	ttcttccacc	960
tcagattctc	cgtaaggctg	ggcgatgggt	cctTcaggag	atggtccatc	agccgctgg	1020
gatatctcta	cgccgggttg	agctccagg	cagaaaaaat	cgctggcgaa	tggyatgacc	1080
gttatgtcka	ttactacgg	tytaagttg	gttttgacca	tctttctgtc	agcttaagaa	1140
cacttggtgag	acttggttca	tgtcggatc	gatttgttc	gtttcgggt	gagtttccaa	1200
ctttgtttta	aattgwttt	ggatcccatg	ttgattctgt	attattcagt	atagttggat	1260
tgttttgtta	taataatag	acagttc				

(2) INFORMATION FOR SEQ ID NO:1384:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..221

(D) OTHER INFORMATION: / Ceres Seq. ID 1569788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384:

Met	Thr	Phe	Leu	Lys	Met	Lys	Ser	Leu	Ser	Phe	Phe	Thr	Ile	Leu
1			5					10					15	
Leu	Ser	Leu	Ser	Thr	Leu	Phe	Thr	Ile	Ser	Asn	Ala	Arg	Lys	Phe
			20					25					30	Asn
Val	Gly	Gly	Ser	Gly	Ala	Trp	Val	Thr	Asn	Pro	Pro	Glu	Asn	Tyr
			35					40				45		Glu
Ser	Trp	Ser	Gly	Lys	Asn	Arg	Phe	Leu	Val	His	Asp	Thr	Leu	Tyr
			50					55				60		Phe
Ser	Tyr	Ala	Lys	Gly	Ala	Asp	Ser	Val	Leu	Glu	Val	Asn	Lys	Ala
			65					70				75		Asp
Tyr	Asp	Ala	Cys	Asn	Thr	Lys	Asn	Pro	Ile	Lys	Arg	Val	Asp	Asp
			85					90				95		Gly
Asp	Ser	Glu	Ile	Ser	Leu	Asp	Arg	Tyr	Gly	Pro	Phe	Tyr	Phe	Ile
			100					105				110		Ser
Gly	Asn	Glu	Asp	Asn	Cys	Lys	Lys	Gly	Gln	Lys	Leu	Asn	Val	Val
			115					120				125		Val
Ile	Ser	Ala	Arg	Ile	Pro	Ser	Thr	Ala	Gln	Ser	Pro	His	Ala	Ala
			130					135				140		Ala
Pro	Gly	Ser	Ser	Thr	Pro	Gly	Ser	Met	Thr	Pro	Pro	Gly	Gly	Ala
			145					150				155		His
Ser	Pro	Lys	Ser	Ser	Ser	Pro	Val	Ser	Pro	Thr	Thr	Ser	Pro	Gly
			165					170				175		Gly
Ser	Thr	Thr	Pro	Gly	Gly	Ala	His	Ser	Pro	Lys	Ser	Ser	Ser	Ala
			180					185				190		Ala
Val	Ser	Pro	Ala	Thr	Ser	Pro	Pro	Gly	Ser	Met	Ala	Pro	Lys	Ser
			195					200				205		Gly
Ser	Pro	Val	Ser	Pro	Thr	Thr	Ser	Arg	Thr	Gly	Thr	Thr		
			210					215				220		

(2) INFORMATION FOR SEQ ID NO:1385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..216
(D) OTHER INFORMATION: / Ceres Seq. ID 1569789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385:

```
Met Lys Ser Leu Ser Phe Phe Phe Thr Ile Leu Leu Ser Leu Ser Thr
1      5      10      15
Leu Phe Thr Ile Ser Asn Ala Arg Lys Phe Asn Val Gly Gly Ser Gly
20     25     30
Ala Trp Val Thr Asn Pro Pro Glu Asn Tyr Glu Ser Trp Ser Gly Lys
35     40     45
Asn Arg Phe Leu Val His Asp Thr Leu Tyr Phe Ser Tyr Ala Lys Gly
50     55     60
Ala Asp Ser Val Leu Glu Val Asn Lys Ala Asp Tyr Asp Ala Cys Asn
65     70     75
Thr Lys Asn Pro Ile Lys Arg Val Asp Asp Gly Asp Ser Glu Ile Ser
85     90     95
Leu Asp Arg Tyr Gly Pro Phe Tyr Phe Ile Ser Gly Asn Glu Asp Asn
100    105    110
Cys Lys Lys Gly Gln Lys Leu Asn Val Val Ile Ser Ala Arg Ile
115    120    125
Pro Ser Thr Ala Gln Ser Pro His Ala Ala Pro Gly Ser Ser Thr
130    135    140
Pro Gly Ser Met Thr Pro Pro Gly Gly Ala His Ser Pro Lys Ser Ser
145    150    155
Ser Pro Val Ser Pro Thr Thr Ser Pro Pro Gly Ser Thr Thr Pro Pro
165    170    175
Gly Gly Ala His Ser Pro Lys Ser Ser Ser Ala Val Ser Pro Ala Thr
180    185    190
Ser Pro Pro Gly Ser Met Ala Pro Lys Ser Gly Ser Pro Val Ser Pro
195    200    205
Thr Thr Ser Arg Thr Gly Thr Thr
210    215
```

(2) INFORMATION FOR SEQ ID NO:1386:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..116
(D) OTHER INFORMATION: / Ceres Seq. ID 1569790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386:

```
Met Thr Ser Pro Pro Ala Pro Met Ala Pro Lys Ser Ser Ser Thr Ile
1      5      10      15
Pro Pro Ser Ser Ala Pro Met Thr Ser Pro Pro Gly Ser Met Ala Pro
20     25     30
Lys Ser Ser Ser Pro Val Ser Asn Ser Pro Thr Val Ser Pro Ser Leu
35     40     45
Ala Pro Gly Gly Ser Thr Ser Ser Ser Pro Ser Asp Ser Pro Ser Gly
50     55     60
Ser Ala Met Gly Pro Ser Gly Asp Gly Pro Ser Ala Ala Gly Asp Ile
65     70     75
Ser Thr Pro Ala Gly Ala Pro Gly Gln Lys Lys Ser Ser Ala Asn Xaa
```

85 90 95
Met Thr Val Met Xaa Ile Thr Thr Val Xaa Ser Leu Val Leu Thr Ile
100 105 110
Phe Leu Ser Ala
115

(2) INFORMATION FOR SEQ ID NO:1387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1481
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387:

gattactt	gt	tctttt	gatt	tctcct	tcca	taga	accgaa	ttgttt	tcag	ctcgagatt	60
ctcctgcg	ca	gaga	acgatt	ttaatc	tatt	tctc	tcgaga	gtaga	aaatg	gctgaggtg	120
aagatatt	ca	accctc	tgct	tgta	caaatg	gaact	ggaat	ggta	aaagct	ggttttgctg	180
gggatgat	gc	accgag	ggct	gtgttt	tcca	gtatt	gttg	ccgtc	ctcg	cacactggag	240
tgatggtg	gc	aatggg	acag	aaggat	gc	atgtt	gcga	tgaag	ctcaa	tccaagcgtg	300
gtattctt	ac	ccttaa	atac	ctattg	agc	gtatt	gt	caaca	aattg	gatgatattg	360
aaaaaatc	gt	gc	atc	act	tctaca	aatg	agctc	cggt	gt	gtcctccgag	420
tctctgtc	ac	tgaag	cgcct	ctta	acccaa	aggcta	acg	tgaga	agatg	actcagatca	480
tgtttga	aac	cttta	acgct	ccgg	ctatgt	atgtc	gccat	tcaag	ctgtc	ctgtgcgttt	540
atgctagt	gg	ctgt	actact	ggtatt	gtgc	ttgact	ctgg	agatg	gtgtg	agtcacacgg	600
tccttatc	ta	tgagg	gttac	gctctc	ccgc	atgc	aatc	acgtc	ttgat	cttgacagtc	660
gtgacctc	ac	agatg	ctctg	atga	agatcc	tcactg	agc	gt	ttact	cttccaccaa	720
cagctgag	cg	tgaa	attgtc	agaga	catca	aggaga	agct	ttg	ctacatt	gctcttgact	780
atgacgag	ga	ctgtg	agac	gctaaa	ac	gctctt	ctgt	agaga	agaac	tatgatgtac	840
ctgatggc	ca	agtgat	cacc	attggat	ctgc	agcg	ttccg	ttgc	ccctgag	gttctttacc	900
agccatct	at	gatc	ggtatg	gaga	atgctg	gtatc	catga	aacc	acctac	aactccataa	960
tgaaatgt	ga	tggtg	acatc	agaa	aggact	tgatg	gtga	cat	gtgtc	agtggtggaa	1020
caactatg	tt	ccctg	gaatt	gctg	acagaa	tgag	c	caatg	ctgt	ttggcaccga	1080
gcagcatg	aa	gatca	aaagtc	gttg	ccacct	ctgag	aggaa	atact	ctgtc	tgagttggag	1140
gatccatc	tt	ggcctc	ccctc	agta	cccttc	agcag	atgtg	gatcg	caaa	gcagaaatg	1200
atgagtc	ag	ccctg	ctgatt	gttc	accgga	aatg	ctttg	agctt	gaagt	taagtctgct	1260
tcgggaga	ag	ccctg	gggggt	tttcc	agttt	gtcct	tactg	ggttt	tta	ctcgttctct	1320
gctctctt	ct	gtttt	ctctc	ttca	atatt	tcag	attctg	gccta	agaca	ttttgaagaa	1380
tttaca	tatt	ctgtt	gttgat	gtt	aaactg	ttgt	cttctg	ctctt	tattt	attttggatg	1440
acacaact	gt	gtttg	agtga	ata	gaactc	ctg	atttttc	c			

(2) INFORMATION FOR SEQ ID NO:1388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..377
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388:

Met	Ala	Asp	Gly	Glu	Asp	Ile	Gln	Pro	Leu	Val	Cys	Asp	Asn	Gly	Thr
1				5					10					15	
Gly	Met	Val	Lys	Ala	Gly	Phe	Ala	Gly	Asp	Asp	Ala	Pro	Arg	Ala	Val
				20					25					30	
Phe	Pro	Ser	Ile	Val	Gly	Arg	Pro	Gly	His	Thr	Gly	Val	Met	Val	Gly
				35					40					45	
Met	Gly	Gln	Lys	Asp	Ala	Tyr	Val	Gly	Asp	Glu	Ala	Gln	Ser	Lys	Arg

(2) INFORMATION FOR SEQ ID NO:1389:

(A) LENGTH: 360 amino acids

(B) TYPE: amino acid

{C} STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..360

(D) OTHER INFORMATION: / Ceres Seq. ID 1569801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389:

Met	Val	Lys	Ala	Gly	Phe	Ala	Gly	Asp	Asp	Ala	Pro	Arg	Ala	Val	Phe
1				5				10					15		
Pro	Ser	Ile	Val	Gly	Arg	Pro	Arg	His	Thr	Gly	Val	Met	Val	Gly	Met
			20					25					30		
Gly	Gln	Lys	Asp	Ala	Tyr	Val	Gly	Asp	Glu	Ala	Gln	Ser	Lys	Arg	Gly
		35				40						45			
Ile	Leu	Thr	Leu	Lys	Tyr	Pro	Ile	Glu	His	Gly	Ile	Val	Asn	Asn	Trp
	50					55				60					

Asp Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg
65 70 75 80
Val Ala Pro Glu Glu His Pro Ile Leu Leu Thr Glu Ala Pro Leu Asn
85 90 95
Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe
100 105 110
Asn Ala Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr
115 120 125
Ala Ser Gly Arg Thr Thr Gly Ile Val Leu Asp Ser Gly Asp Gly Val
130 135 140
Ser His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile
145 150 155 160
Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Ala Leu Met Lys
165 170 175
Ile Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala Glu Arg Glu
180 185 190
Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Ile Ala Leu Asp Tyr
195 200 205
Glu Gln Glu Leu Glu Thr Ala Lys Thr Ser Ser Ser Val Glu Lys Asn
210 215 220
Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Ser Glu Arg Phe
225 230 235 240
Arg Cys Pro Glu Val Leu Tyr Gln Pro Ser Met Ile Gly Met Glu Asn
245 250 255
Ala Gly Ile His Glu Thr Thr Tyr Asn Ser Ile Met Lys Cys Asp Val
260 265 270
Asp Ile Arg Lys Asp Leu Tyr Gly Asn Ile Val Leu Ser Gly Gly Thr
275 280 285
Thr Met Phe Pro Gly Ile Ala Asp Arg Met Ser Lys Glu Ile Thr Ala
290 295 300
Leu Ala Pro Ser Ser Met Lys Ile Lys Val Val Ala Pro Pro Glu Arg
305 310 315 320
Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr
325 330 335
Phe Gln Gln Met Trp Ile Ala Lys Ala Glu Tyr Asp Glu Ser Gly Pro
340 345 350
Ser Ile Val His Arg Lys Cys Phe
355 360

(2) INFORMATION FOR SEQ ID NO:1390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..332
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390:

Met Val Gly Met Gly Gln Lys Asp Ala Tyr Val Gly Asp Glu Ala Gln
1 5 10 15
Ser Lys Arg Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile
20 25 30
Val Asn Asn Trp Asp Asp Met Glu Lys Ile Trp His His Thr Phe Tyr
35 40 45
Asn Glu Leu Arg Val Ala Pro Glu Glu His Pro Ile Leu Leu Thr Glu
50 55 60
Ala Pro Leu Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met
65 70 75 80
Phe Glu Thr Phe Asn Ala Pro Ala Met Tyr Val Ala Ile Gln Ala Val

85 90 95
Leu Ser Leu Tyr Ala Ser Gly Arg Thr Thr Gly Ile Val Leu Asp Ser
100 105 110
Gly Asp Gly Val Ser His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu
115 120 125
Pro His Ala Ile Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp
130 135 140
Ala Leu Met Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr
145 150 155 160
Ala Glu Arg Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Ile
165 170 175
Ala Leu Asp Tyr Glu Gln Glu Leu Glu Thr Ala Lys Thr Ser Ser Ser
180 185 190
Val Glu Lys Asn Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly
195 200 205
Ser Glu Arg Phe Arg Cys Pro Glu Val Leu Tyr Gln Pro Ser Met Ile
210 215 220
Gly Met Glu Asn Ala Gly Ile His Glu Thr Tyr Asn Ser Ile Met
225 230 235 240
Lys Cys Asp Val Asp Ile Arg Lys Asp Leu Tyr Gly Asn Ile Val Leu
245 250 255
Ser Gly Gly Thr Thr Met Phe Pro Gly Ile Ala Asp Arg Met Ser Lys
260 265 270
Glu Ile Thr Ala Leu Ala Pro Ser Ser Met Lys Ile Lys Val Val Ala
275 280 285
Pro Pro Glu Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala
290 295 300
Ser Leu Ser Thr Phe Gln Gln Met Trp Ile Ala Lys Ala Glu Tyr Asp
305 310 315 320
Glu Ser Gly Pro Ser Ile Val His Arg Lys Cys Phe
325 330

(2) INFORMATION FOR SEQ ID NO:1391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1439
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391:

caagaaaaaa	aagaaacgat	gaggcttaat	ggggattcgg	gtccgggtca	ggatgaaccc	60
ggttcgagcg	ggtttccagg	cggaaatcaga	cgattccogt	tagcagctca	gcggagatt	120
atgagagctg	ctgagaaaga	cgatcaatac	gcttctttca	tccacgaagc	ttgccgcgat	180
gccttcgcgac	accttttcgg	tacaagaatc	gctcttgctt	accagaagga	gatgaagcta	240
cttggaacaga	tgctttacta	tgttcttacg	acagggttcag	ggcaacaaac	tttaggagag	300
gaatattgtg	acattatata	ggttgcaggg	ccttatggac	tctctctact	accagctaga	360
cgtgctttgt	tcatattgta	ccagaccgca	gttccatata	tcgcagagag	aattagcaat	420
cgagctgtcta	cgcaagcagt	cacctttgat	gagtcctgat	agtttttttg	tgatagctat	480
atccactcac	caagaatgat	agatcttcca	tcttcatctc	aagttgaaac	ttcaactctc	540
gtagtatcta	gggttaaacga	tagacttaag	agatbttggc	accgagctWt	tcacgcgatg	600
cctgggtgttc	ttctgtttgc	cgcggaagtc	ttacaactgg	ttttgcgtgc	caatctgatg	660
cttttctact	ctgaaggttt	ttattatcat	atatcgaaac	gtgcatcccg	ggtttcgttat	720
gttttctatg	gaaagcaact	gaatcagaga	cctagatacc	aaattcttgg	ggttttccct	780
ctaattccaat	tgtgctatct	tgctgctgag	ggcttcgcgc	ggagtaattt	gtcatctatc	840
acctgttcca	ttcagcaggc	ttctatagga	tcttatcaaa	cttcaggagg	gagaggttta	900
cctgtttttca	atgaagaggg	gaatttgata	acttcggaag	ctgaaaaggg	aaactgtgct	960
acctccgatt	caacttcaac	ggaggcgata	gggaaatgca	ctctctgctt	aagcaccogt	1020
cagcaccocaa	cggccaactc	ttgtgggtcat	gtgtttttgt	ggagctgcgat	tatggaatgg	1080

tgcaacgaga atcaagaatg cctcttttgt cgaacgcccc ataccattc aagtttggtt	1140
tgtttgtatc attctgattt ttaggcacaa tgggatcaac aaggacaggc actgcagaaa	1200
ggcaaaagcag ctaagacagt gacacctaa gacagtgcac ctgctacagg aatggaatct	1260
gcttcggcgt cagacttttt gagtaagatc aacaagttat gagagaagac agaataaata	1320
tattttcgac atcattctcg atcccatgcc tacctttttc tctatgat ttatgtcaga	1380
aaccacagag gtttggtgtt ttacatttca ttaaaaagag ttggagatgt taggtggtt	

(2) INFORMATION FOR SEQ ID NO:1392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..387

(D) OTHER INFORMATION: / Ceres Seq. ID 1569808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392:

His Glu Lys Lys Lys Glu Thr Met Arg Leu Asn Gly Asp Ser Gly Pro Gly	
1 5 10 15	
Gln Asp Glu Pro Gly Ser Ser Gly Phe His Gly Gly Ile Arg Arg Phe	
20 25 30	
Pro Leu Ala Ala Gln Pro Glu Ile Met Arg Ala Ala Glu Lys Asp Asp	
35 40 45	
Gln Tyr Ala Ser Phe Ile His Glu Ala Cys Arg Asp Ala Phe Arg His	
50 55 60	
Leu Phe Gly Thr Arg Ile Ala Leu Ala Tyr Gln Lys Glu Met Lys Leu	
65 70 75 80	
Leu Gly Gln Met Leu Tyr Tyr Val Leu Thr Thr Gly Ser Gly Gln Gln	
85 90 95	
Thr Leu Gly Glu Glu Tyr Cys Asp Ile Ile Gln Val Ala Gly Pro Tyr	
100 105 110	
Gly Leu Ser Pro Thr Pro Ala Arg Arg Ala Leu Phe Ile Leu Tyr Gln	
115 120 125	
Thr Ala Val Pro Tyr Ile Ala Glu Arg Ile Ser Thr Arg Ala Ala Thr	
130 135 140	
Gln Ala Val Thr Phe Asp Glu Ser Asp Glu Phe Phe Gly Asp Ser His	
145 150 155 160	
Ile His Ser Pro Arg Met Ile Asp Leu Pro Ser Ser Ser Gln Val Glu	
165 170 175	
Thr Ser Thr Ser Val Val Ser Arg Leu Asn Asp Arg Leu Lys Arg Xaa	
180 185 190	
Trp His Arg Ala Xaa Gln Arg Trp Pro Val Val Leu Pro Val Ala Arg	
195 200 205	
Glu Val Leu Gln Leu Val Leu Arg Ala Asn Leu Met Leu Phe Tyr Ser	
210 215 220	
Glu Gly Phe Tyr Tyr His Ile Ser Lys Arg Ala Ser Gly Val Arg Tyr	
225 230 235 240	
Val Phe Ile Gly Lys Gln Leu Asn Gln Arg Pro Arg Tyr Gln Ile Leu	
245 250 255	
Gly Val Phe Leu Leu Ile Gln Leu Cys Ile Leu Ala Ala Glu Gly Leu	
260 265 270	
Arg Arg Ser Asn Leu Ser Ser Ile Thr Ser Ser Ile Gln Gln Ala Ser	
275 280 285	
Ile Gly Ser Tyr Gln Thr Ser Gly Gly Arg Gly Leu Pro Val Leu Asn	
290 295 300	
Glu Glu Gly Asn Leu Ile Thr Ser Glu Ala Glu Lys Gly Asn Trp Ser	
305 310 315 320	
Thr Ser Asp Ser Thr Ser Thr Glu Ala Val Gly Lys Cys Thr Leu Cys	
325 330 335	
Leu Ser Thr Arg Gln His Pro Thr Ala Thr Pro Cys Gly His Val Phe	

340 345 350
Cys Trp Ser Cys Ile Met Glu Trp Cys Asn Glu Asn Gln Glu Cys Pro
355 360 365
Leu Cys Arg Thr Pro Asn Thr His Ser Ser Leu Val Cys Leu Tyr His
370 375 380
Ser Asp Phe
385

(2) INFORMATION FOR SEQ ID NO:1393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..381
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393:

Met	Arg	Leu	Asn	Gly	Asp	Ser	Gly	Pro	Gly	Gln	Asp	Glu	Pro	Gly	Ser
1			5					10						15	
Ser	Gly	Phe	His	Gly	Gly	Ile	Arg	Arg	Phe	Pro	Leu	Ala	Ala	Gln	Pro
			20					25					30		
Glu	Ile	Met	Arg	Ala	Ala	Glu	Lys	Asp	Asp	Gln	Tyr	Ala	Ser	Phe	Ile
		35					40					45			
His	Glu	Ala	Cys	Arg	Asp	Ala	Phe	Arg	His	Leu	Phe	Gly	Thr	Arg	Ile
		50				55					60				
Ala	Leu	Ala	Tyr	Gln	Lys	Glu	Met	Lys	Leu	Leu	Gly	Gln	Met	Leu	Tyr
		65			70					75				80	
Tyr	Val	Leu	Thr	Thr	Gly	Ser	Gly	Gln	Gln	Thr	Leu	Gly	Glu	Glu	Tyr
			85					90					95		
Cys	Asp	Ile	Ile	Gln	Val	Ala	Gly	Pro	Tyr	Gly	Leu	Ser	Pro	Thr	Pro
			100					105					110		
Ala	Arg	Arg	Ala	Leu	Phe	Ile	Leu	Tyr	Gln	Thr	Ala	Val	Pro	Tyr	Ile
			115					120				125			
Ala	Glu	Arg	Ile	Ser	Thr	Arg	Ala	Ala	Thr	Gln	Ala	Val	Thr	Phe	Asp
			130			135						140			
Glu	Ser	Asp	Glu	Phe	Phe	Gly	Asp	Ser	His	Ile	His	Ser	Pro	Arg	Met
			145			150				155				160	
Ile	Asp	Leu	Pro	Ser	Ser	Ser	Gln	Val	Glu	Thr	Ser	Thr	Ser	Val	Val
			165					170					175		
Ser	Arg	Leu	Asn	Asp	Arg	Leu	Lys	Arg	Xaa	Trp	His	Arg	Ala	Xaa	Gln
			180					185					190		
Arg	Trp	Pro	Val	Val	Leu	Pro	Val	Ala	Arg	Glu	Val	Leu	Gln	Leu	Val
			195				200					205			
Leu	Arg	Ala	Asn	Leu	Met	Leu	Phe	Tyr	Ser	Glu	Gly	Phe	Tyr	Tyr	His
			210			215					220				
Ile	Ser	Lys	Arg	Ala	Ser	Gly	Val	Arg	Tyr	Val	Phe	Ile	Gly	Lys	Gln
			225			230				235				240	
Leu	Asn	Gln	Arg	Pro	Arg	Tyr	Gln	Ile	Leu	Gly	Val	Phe	Leu	Leu	Ile
			245					250					255		
Gln	Leu	Cys	Ile	Leu	Ala	Ala	Glu	Gly	Leu	Arg	Arg	Ser	Asn	Leu	Ser
			260				265					270			
Ser	Ile	Thr	Ser	Ser	Ile	Gln	Gln	Ala	Ser	Ile	Gly	Ser	Tyr	Gln	Thr
			275			280					285				
Ser	Gly	Gly	Arg	Gly	Leu	Pro	Val	Leu	Asn	Glu	Glu	Gly	Asn	Leu	Ile
			290			295					300				
Thr	Ser	Glu	Ala	Glu	Lys	Gly	Asn	Trp	Ser	Thr	Ser	Asp	Ser	Thr	Ser
			305			310				315				320	
Thr	Glu	Ala	Val	Gly	Lys	Cys	Thr	Leu	Cys	Leu	Ser	Thr	Arg	Gln	His
			325					330					335		

Pro Thr Ala Thr Pro Cys Gly His Val Phe Cys Trp Ser Cys Ile Met
340 345 350
Glu Trp Cys Asn Glu Asn Gln Glu Cys Pro Leu Cys Arg Thr Pro Asn
355 360 365
Thr His Ser Ser Leu Val Cys Leu Tyr His Ser Asp Phe
370 375 380

(2) INFORMATION FOR SEQ ID NO:1394:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 347 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..347

(D) OTHER INFORMATION: / Ceres Seq. ID 1569810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394:

Met Arg Ala Ala Glu Lys Asp Asp Gln Tyr Ala Ser Phe Ile His Glu
1 5 10 15
Ala Cys Arg Asp Ala Phe Arg His Leu Phe Gly Thr Arg Ile Ala Leu
20 25 30
Ala Tyr Gln Lys Glu Met Lys Leu Leu Gly Gln Met Leu Tyr Tyr Val
35 40 45
Leu Thr Thr Gly Ser Gly Gln Gln Thr Leu Gly Glu Glu Tyr Cys Asp
50 55 60
Ile Ile Gln Val Ala Gly Pro Tyr Gly Leu Ser Pro Thr Pro Ala Arg
65 70 75 80
Arg Ala Leu Phe Ile Leu Tyr Gln Thr Ala Val Pro Tyr Ile Ala Glu
85 90 95
Arg Ile Ser Thr Arg Ala Ala Thr Gln Ala Val Thr Phe Asp Glu Ser
100 105 110
Asp Glu Phe Phe Gly Asp Ser His Ile His Ser Pro Arg Met Ile Asp
115 120 125
Leu Pro Ser Ser Ser Gln Val Glu Thr Ser Thr Ser Val Val Ser Arg
130 135 140
Leu Asn Asp Arg Leu Lys Arg Xaa Trp His Arg Ala Xaa Gln Arg Trp
145 150 155 160
Pro Val Val Leu Pro Val Ala Arg Glu Val Leu Gln Leu Val Leu Arg
165 170 175
Ala Asn Leu Met Leu Phe Tyr Ser Glu Gly Phe Tyr Tyr His Ile Ser
180 185 190
Lys Arg Ala Ser Gly Val Arg Tyr Val Phe Ile Gly Lys Gln Leu Asn
195 200 205
Gln Arg Pro Arg Tyr Gln Ile Leu Gly Val Phe Leu Leu Ile Gln Leu
210 215 220
Cys Ile Leu Ala Ala Glu Gly Leu Arg Arg Ser Asn Leu Ser Ser Ile
225 230 235 240
Thr Ser Ser Ile Gln Gln Ala Ser Ile Gly Ser Tyr Gln Thr Ser Gly
245 250 255
Gly Arg Gly Leu Pro Val Leu Asn Glu Glu Gly Asn Leu Ile Thr Ser
260 265 270
Glu Ala Glu Lys Gly Asn Trp Ser Thr Ser Asp Ser Thr Ser Thr Glu
275 280 285
Ala Val Gly Lys Cys Thr Leu Cys Leu Ser Thr Arg Gln His Pro Thr
290 295 300
Ala Thr Pro Cys Gly His Val Phe Cys Trp Ser Cys Ile Met Glu Trp
305 310 315 320
Cys Asn Glu Asn Gln Glu Cys Pro Leu Cys Arg Thr Pro Asn Thr His
325 330 335
Ser Ser Leu Val Cys Leu Tyr His Ser Asp Phe

2025 RELEASE UNDER E.O. 14176

340 345
(2) INFORMATION FOR SEQ ID NO:1395:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1824 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1824
(D) OTHER INFORMATION: / Ceres Seq. ID 1569815
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395:
aagggtgacct tggctcttgg ttgaccatca aaaaactacaa cgctctttct ccgtaGgaaa 60
ggggaagcaa ataaattatc gaagcccaact ggtttcggag ctgatcggtc tctatttctc 120
ctttcataca tatctcaagc agataaagt ttgatcgatc tagaatggga ggaggattta 180
gagtttttga tttggtgagg ccattcttgg cttttctgcc tgaggttcag agtgctgata 240
ggaaggttcc attcagagag aaggttatct acactgtcat ctctctcttc atctttctgt 300
ctcgagtcga gctctctctt tatggaatcc attccaccac cggtgcggat ccattctatt 360
ggatgcgtgt cattcttggc tccaaccgtg gaactgtcat ggagctcggg attactctca 420
ttgttacatc tggacttggg atgcaactct tggctgggtc caagattatt gaggttgaca 480
acaatgttgc tgaggatcgt gccctcttga atggtgtcga gaagctctca ggtattctga 540
ttgccattgt tgagcgtggt gcatatgttc tttctggaat gtatgggtccc gttggacagc 600
ttggtgttgg aaatgccatt ctgatcatcc ttacagctttt cttgtctgga atcatttgtta 660
ctgctcgtga tgaactcctt cagaagggat atggctctcg atcaggaatc tcccttttca 720
ttgccaccaa cattttgtaa agcattatct ggaaggaatt tagcccaact accatcaaca 780
ccgggcgtgg agctgagttt gaaggtgctg ttattgcact gtcccatatg ctgataacca 840
agtcacacaa ggttgcgggt ctccgccaag ctttctaacc gcaaaacctt ccaaatgtta 900
ccaacttggc tgccacagtc ttgatcttcc tgatttgtat ctacttccaa ggtttccgtg 960
tggttttgcc tgtgagatca aagaatgccc gtggacaaca ggttctttac ccaatcaagc 1020
tgtttacac ctctaaacat cccatcatcc tccaatccgc cctgtctca aatctttact 1080
tcatttctca gcttctctac cgggaagtta cgggaaattt ctttggtaac cttttgggac 1140
aatggaagaa atctgagtac agtggacaat ctattccagt tagtggtctg gcttacctca 1200
tcacagctcc agcaagtttc tctgacatgg cagctcaacc ctgccatgca ctggtctaca 1260
tcgtcttcat gctcactgct tgtgctcttt tctcaaaagc atggattgaa gtctctggat 1320
cttctgctag ggatgtagct aagcagctaa aggaacaaca aatggtgatg ccaggacaca 1380
gagaatcaaa cttacagaag gaactgaaca gatacatccc aacagcagca gcttttgag 1440
gagtttgtat cgggtgcactt accgttttgg ctgatttcat gggagccatc gggctcggaa 1500
ccggaattct gttggcggtc acgatcatat accagatttt cgagaccttt gagaaggaaa 1560
aagccagtga actcggcttc ttccgggttct aagttagctt aaagaagggt taaactttgc 1620
ctgaggcaaa aaagcagagc aagaagaggct ttgctctctg tgcccacctc aaacacagac 1680
aattttgtgt ggcacttggg ttgactactt ttttttgtt gttgttgtaa cgaatttttc 1740
tcattagtca tttatgtttt ttgttactt tttaacaagt aaaaaactta tgtgatagac 1800
gcttttctaa tgtatgtttc twgc
(2) INFORMATION FOR SEQ ID NO:1396:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 475 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..475
(D) OTHER INFORMATION: / Ceres Seq. ID 1569816
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396:
Met Gly Gly Gly Phe Arg Val Leu His Leu Val Arg Pro Phe Leu Ala
1 5 10 15
Phe Leu Pro Glu Val Gln Ser Ala Asp Arg Lys Val Pro Phe Arg Glu
20 25 30
Lys Val Ile Tyr Thr Val Ile Ser Leu Phe Ile Phe Leu Val Cys Ser

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..409

(D) OTHER INFORMATION: / Ceres Seq. ID 1569817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1397:

Met	Arg	Val	Ile	Leu	Ala	Ser	Asn	Arg	Gly	Thr	Val	Met	Glu	Leu	Gly	
1			5						10				15			
Ile	Thr	Pro	Ile	Val	Thr	Ser	Gly	Leu	Val	Met	Gln	Leu	Leu	Ala	Gly	
			20					25					30			
Ser	Lys	Ile	Ile	Glu	Val	Asp	Asn	Asn	Val	Arg	Glu	Asp	Arg	Ala	Leu	
			35					40					45			
Leu	Asn	Gly	Ala	Gln	Lys	Leu	Leu	Gly	Ile	Leu	Ile	Ala	Ile	Gly	Glu	
			50					55				60				
Ala	Val	Ala	Tyr	Val	Leu	Ser	Gly	Met	Tyr	Gly	Pro	Val	Gly	Gln	Leu	
			65					70					75			
Gly	Val	Gly	Asn	Ala	Ile	Leu	Ile	Ile	Leu	Gln	Leu	Phe	Phe	Ala	Gly	
			85						90					95		
Ile	Ile	Val	Ile	Cys	Leu	Asp	Glu	Leu	Leu	Gln	Lys	Gly	Tyr	Gly	Leu	
			100					105					110			
Gly	Ser	Gly	Ile	Ser	Leu	Phe	Ile	Ala	Thr	Asn	Ile	Cys	Gly	Ser	Ile	
			115					120					125			
Ile	Trp	Lys	Ala	Phe	Ser	Pro	Thr	Thr	Ile	Asn	Thr	Gly	Arg	Gly	Ala	
			130					135					140			
Glu	Phe	Glu	Gly	Ala	Val	Ile	Ala	Leu	Phe	His	Met	Leu	Ile	Thr	Lys	
			145					150				155				
Ser	Asn	Lys	Val	Ala	Ala	Leu	Arg	Gln	Ala	Phe	Tyr	Arg	Gln	Asn	Leu	
			165					170					175			
Pro	Asn	Val	Thr	Asn	Leu	Leu	Ala	Thr	Val	Leu	Ile	Phe	Leu	Ile	Val	
			180					185					190			
Ile	Tyr	Phe	Gln	Gly	Phe	Arg	Val	Val	Leu	Pro	Val	Arg	Ser	Lys	Asn	
			195					200					205			
Ala	Arg	Gly	Gln	Gln	Gly	Ser	Tyr	Pro	Ile	Lys	Leu	Phe	Tyr	Thr	Ser	
			210					215					220			
Asn	Met	Pro	Ile	Ile	Leu	Gln	Ser	Ala	Leu	Val	Ser	Asn	Leu	Tyr	Phe	
			225					230					235			
Ile	Ser	Gln	Leu	Leu	Tyr	Arg	Lys	Phe	Ser	Gly	Asn	Phe	Phe	Val	Asn	
			245					250					255			
Leu	Leu	Gly	Gln	Trp	Lys	Glu	Ser	Glu	Tyr	Ser	Gly	Gln	Ser	Ile	Pro	
			260					265					270			
Val	Ser	Gly	Leu	Ala	Tyr	Leu	Ile	Thr	Ala	Pro	Ala	Ser	Phe	Ser	Asp	
			275					280					285			
Met	Ala	Ala	His	Pro	Phe	His	Ala	Leu	Phe	Tyr	Ile	Val	Phe	Met	Leu	
			290					295					300			
Thr	Ala	Cys	Ala	Leu	Phe	Ser	Lys	Thr	Trp	Ile	Glu	Val	Ser	Gly	Ser	
			305					310					315			
Ser	Ala	Arg	Asp	Val	Ala	Lys	Gln	Leu	Lys	Glu	Gln	Gln	Met	Val	Met	
			325					330					335			
Pro	Gly	His	Arg	Glu	Ser	Asn	Leu	Gln	Lys	Glu	Leu	Asn	Arg	Tyr	Ile	
			340					345					350			
Pro	Thr	Ala	Ala	Ala	Phe	Gly	Gly	Val	Cys	Ile	Gly	Ala	Leu	Thr	Val	
			355					360					365			
Leu	Ala	Asp	Phe	Met	Gly	Ala	Ile	Gly	Ser	Gly	Thr	Gly	Ile	Leu	Leu	
			370					375					380			
Ala	Val	Thr	Ile	Ile	Tyr	Gln	Tyr	Phe	Glu	Thr	Phe	Glu	Lys	Glu	Lys	
			385					390					395			
Ala	Ser	Glu	Leu	Gly	Phe	Phe	Gly	Phe								
			405													

(2) INFORMATION FOR SEQ ID NO:1398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 397 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..397
(D) OTHER INFORMATION: / Ceres Seq. ID 1569818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398:
Met Glu Leu Gly Ile Thr Pro Ile Val Thr Ser Gly Leu Val Met Gln
1 5 10 15
Leu Leu Ala Gly Ser Lys Ile Ile Glu Val Asp Asn Asn Val Arg Glu
20 25 30
Asp Arg Ala Leu Leu Asn Gly Ala Gln Lys Leu Gly Ile Leu Ile
35 40 45
Ala Ile Gly Glu Ala Val Ala Tyr Val Leu Ser Gly Met Tyr Gly Pro
50 55 60
Val Gly Gln Leu Gly Val Gly Asn Ala Ile Leu Ile Leu Gln Leu
65 70 75 80
Phe Phe Ala Gly Ile Ile Val Ile Cys Leu Asp Glu Leu Leu Gln Lys
85 90 95
Gly Tyr Gly Leu Gly Ser Gly Ile Ser Leu Phe Ile Ala Thr Asn Ile
100 105 110
Cys Glu Ser Ile Ile Trp Lys Ala Phe Ser Pro Thr Thr Ile Asn Thr
115 120 125
Gly Arg Gly Ala Glu Phe Glu Gly Ala Val Ile Ala Leu Phe His Met
130 135 140
Leu Ile Thr Lys Ser Asn Lys Val Ala Ala Leu Arg Gln Ala Phe Tyr
145 150 155 160
Arg Gln Asn Leu Pro Asn Val Thr Asn Leu Leu Ala Thr Val Leu Ile
165 170 175
Phe Leu Ile Val Ile Tyr Phe Gln Gly Phe Arg Val Val Leu Pro Val
180 185 190
Arg Ser Lys Asn Ala Arg Gly Gln Gln Gly Ser Tyr Pro Ile Lys Leu
195 200 205
Phe Tyr Thr Ser Asn Met Pro Ile Ile Leu Gln Ser Ala Leu Val Ser
210 215 220
Asn Leu Tyr Phe Ile Ser Gln Leu Leu Tyr Arg Lys Phe Ser Gly Asn
225 230 235 240
Phe Phe Val Asn Leu Leu Gly Gln Trp Lys Glu Ser Glu Tyr Ser Gly
245 250 255
Gln Ser Ile Pro Val Ser Gly Leu Ala Tyr Leu Ile Thr Ala Pro Ala
260 265 270
Ser Phe Ser Asp Met Ala Ala His Pro Phe His Ala Leu Phe Tyr Ile
275 280 285
Val Phe Met Leu Thr Ala Cys Ala Leu Phe Ser Lys Thr Trp Ile Glu
290 295 300
Val Ser Gly Ser Ser Ala Arg Asp Val Ala Lys Gln Leu Lys Glu Gln
305 310 315 320
Gln Met Val Met Pro Gly His Arg Glu Ser Asn Leu Gln Lys Glu Leu
325 330 335
Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly Val Cys Ile Gly
340 345 350
Ala Leu Thr Val Leu Ala Asp Phe Met Gly Ala Ile Gly Ser Gly Thr
355 360 365
Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr Phe Glu Thr Phe
370 375 380
Glu Lys Glu Lys Ala Ser Glu Leu Gly Phe Phe Gly Phe
385 390 395

(2) INFORMATION FOR SEQ ID NO:1399:
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1853 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1853
(D) OTHER INFORMATION: / Ceres Seq. ID 1569834
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399:

```

attccttgcg  atcttttttcg  tcacctatgc  cgcttttactc  tctttgcgata  tctctgaggt  60
aattctgtgag  cagcataaaac  aatcaattga  ttcatctcttc  ttgatacccaa  gttgtggaaa  120
ctctagagatt  gtttctgtgta  tatctccaga  attgctgtttt  tgattgaatt  taggtcgcttt  180
agctcagttg  atagagcacc  acattttttg  tggtagaaaat  cgatttgttt  gacagtctct  240
aaccatgggt  aaagagaatt  ttcacatcaa  catttggtgc  attggccacg  tcgattctcg  300
aaagtgcacc  accactggac  acttgatcta  caagtgggtg  ggtattgaca  agcgtgtcat  360
tgagaggttc  gagaaggagg  ctgctgagat  gaacaaggag  tccttcaagt  acgcatgggt  420
tttggacaaa  cttaaggctg  agcgtgagcg  tggatatcacc  attgacattg  ctctctggaa  480
gttcgagacc  accaagtact  actgcactgt  cattgatgct  cctggccattg  gtgatttcat  540
caagaacatg  atcactggta  cctcccagcg  tgatttgtct  gtccttatca  tcgactccac  600
cactgttggt  tttgaggtgc  gtatctccaa  ggaatggtcag  acccgtgagc  acgctctcct  660
tgcttttacc  ttgtgtgtca  aacagatgat  ctgctgttgt  aacaagatgg  atgccactac  720
cccacaatga  tccaaggcca  ggtacgatga  aattatcaag  gaggtgtctt  cctacttgaa  780
gaaggttggt  tacaaccccc  acaaaatccc  atttgtgccc  atctctggat  tcgagggtga  840
caacatgatt  gagagggtca  ccaacctaga  ctggtacaag  ggaccaactc  ttcttgaggc  900
tcttgaccag  atcaacgagc  ccaagaggcc  atcagacaag  ccccttcgtc  tcccacttca  960
ggatgtctac  aagattgggt  gtattggaac  ggtgccagtg  ggacgtgttg  agactgggat  1020
gatcaagctc  ggtatgggtg  tgacotttgc  tcccaacagg  ttgaccaact  agctgcaagt  1080
tgttgagatg  caccacagtg  ctcttcttga  ggcacttcca  ggtgacaacg  ttgggttcaa  1140
gtttaagaat  gttgtgtcta  aggatcttaa  gagaggggtc  ctgcactcca  acctcaagga  1200
tgaccctgcc  aagggtgtcg  ctaacttcaa  ctcccagctc  atcatcaTda  accaccctgg  1260
tcagattggt  aacggttacg  cccagtcctc  ggattgcgac  actctcaca  ttgcagtcaa  1320
gttctctgag  atcttgacca  agattgacag  cggttctggt  aaggagatgt  agaaggagcc  1380
caagttcttg  aagaatgggt  atgctggtat  ggtgaagatg  actccaacca  agcccatggt  1440
tgttgagacc  ttctctgagt  acccaccact  tggacgtttc  gctgtgaggg  acatgaggca  1500
gactgttgca  tgcggtgtta  tcaagatgtg  tgacaagaag  gaccacaacc  gagccaaggt  1560
taccaaggtc  gccgtcaaga  aggtgtcgaa  gtgaaccatc  ctcaaaaact  tatctgccgc  1620
aggtgaatca  aaggacagtg  ttagttttat  tacaatagtt  tggtaatttg  tcgcgtgtct  1680
gtgtctctgt  ttcgttttct  ccccgtaaga  cggttgttct  cgtaattggg  tcttctgatc  1740
gaggtggcgg  atctacacac  acattcttcc  tgttttttgc  tttttatttg  ttttctcatt  1800
tgaaactggt  taaaatttct  gttatatgaa  tgaatgtttt  ccctgcgggt  att

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(2) INFORMATION FOR SEQ ID NO:1400:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 449 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..449
(D) OTHER INFORMATION: / Ceres Seq. ID 1569835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400:

```

Met Gly Lys Glu Asn Phe His Ile Asn Ile Val Val Ile Gly His Val
1           5           10           15
Asp Ser Gly Lys Ser Thr Thr Thr Gly His Leu Ile Tyr Lys Leu Gly
20          25          30
Gly Ile Asp Lys Arg Val Ile Glu Arg Phe Glu Lys Glu Ala Ala Glu
35          40          45
Met Asn Lys Arg Ser Phe Lys Tyr Ala Trp Val Leu Asp Lys Leu Lys
50          55          60

```

Ala Glu Arg Glu Arg Gly Ile Thr Ile Asp Ile Ala Leu Trp Lys Phe
65 70 75 80
Glu Thr Thr Lys Tyr Cys Thr Val Ile Asp Ala Pro Gly His Arg
85 90 95
Asp Phe Ile Lys Asn Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala
100 105 110
Val Leu Ile Ile Asp Ser Thr Thr Gly Gly Phe Glu Ala Gly Ile Ser
115 120 125
Lys Asp Gly Gln Thr Arg Glu His Ala Leu Leu Ala Phe Thr Leu Gly
130 135 140
Val Lys Gln Met Ile Cys Cys Asn Lys Met Asp Ala Thr Thr Pro
145 150 155 160
Lys Tyr Ser Lys Ala Arg Tyr Asp Glu Ile Ile Lys Glu Val Ser Ser
165 170 175
Tyr Leu Lys Lys Val Gly Tyr Asn Pro Asp Lys Ile Pro Phe Val Pro
180 185 190
Ile Ser Gly Phe Glu Gly Asp Asn Met Ile Glu Arg Ser Thr Asn Leu
195 200 205
Asp Trp Tyr Lys Gly Pro Thr Leu Leu Glu Ala Leu Asp Gln Ile Asn
210 215 220
Glu Pro Lys Arg Pro Ser Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp
225 230 235 240
Val Tyr Lys Ile Gly Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu
245 250 255
Thr Gly Met Ile Lys Pro Gly Met Val Val Thr Phe Ala Pro Thr Gly
260 265 270
Leu Thr Thr Glu Val Lys Ser Val Glu Met His His Glu Ser Leu Leu
275 280 285
Glu Ala Leu Pro Gly Asp Asn Val Gly Phe Asn Val Lys Asn Val Ala
290 295 300
Val Lys Asp Leu Lys Arg Gly Tyr Val Ala Ser Asn Ser Lys Asp Asp
305 310 315 320
Pro Ala Lys Gly Ala Ala Asn Phe Thr Ser Gln Val Ile Ile Xaa Asn
325 330 335
His Pro Gly Gln Ile Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His
340 345 350
Thr Ser His Ile Ala Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp
355 360 365
Arg Arg Ser Gly Lys Glu Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn
370 375 380
Gly Asp Ala Gly Met Val Lys Met Thr Pro Thr Lys Pro Met Val Val
385 390 395 400
Glu Thr Phe Ser Glu Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp
405 410 415
Met Arg Gln Thr Val Ala Val Gly Val Ile Lys Ser Val Asp Lys Lys
420 425 430
Asp Pro Thr Gly Ala Lys Val Thr Lys Ala Ala Val Lys Lys Gly Ala
435 440 445
Lys

(2) INFORMATION FOR SEQ ID NO:1401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..401
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401:

Met	Asn	Lys	Arg	Ser	Phe	Lys	Tyr	Ala	Trp	Val	Leu	Asp	Lys	Leu	Lys
1			5						10					15	
Ala	Glu	Arg	Glu	Arg	Gly	Ile	Thr	Ile	Asp	Ile	Ala	Leu	Trp	Lys	Phe
			20					25					30		
Glu	Thr	Thr	Lys	Tyr	Tyr	Cys	Thr	Val	Ile	Asp	Ala	Pro	Gly	His	Arg
		35					40					45			
Asp	Phe	Ile	Lys	Asn	Met	Ile	Thr	Gly	Thr	Ser	Gln	Ala	Asp	Cys	Ala
	50				55						60				
Val	Leu	Ile	Ile	Asp	Ser	Thr	Thr	Gly	Gly	Phe	Glu	Ala	Gly	Ile	Ser
65				70						75				80	
Lys	Asp	Gly	Gln	Thr	Arg	Glu	His	Ala	Leu	Ala	Phe	Thr	Leu	Gly	
			85					90					95		
Val	Lys	Gln	Met	Ile	Cys	Cys	Cys	Asn	Lys	Met	Asp	Ala	Thr	Thr	Pro
		100						105					110		
Lys	Tyr	Ser	Lys	Ala	Arg	Tyr	Asp	Glu	Ile	Ile	Lys	Glu	Val	Ser	Ser
		115					120					125			
Tyr	Leu	Lys	Lys	Val	Gly	Tyr	Asn	Pro	Asp	Lys	Ile	Pro	Phe	Val	Pro
	130					135					140				
Ile	Ser	Gly	Phe	Glu	Gly	Asp	Asn	Met	Ile	Glu	Arg	Ser	Thr	Asn	Leu
145				150						155				160	
Asp	Trp	Tyr	Lys	Gly	Pro	Thr	Leu	Leu	Glu	Ala	Leu	Asp	Gln	Ile	Asn
			165						170					175	
Glu	Pro	Lys	Arg	Pro	Ser	Asp	Lys	Pro	Leu	Arg	Leu	Pro	Leu	Gln	Asp
			180					185					190		
Val	Tyr	Lys	Ile	Gly	Gly	Ile	Gly	Thr	Val	Pro	Val	Gly	Arg	Val	Glu
		195					200					205			
Thr	Gly	Met	Ile	Lys	Pro	Gly	Met	Val	Val	Thr	Phe	Ala	Pro	Thr	Gly
	210					215					220				
Leu	Thr	Thr	Glu	Val	Lys	Ser	Val	Glu	Met	His	His	Glu	Ser	Leu	Leu
225					230					235				240	
Glu	Ala	Leu	Pro	Gly	Asp	Asn	Val	Gly	Phe	Asn	Val	Lys	Asn	Val	Ala
			245						250					255	
Val	Lys	Asp	Leu	Lys	Arg	Gly	Tyr	Val	Ala	Ser	Asn	Ser	Lys	Asp	Asp
		260					265						270		
Pro	Ala	Lys	Gly	Ala	Ala	Asn	Phe	Thr	Ser	Gln	Val	Ile	Ile	Xaa	Asn
		275					280					285			
His	Pro	Gly	Gln	Ile	Gly	Asn	Gly	Tyr	Ala	Pro	Val	Leu	Asp	Cys	His
	290					295						300			
Thr	Ser	His	Ile	Ala	Val	Lys	Phe	Ser	Glu	Ile	Leu	Thr	Lys	Ile	Asp
305				310						315				320	
Arg	Arg	Ser	Gly	Lys	Glu	Ile	Glu	Lys	Glu	Pro	Lys	Phe	Leu	Lys	Asn
			325						330					335	
Gly	Asp	Ala	Gly	Met	Val	Lys	Met	Thr	Pro	Thr	Lys	Pro	Met	Val	Val
		340						345					350		
Glu	Thr	Phe	Ser	Glu	Tyr	Pro	Pro	Leu	Gly	Arg	Phe	Ala	Val	Arg	Asp
		355					360					365			
Met	Arg	Gln	Thr	Val	Ala	Val	Gly	Val	Ile	Lys	Ser	Val	Asp	Lys	Lys
		370				375					380				
Asp	Pro	Thr	Gly	Ala	Lys	Val	Thr	Lys	Ala	Ala	Val	Lys	Lys	Gly	Ala
					390					395				400	
Lys															

(2) INFORMATION FOR SEQ ID NO:1402:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..348
(D) OTHER INFORMATION: / Ceres Seq. ID 1569837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402:

```
Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala Val Leu Ile Ile Asp
1      5      10      15
Ser Thr Thr Gly Gly Phe Glu Ala Gly Ile Ser Lys Asp Gly Gln Thr
20      25      30
Arg Glu His Ala Leu Leu Ala Phe Thr Leu Gly Val Lys Gln Met Ile
35      40      45
Cys Cys Cys Asn Lys Met Asp Ala Thr Thr Pro Lys Tyr Ser Lys Ala
50      55      60
Arg Tyr Asp Glu Ile Ile Lys Glu Val Ser Ser Tyr Leu Lys Lys Val
65      70      75      80
Gly Tyr Asn Pro Asp Lys Ile Pro Phe Val Pro Ile Ser Gly Phe Glu
85      90      95
Gly Asp Asn Met Ile Glu Arg Ser Thr Asn Leu Asp Trp Tyr Lys Gly
100      105      110
Pro Thr Leu Leu Glu Ala Leu Asp Gln Ile Asn Glu Pro Lys Arg Pro
115      120      125
Ser Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp Val Tyr Lys Ile Gly
130      135      140
Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu Thr Gly Met Ile Lys
145      150      155      160
Pro Gly Met Val Val Thr Phe Ala Pro Thr Gly Leu Thr Thr Glu Val
165      170      175
Lys Ser Val Glu Met His His Glu Ser Leu Leu Glu Ala Leu Pro Gly
180      185      190
Asp Asn Val Gly Phe Asn Val Lys Asn Val Ala Val Lys Asp Leu Lys
195      200      205
Arg Gly Tyr Val Ala Ser Asn Ser Lys Asp Asp Pro Ala Lys Gly Ala
210      215      220
Ala Asn Phe Thr Ser Gln Val Ile Ile Xaa Asn His Pro Gly Gln Ile
225      230      235      240
Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His Thr Ser His Ile Ala
245      250      255
Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp Arg Arg Ser Gly Lys
260      265      270
Glu Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn Gly Asp Ala Gly Met
275      280      285
Val Lys Met Thr Pro Thr Lys Pro Met Val Val Glu Thr Phe Ser Glu
290      295      300
Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr Val
305      310      315      320
Ala Val Gly Val Ile Lys Ser Val Asp Lys Lys Asp Pro Thr Gly Ala
325      330      335
Lys Val Thr Lys Ala Ala Val Lys Lys Gly Ala Lys
340      345
```

(2) INFORMATION FOR SEQ ID NO:1403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1442 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1442
(D) OTHER INFORMATION: / Ceres Seq. ID 1569846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403:

gccaatTTta aaccgagact gatgattgag aagaaactgt cgaagatgaa gatgagaacc

aaatcgattc	cggtttaggtc	ttcgcgcgaaa	tcctctgatt	cgctttctgga	tgatgaagct	120
aatgaaaaca	cacaatgtga	tgaagagat	gtgccacaca	agaagcgtcg	ttgtcttggg	180
actagttaga	ctactgatag	aggaggatct	gtagagccgc	tgctggactt	ggatccttgt	240
attgtatgtg	aagtttcaga	cgagcgggta	tctcgttgtt	cgcggttgga	ctgtcttctt	300
tcgttttcacg	gcgagtggtt	gtatgctgat	ttgggttagta	ctagttagta	tagtagtagt	360
agtagtgagg	atgttttcgaa	tcatttttgt	ccttatttgt	ggctcaagat	tggtgcactg	420
aaatccaaaa	cattgagaga	aaagaccctt	gagggcgga	aggcggctcg	caagtatcta	480
gataaagaga	tgaamAgcAg	ggatgaggat	ataaccttat	ctgtgttagta	aattgggaaac	540
caagagcaga	gtacagacat	tgtaatgtat	catgagttac	aaggagagaa	ggatggctgt	600
tcatacaaac	cagatgcgga	tcaagggaaa	gtgggtactg	gtaaagtgtat	tgacgaagtt	660
ggagcatcag	agaaggtagc	tacagaaaaa	tttcaagacg	ctgaagtga	tgaacacagct	720
aaagatcaag	gtacaagaat	ctcgaatata	gggtgcaggga	aaaagagaga	ggtttctctg	780
tttttgccta	tgcaagaatc	gttttcagca	aaagaacagg	accaggtcca	gcagaatgag	840
aagcgaagaa	ggagaggagt	gaaaattatc	gatagtga	ttcatcaaa	gggatacagt	900
aacgaacgaa	atggagaaga	tgtaaactgag	caggtaactt	catcggtcca	agtaacctcc	960
ccgtcaggga	gaatgaggaa	ccagcaggga	acaaccaaa	tggttaagtc	aaagacagt	1020
agggacattt	ctttctttaa	gatggatcaa	agaaggaggc	tactttggac	gtacgaagaa	1080
gaagagatgc	taaaagtggt	agtgaggaaa	tttgagcagc	aagcaaacaa	gaacatgcc	1140
tgaggagaaa	ttctggaat	gggagagaa	gtgttcacg	aaacacgtac	tcacagctgt	1200
ctcaaggaaa	atgtggaggag	catgggtcaag	attatgaaca	aaaacgaaca	aggcagcaca	1260
ctaaccctca	ctgctatgta	atcaaatagt	agtgtagctt	attgagatga	agccagactt	1320
ggtgaactaa	tgtgggagtt	gatctgtgta	atagacaaaa	gttcctcctt	tacaagaact	1380
gactctact	ttttgtgtat	cttcgacatc	tttagatttt	cagtatagat	aatatatggc	1440
tc						

(2) INFORMATION FOR SEQ ID NO:1404:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1569847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404:

Ala	Asn	Phe	Lys	Pro	Arg	Leu	Met	Ile	Glu	Lys	Lys	Leu	Ser	Lys	Met
1				5					10					15	
Lys	Met	Arg	Thr	Lys	Ser	Ile	Pro	Val	Arg	Ser	Ser	Arg	Lys	Ser	Leu
			20					25					30		
Asp	Ser	Leu	Leu	Asp	Asp	Glu	Ala	Asn	Glu	Asn	Thr	Gln	Cys	Asp	Glu
			35				40					45			
Arg	Asp	Val	Pro	His	Lys	Lys	Arg	Arg	Cys	Leu	Gly	Thr	Ser	Glu	Thr
			50				55				60				
Thr	Asp	Arg	Gly	Gly	Ser	Val	Glu	Pro	Leu	Leu	Asp	Leu	Asp	Ala	Cys
			65				70				75			80	
Ile	Val	Cys	Glu	Val	Ser	Asp	Glu	Arg	Val	Ser	Arg	Cys	Cys	Gly	Val
			85				90							95	
Asp	Cys	Leu	Leu	Ser	Phe	His	Gly	Glu	Cys	Leu	Tyr	Ala	Asp	Leu	Gly
			100				105						110		
Ser	Thr	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Glu	Asp	Val	Ser	Asn	Pro
			115				120					125			
Phe	Cys	Pro	Tyr	Cys	Trp	Leu	Lys	Ile	Val	Ala	Leu	Lys	Ser	Lys	Thr
			130				135					140			
Leu	Arg	Glu	Lys	Thr	Leu	Glu	Ala	Glu	Lys	Ala	Val	Cys	Lys	Tyr	Leu
			145				150				155				160
Asp	Lys	Glu	Met	Xaa	Ser	Arg	Asp	Glu	Asp	Ile	Thr	Leu	Ser	Gly	Asp
			165				170							175	
Glu	Ile	Gly	Asn	Gln	Glu	Gln	Ser	Thr	Asp	Ile	Val	Ser	Asp	His	Glu
			180				185						190		
Leu	Gln	Gly	Glu	Lys	Asp	Gly	Cys	Ser	Ser	Lys	Pro	Asp	Ala	Asp	Gln

195 200 205
Gly Lys Val Gly Thr Gly Lys Val Ile Asp Glu Val Gly Ala Ser Glu
210 215 220
Lys Val Ala Thr Glu Lys Phe Gln Asp Ala Glu Asp Asp Glu Thr Ala
225 230 240
Lys Asp Gln Gly Thr Arg Ile Leu Asn Thr Gly Ala Gly Lys Lys Arg
245 250 255
Glu Val Ser Ser Phe Leu Ser Met Gln Glu Ser Phe Ser Ala Lys Glu
260 265 270
Gln Asp Gln Val Gln Gln Asn Glu Lys Arg Arg Arg Arg Gly Leu Lys
275 280 285
Ile Ile Asp Ser Asp Ile Ser Ser Lys Gly Ser Ser Asn Glu Arg Asn
290 295 300
Gly Glu Asp Val Thr Glu Gln Val Thr Ser Ser Val Gln Val Thr Ser
305 310 315 320
Pro Ser Gly Arg Met Arg Asn Gln Gln Ala Thr Thr Lys Val Ala Lys
325 330 335
Ser Lys Thr Val Arg Asp Ile Ser Phe Phe Lys Met Asp Gln Arg Arg
340 345 350
Arg Leu Leu Trp Thr Tyr Glu Glu Glu Glu Met Leu Lys Val Gly Val
355 360 365
Glu Lys Phe Ala Ala Glu Ala Asn Lys Asn Met Pro Trp Arg Lys Ile
370 375 380
Leu Glu Met Gly Glu Lys Val Phe His Glu Thr Arg Thr Pro Ala Asp
385 390 395 400
Leu Lys Asp Lys Trp Arg Ser Met Val Lys Ile Met Asn Lys Asn Glu
405 410 415
Gln Gly Ser Thr Leu Thr Pro Thr Ala Met
420 425

(2) INFORMATION FOR SEQ ID NO:1405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..419
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:

Met Ile Glu Lys Lys Leu Ser Lys Met Lys Met Arg Thr Lys Ser Ile
1 5 10 15
Pro Val Arg Ser Ser Arg Lys Ser Leu Asp Ser Leu Leu Asp Asp Glu
20 25 30
Ala Asn Glu Asn Thr Gln Cys Asp Glu Arg Asp Val Pro His Lys Lys
35 40 45
Arg Arg Cys Leu Gly Thr Ser Glu Thr Thr Asp Arg Gly Gly Ser Val
50 55 60
Glu Pro Leu Leu Asp Leu Asp Ala Cys Ile Val Cys Glu Val Ser Asp
65 70 75 80
Glu Arg Val Ser Arg Cys Cys Gly Val Asp Cys Leu Leu Ser Phe His
85 90 95
Gly Glu Cys Leu Tyr Ala Asp Leu Gly Ser Thr Ser Ser Ser Ser
100 105 110
Ser Ser Ser Glu Asp Val Ser Asn Pro Phe Cys Pro Tyr Cys Trp Leu
115 120 125
Lys Ile Val Ala Leu Lys Ser Lys Thr Leu Arg Glu Lys Thr Leu Glu
130 135 140
Ala Glu Lys Ala Val Cys Lys Tyr Leu Asp Lys Glu Met Xaa Ser Arg
145 150 155 160

Asp Glu Asp Ile Thr Leu Ser Gly Asp Glu Ile Gly Asn Gln Glu Gln
165 170 175
Ser Thr Asp Ile Val Ser Asp His Glu Leu Gln Gly Glu Lys Asp Gly
180 185 190
Cys Ser Ser Lys Pro Asp Ala Asp Gln Gly Lys Val Gly Thr Gly Lys
195 200 205
Val Ile Asp Glu Val Gly Ala Ser Glu Lys Val Ala Thr Glu Lys Phe
210 215 220
Gln Asp Ala Glu Asp Asp Glu Thr Ala Lys Asp Gln Gly Thr Arg Ile
225 230 235 240
Leu Asn Thr Gly Ala Gly Lys Lys Arg Glu Val Ser Ser Phe Leu Ser
245 250 255
Met Gln Glu Ser Phe Ser Ala Lys Glu Gln Asp Gln Val Gln Gln Asn
260 265 270
Glu Lys Arg Arg Arg Arg Gly Leu Lys Ile Ile Asp Ser Asp Ile Ser
275 280 285
Ser Lys Gly Ser Ser Asn Glu Arg Asn Gly Glu Asp Val Thr Glu Gln
290 295 300
Val Thr Ser Ser Val Gln Val Thr Ser Pro Ser Gly Arg Met Arg Asn
305 310 315 320
Gln Gln Ala Thr Thr Lys Val Ala Lys Ser Lys Thr Val Arg Asp Ile
325 330 335
Ser Phe Phe Lys Met Asp Gln Arg Arg Arg Leu Leu Trp Thr Tyr Glu
340 345 350
Glu Glu Glu Met Leu Lys Val Gly Val Glu Lys Phe Ala Ala Glu Ala
355 360 365
Asn Lys Asn Met Pro Trp Arg Lys Ile Leu Glu Met Gly Glu Lys Val
370 375 380
Phe His Glu Thr Arg Thr Pro Ala Asp Leu Lys Asp Lys Trp Arg Ser
385 390 395 400
Met Val Lys Ile Met Asn Lys Asn Glu Gln Gly Ser Thr Leu Thr Pro
405 410 415
Thr Ala Met

(2) INFORMATION FOR SEQ ID NO:1406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..411

(D) OTHER INFORMATION: / Ceres Seq. ID 1569849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406:

Met Lys Met Arg Thr Lys Ser Ile Pro Val Arg Ser Ser Arg Lys Ser
1 5 10
Leu Asp Ser Leu Leu Asp Asp Glu Ala Asn Glu Asn Thr Gln Cys Asp
20 25 30
Glu Arg Asp Val Pro His Lys Lys Arg Arg Cys Leu Gly Thr Ser Glu
35 40 45
Thr Thr Asp Arg Gly Gly Ser Val Glu Pro Leu Leu Asp Leu Asp Ala
50 55 60
Cys Ile Val Cys Glu Val Ser Asp Glu Arg Val Ser Arg Cys Cys Gly
65 70 75 80
Val Asp Cys Leu Leu Ser Phe His Gly Glu Cys Leu Tyr Ala Asp Leu
85 90 95
Gly Ser Thr Ser Ser Ser Ser Ser Ser Ser Glu Asp Val Ser Asn
100 105 110
Pro Phe Cys Pro Tyr Cys Trp Leu Lys Ile Val Ala Leu Lys Ser Lys

115	120	125
Thr Leu Arg Glu Lys	Thr Leu Glu Ala Glu Lys	Ala Val Cys Lys Tyr
130	135	140
Leu Asp Lys Glu Met	Xaa Ser Arg Asp	Glu Asp Ile Thr Leu Ser Gly
145	150	155
Asp Glu Ile Gly Asn	Gln Glu Gln Ser	Thr Asp Ile Val Ser Asp His
165	170	175
Glu Leu Gln Gly Glu	Lys Asp Gly Cys Ser	Ser Lys Pro Asp Ala Asp
180	185	190
Gln Gly Lys Val Gly	Thr Gly Lys Val Ile	Asp Glu Val Gly Ala Ser
195	200	205
Glu Lys Val Ala Thr	Glu Lys Phe Gln Asp	Ala Glu Asp Asp Glu Thr
210	215	220
Ala Lys Asp Gln Gly	Thr Arg Ile Leu Asn	Thr Gly Ala Gly Lys Lys
225	230	235
Arg Glu Val Ser Ser	Phe Leu Ser Met	Gln Glu Ser Phe Ser Ala Lys
245	250	255
Glu Gln Asp Gln Val	Gln Gln Asn Glu Lys	Arg Arg Arg Arg Gly Leu
260	265	270
Lys Ile Ile Asp Ser	Asp Ile Ser Ser	Lys Gly Ser Ser Asn Glu Arg
275	280	285
Asn Gly Glu Asp Val	Thr Glu Gln Val	Thr Ser Ser Val Gln Val Thr
290	295	300
Ser Pro Ser Gly Arg	Met Arg Asn Gln	Gln Ala Thr Thr Lys Val Ala
305	310	315
Lys Ser Lys Thr Val	Arg Asp Ile Ser	Phe Phe Lys Met Asp Gln Arg
325	330	335
Arg Arg Leu Leu Trp	Thr Tyr Glu Glu Glu	Met Leu Lys Val Gly
340	345	350
Val Glu Lys Phe Ala	Ala Glu Ala Asn	Lys Asn Met Pro Trp Arg Lys
355	360	365
Ile Leu Glu Met Gly	Glu Lys Val Phe His	Glu Thr Arg Thr Pro Ala
370	375	380
Asp Leu Lys Asp Lys	Trp Arg Ser Met	Val Lys Ile Met Asn Lys Asn
385	390	395
Glu Gln Gly Ser Thr	Leu Thr Pro Thr	Ala Met
405	410	

(2) INFORMATION FOR SEQ ID NO:1407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 986 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..986
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:

aattcacc	cctccctccc	ttaagtctgt	ttgaattctgc	tgaattgttt	tataaagagt	60
tactttcgca	aaatggaaaa	tccggcggaag	agagtgttga	tgcacatccaa	cggcgcagag	120
gtgtcccgaa	acatcgcttt	ccatctagcc	aaacacgggtt	gcaagtgtgt	aatgatggga	180
aatgagggtt	ccctaaggag	catgttagag	attccattga	gggagccttc	cotgcccgatg	240
ttatagcact	cgacatggaa	tctgactctg	aagttgcttt	tcattgcgct	gtccaaaagg	300
catgggaact	ttccggccat	tctgatgctt	ttctcaactc	ttatacctac	caaggaaaagg	360
tgccagacat	tcttcaagtc	tctcaagatg	agttccacag	aatcacaaaag	atcaatctca	420
ccgcctcatg	gtttctctaa	aggctgtagc	cacaaggatg	aaggaccatg	gatcaggagg	480
ctccattgtc	ttcatggcca	ctatcgccag	cggagagagg	gcgctttacc	ctggcgctga	540
tgccatagct	tcaacttctg	ccgctattca	ccagctcgtt	cgggcatcag	ccatgagtct	600
cggggaagc	aagatcacgg	tcaactgat	ctctagaggg	ctgcatctg	atgatgagta	660
tacagcttct	gtgggaagag	accgagcaca	gaagctggtc	aaggacgctg	caccctcgg	720

```
ccagtggtc aaccgggaga cagacctcta ctccactgtt atctacttga tcagcgtatg 780
Ctcacgcttc atgacaggga ccaactgtctt ggtggatgga gcgcagtcctc ttacgcgacc 840
cgtgtcaaaa tcttactatgt gatcaacgcg tagtattata attctatgtt gctgtgtaaaa 900
agtgaatatg aatcaagttt gaataacttt ggagggatta ataatccatg gaatcaatga 960
ttacataactt ttgacaagta tagaag
```

(2) INFORMATION FOR SEQ ID NO:1408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1569868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:

```
Met Val Ser Leu Lys Ala Val Ala Thr Arg Met Lys Asp His Gly Ser
1 5 10 15
Gly Gly Ser Ile Val Phe Met Ala Thr Ile Ala Ser Gly Glu Arg Ala
20 25 30
Leu Tyr Pro Gly Ala Asp Ala Tyr Ala Ser Thr Ser Ala Ala Ile His
35 40 45
Gln Leu Val Arg Ala Ser Ala Met Ser Leu Gly Lys His Lys Ile Arg
50 55 60
Val Asn Met Ile Ser Arg Gly Leu His Leu Asp Asp Glu Tyr Thr Ala
65 70 75 80
Ser Val Gly Arg Asp Arg Ala Gln Lys Leu Val Lys Asp Ala Ala Pro
85 90 95
Leu Gly Gln Trp Leu Asn Pro Glu Thr Asp Leu Tyr Ser Thr Val Ile
100 105 110
Tyr Leu Ile Ser Asp Gly Ser Arg Phe Met Thr Gly Thr Thr Val Leu
115 120 125
Val Asp Gly Ala Gln Ser Leu Thr Arg Pro Arg Leu Lys Ser Tyr Met
130 135 140
```

(2) INFORMATION FOR SEQ ID NO:1409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1569869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:

```
Met Lys Asp His Gly Ser Gly Gly Ser Ile Val Phe Met Ala Thr Ile
1 5 10 15
Ala Ser Gly Glu Arg Ala Leu Tyr Pro Gly Ala Asp Ala Tyr Ala Ser
20 25 30
Thr Ser Ala Ala Ile His Gln Leu Val Arg Ala Ser Ala Met Ser Leu
35 40 45
Gly Lys His Lys Ile Arg Val Asn Met Ile Ser Arg Gly Leu His Leu
50 55 60
Asp Asp Glu Tyr Thr Ala Ser Val Gly Arg Asp Arg Ala Gln Lys Leu
65 70 75 80
Val Lys Asp Ala Ala Pro Leu Gly Gln Trp Leu Asn Pro Glu Thr Asp
85 90 95
```

Leu Tyr Ser Thr Val Ile Tyr Leu Ile Ser Asp Gly Ser Arg Phe Met
100 105 110
Thr Gly Thr Thr Val Leu Val Asp Gly Ala Gln Ser Leu Thr Arg Pro
115 120 125
Arg Leu Lys Ser Tyr Met
130

(2) INFORMATION FOR SEQ ID NO:1410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410:

Met Ala Thr Ile Ala Ser Gly Glu Arg Ala Leu Tyr Pro Gly Ala Asp
1 5 10 15
Ala Tyr Ala Ser Thr Ser Ala Ala Ile His Gln Leu Val Arg Ala Ser
20 25 30
Ala Met Ser Leu Gly Lys His Lys Ile Arg Val Asn Met Ile Ser Arg
35 40 45
Gly Leu His Leu Asp Asp Glu Tyr Thr Ala Ser Val Gly Arg Asp Arg
50 55 60
Ala Gln Lys Leu Val Lys Asp Ala Ala Pro Leu Gly Gln Trp Leu Asn
65 70 75 80
Pro Glu Thr Asp Leu Tyr Ser Thr Val Ile Tyr Leu Ile Ser Asp Gly
85 90 95
Ser Arg Phe Met Thr Gly Thr Thr Val Leu Val Asp Gly Ala Gln Ser
100 105 110
Leu Thr Arg Pro Arg Leu Lys Ser Tyr Met
115 120

(2) INFORMATION FOR SEQ ID NO:1411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1573
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411:

ctctctctct ctctctccct ctctaaactgt atctctctct tcttcttcaa ccttcagact 60
ttcttagttg caactctcat tcaattgttc aattctctctg taataaatcaa agcttttttg 120
aatcttttctt cggcgagata ttctttcacc ggcgcaagct tctcttgagc gtgattcatc 180
actgggtttg cattttttcc tgggtgggtat tcttcaaatg gtccaaagct ccgacctttt 240
cttctcttga atctgattac tggaaatcttg aagctggaga gactcagatt tatatggttt 300
caagactcgt tgagctcaatc attgagttgt gtagaagaaa ggtttggttt tcttctccgt 360
ttaagtgggt ttgggttttg taggatttgg tgtaaatctgg gagataaaga aagatgaata 420
tgagtgattt aggttgggat gatgaagata aatcgggtgt tagtgcgtgt ttaggcatt 480
tagcttctga ttttctctga gcaaacctcta attcgaatca gaatctcttt cttgttatgg 540
gaactcatga tactctgaat aagaagctct ctagtctcgt tgatttggcca aactcggaga 600
atttcagctg gaactacgct attttctggc aacaaacctat gctcagatcc ggacaacaag 660
tcttaggttg gggagatggg tgttgcgcag agcctaataa ggaagaggaa tcaaaagtgt 720
ttaggtctta taatttttaac aacatggggg cagaggaaga gacatggcaa gatatgagga 780
agagagtgtt gcagaagctt cataggttgt ttggtggatc tgatgaagac aattatgctt 840
tgagcttaga gaaagtact gctactgaga ttttctctt agcttccatg tattttctt 900

tcaatcacgg	tgaaggcgg	cctggggaggt	gttattcttc	agggaacat	gtgtggctct	960
ctgatcggt	taactctgag	tctgactatt	gtttcaggtc	ttttatggcg	aaatctgcgg	1020
gaatcagaag	gatcgttatg	gttctctactg	atgctgggtg	tcttgagcgt	ggttctgttt	1080
ggctcttggc	tgaaaacatt	ggctgtgtta	agtctgttca	agctttgttc	atgaggagag	1140
ttacgcaacc	agtaatgggtg	acttcaaaca	ctaactgac	tggaggggatt	cacaagcctt	1200
tcggggcagg	tttgagtggg	gCtcacgggt	atcctaagaa	gctcgaagtg	agaagaaact	1260
tggatgagag	atcactcct	caaagttggg	aaggctataa	taacaataaa	gggtccaacat	1320
ttggttacac	acctcagagg	gatgatgtga	aagtgcctaga	gaatgtgaat	atggttgtag	1380
ataataacaa	ttacaagacg	cagattgagt	ttgcgggatc	atcagttgct	gcttcttcga	1440
atccatctac	aaacactcag	caagaaaaat	cagaatcttg	tacagagaaa	agaccagtga	1500
gcttgtagc	aggagcagg	atagtttctg	ttgttgatga	gaagagaccg	agaaaagagag	1560
ggagaaagcc	tgc					

(2) INFORMATION FOR SEQ ID NO:1412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..386
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412:

Met	Asn	Met	Ser	Asp	Leu	Gly	Trp	Asp	Asp	Glu	Asp	Lys	Ser	Val	Val
1			5					10						15	
Ser	Ala	Val	Leu	Gly	His	Leu	Ala	Ser	Asp	Phe	Leu	Arg	Ala	Asn	Ser
			20					25					30		
Asn	Ser	Asn	Gln	Asn	Leu	Phe	Leu	Val	Met	Gly	Thr	Asp	Asp	Thr	Leu
		35				40						45			
Asn	Lys	Lys	Leu	Ser	Ser	Leu	Val	Asp	Trp	Pro	Asn	Ser	Glu	Asn	Phe
		50				55					60				
Ser	Trp	Asn	Tyr	Ala	Ile	Phe	Trp	Gln	Gln	Thr	Met	Ser	Arg	Ser	Gly
65			70							75				80	
Gln	Gln	Val	Leu	Gly	Trp	Gly	Asp	Gly	Cys	Cys	Arg	Glu	Pro	Asn	Glu
			85						90					95	
Glu	Glu	Glu	Ser	Lys	Val	Val	Arg	Ser	Tyr	Asn	Phe	Asn	Asn	Met	Gly
			100					105					110		
Ala	Glu	Glu	Glu	Thr	Trp	Gln	Asp	Met	Arg	Lys	Arg	Val	Leu	Gln	Lys
			115					120				125			
Leu	His	Arg	Leu	Phe	Gly	Gly	Ser	Asp	Glu	Asp	Asn	Tyr	Ala	Leu	Ser
			130			135					140				
Leu	Glu	Lys	Val	Thr	Ala	Thr	Glu	Ile	Phe	Phe	Leu	Ala	Ser	Met	Tyr
145					150				155					160	
Phe	Phe	Phe	Asn	His	Gly	Glu	Gly	Gly	Pro	Gly	Arg	Cys	Tyr	Ser	Ser
			165						170					175	
Gly	Lys	His	Val	Trp	Leu	Ser	Asp	Ala	Val	Asn	Ser	Glu	Ser	Asp	Tyr
			180					185					190		
Cys	Phe	Arg	Ser	Phe	Met	Ala	Lys	Ser	Ala	Gly	Ile	Arg	Thr	Ile	Val
			195				200					205			
Met	Val	Pro	Thr	Asp	Ala	Gly	Val	Leu	Glu	Leu	Gly	Ser	Val	Trp	Ser
			210			215						220			
Leu	Pro	Glu	Asn	Ile	Gly	Leu	Val	Lys	Ser	Val	Gln	Ala	Leu	Phe	Met
225					230					235				240	
Arg	Arg	Val	Thr	Gln	Pro	Val	Met	Val	Thr	Ser	Asn	Thr	Asn	Met	Thr
			245						250					255	
Gly	Gly	Ile	His	Lys	Leu	Phe	Gly	Gln	Asp	Leu	Ser	Gly	Ala	His	Ala
			260					265					270		
Tyr	Pro	Lys	Lys	Leu	Glu	Val	Arg	Arg	Asn	Leu	Asp	Glu	Arg	Phe	Thr
			275				280					285			
Pro	Gln	Ser	Trp	Glu	Gly	Tyr	Asn	Asn	Lys	Gly	Pro	Thr	Phe	Gly	

(2) INFORMATION FOR SEQ ID NO:1413:

(A) LENGTH: 384 amino acids

(C) STRANDEDNESS:

MOLECULE TYPE: peptid

(IX) FEATURE:
(A) NAME/KEY: peptide

(D) OTHER INFORMATION

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1413:
Ser Asp Lys Gly Trp Asp Asp Glu Asp Lys Se

Met	Ser	Asp	Leu	Gly	Trp	Asp	Asp	Glu	Asp	Lys	Ser	Val	Val	Ala
1			5					10					15	
Val	Leu	Gly	His	Leu	Ala	Ser	Asp	Phe	Leu	Arg	Ala	Asn	Ser	Ser
			20					25				30		
Asn	Gln	Asn	Leu	Phe	Leu	Val	Met	Gly	Thr	Asp	Asp	Thr	Leu	Asn
		35					40					45		Lys
Lys	Leu	Ser	Ser	Leu	Val	Asp	Trp	Pro	Asn	Ser	Glu	Asn	Phe	Ser
	50					55					60			Trp
Asn	Tyr	Ala	Ile	Phe	Trp	Gln	Gln	Thr	Met	Ser	Arg	Ser	Gly	Gln
					70					75				80
Val	Leu	Gly	Trp	Gly	Asp	Gly	Cys	Cys	Arg	Glu	Pro	Asn	Glu	Glu
				85				90					95	
Glu	Ser	Lys	Val	Val	Arg	Ser	Tyr	Asn	Phe	Asn	Asn	Met	Gly	Ala
			100					105					110	Glu
Glu	Glu	Thr	Trp	Gln	Asp	Met	Arg	Lys	Arg	Val	Leu	Gln	Lys	Leu
			115				120					125		His
Arg	Leu	Phe	Gly	Gly	Ser	Asp	Glu	Asn	Tyr	Ala	Leu	Ser	Leu	Glu
	130					135					140			
Lys	Val	Thr	Ala	Thr	Glu	Ile	Phe	Phe	Leu	Ala	Ser	Met	Tyr	Phe
	145				150					155				160
Phe	Asn	His	Gly	Glu	Gly	Gly	Pro	Gly	Arg	Cys	Tyr	Ser	Ser	Gly
				165					170					175
His	Val	Trp	Leu	Ser	Asp	Ala	Val	Asn	Ser	Glu	Ser	Asp	Tyr	Cys
			180					185					190	Phe
Arg	Ser	Phe	Met	Ala	Lys	Ser	Ala	Gly	Ile	Arg	Thr	Ile	Val	Met
		195					200					205		Val
Pro	Thr	Asp	Ala	Gly	Val	Leu	Glu	Leu	Gly	Ser	Val	Trp	Ser	Leu
	210					215					220			Pro
Glu	Asn	Ile	Gly	Leu	Val	Lys	Ser	Val	Gln	Ala	Leu	Phe	Met	Arg
	225				230					235				240
Val	Thr	Gln	Pro	Val	Met	Val	Thr	Ser	Asn	Thr	Asn	Met	Thr	Gly
				245					250					255
Ile	His	Lys	Leu	Phe	Gly	Gln	Asp	Leu	Ser	Gly	Ala	His	Ala	Tyr
		260						265					270	Pro
Lys	Lys	Leu	Glu	Val	Arg	Arg	Asn	Leu	Asp	Glu	Arg	Phe	Thr	Gln
		275					280					285		

Ser	Trp	Glu	Gly	Tyr	Asn	Asn	Asn	Lys	Gly	Pro	Thr	Phe	Gly	Tyr	Thr
290					295						300				
Pro	Gln	Arg	Asp	Asp	Val	Lys	Val	Leu	Glu	Asn	Val	Asn	Met	Val	Val
305					310					315				320	
Asp	Asn	Asn	Asn	Tyr	Lys	Thr	Gln	Ile	Glu	Phe	Ala	Gly	Ser	Ser	Val
				325					330					335	
Ala	Ala	Ser	Ser	Asn	Pro	Ser	Thr	Asn	Thr	Gln	Gln	Glu	Lys	Ser	Glu
				340					345				350		
Ser	Cys	Thr	Glu	Lys	Arg	Pro	Val	Ser	Leu	Leu	Ala	Gly	Ala	Gly	Ile
				355					360				365		
Val	Ser	Val	Val	Asp	Glu	Lys	Arg	Pro	Arg	Lys	Arg	Gly	Arg	Lys	Pro
370					375										

(2) INFORMATION FOR SEQ ID NO:1414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..345

(D) OTHER INFORMATION: / Ceres Seq. ID 1569874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414:

Met	Gly	Thr	Asp	Asp	Thr	Leu	Asn	Lys	Lys	Leu	Ser	Ser	Leu	Val	Asp
1			5					10					15		
Trp	Pro	Asn	Ser	Glu	Asn	Phe	Ser	Trp	Asn	Tyr	Ala	Ile	Phe	Trp	Gln
			20					25					30		
Gln	Thr	Met	Ser	Arg	Ser	Gly	Gln	Gln	Val	Leu	Gly	Trp	Gly	Asp	Gly
			35				40					45			
Cys	Cys	Arg	Glu	Pro	Asn	Glu	Glu	Glu	Ser	Lys	Val	Val	Arg	Ser	
			50				55				60				
Tyr	Asn	Phe	Asn	Asn	Met	Gly	Ala	Glu	Glu	Glu	Thr	Trp	Gln	Asp	Met
					70					75				80	
Arg	Lys	Arg	Val	Leu	Gln	Lys	Leu	His	Arg	Leu	Phe	Gly	Gly	Ser	Asp
				85					90				95		
Glu	Asp	Asn	Tyr	Ala	Leu	Ser	Leu	Glu	Lys	Val	Thr	Ala	Thr	Glu	Ile
				100				105					110		
Phe	Phe	Leu	Ala	Ser	Met	Tyr	Phe	Phe	Phe	Asn	His	Gly	Glu	Gly	Gly
				115				120				125			
Pro	Gly	Arg	Cys	Tyr	Ser	Ser	Gly	Lys	His	Val	Trp	Leu	Ser	Asp	Ala
					135						140				
Val	Asn	Ser	Glu	Ser	Asp	Tyr	Cys	Phe	Arg	Ser	Phe	Met	Ala	Lys	Ser
					150				155					160	
Ala	Gly	Ile	Arg	Thr	Ile	Val	Met	Val	Pro	Thr	Asp	Ala	Gly	Val	Leu
				165					170					175	
Glu	Leu	Gly	Ser	Val	Trp	Ser	Leu	Pro	Glu	Asn	Ile	Gly	Leu	Val	Lys
				180				185					190		
Ser	Val	Gln	Ala	Leu	Phe	Met	Arg	Arg	Val	Thr	Gln	Pro	Val	Met	Val
				195				200				205			
Thr	Ser	Asn	Thr	Asn	Met	Thr	Gly	Gly	Ile	His	Lys	Leu	Phe	Gly	Gln
					215						220				
Asp	Leu	Ser	Gly	Ala	His	Ala	Tyr	Pro	Lys	Lys	Leu	Glu	Val	Arg	Arg
				230						235					240
Asn	Leu	Asp	Glu	Arg	Phe	Thr	Pro	Gln	Ser	Trp	Glu	Gly	Tyr	Asn	Asn
				245					250					255	
Asn	Lys	Gly	Pro	Thr	Phe	Gly	Tyr	Thr	Pro	Gln	Arg	Asp	Asp	Val	Lys
				260				265					270		
Val	Leu	Glu	Asn	Val	Asn	Met	Val	Val	Asp	Asn	Asn	Asn	Tyr	Lys	Thr

	275		280		285
Gln Ile Glu Phe Ala Gly Ser Ser Val Ala Ala Ser Ser Asn Pro Ser					
290		295		300	
Thr Asn Thr Gln Gln Glu Lys Ser Glu Ser Cys Thr Glu Lys Arg Pro					
305		310		315	320
Val Ser Leu Leu Ala Gly Ala Gly Ile Val Ser Val Val Asp Glu Lys					
	325		330		335
Arg Pro Arg Lys Arg Gly Arg Lys Pro					
	340		345		

(2) INFORMATION FOR SEQ ID NO:1415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1215
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415:

ggtttaaAtt	gtttctctctg	atcgaaaagg	aatcagttta	ggtctttggcc	tcctctctcc	60
ggccagctca	attctcgtatc	aaaggtgacg	tgatataatg	aagcagatgt	tttggggaac	120
cagagtctctg	taaatagaaa	ccttcacgcg	acgttgaaag	gttttttgaga	cgaatatagg	180
aggagaagat	gggatgtgtt	tcttcttctg	tccgggttga	ggacattgat	gagtcacatg	240
atccaaacag	ctctgtctat	aggaactgtc	cctgcataag	atgccttctg	cataatttcc	300
ttaacctgtg	tatttcggct	ttcagaagag	gggaaactcg	ctctctccca	tcttcggctc	360
aagctactgc	atcgataact	tctctctctt	cacacgataa	ctttttgtct	gaagcattcc	420
gttctactcc	aaagcctctg	ccttatgatg	ctgatcctag	atacttcocg	tcactcgtct	480
caaggcgagg	gaagggttca	agtcattctc	atgaggaagt	tgaaccttta	agaagcgata	540
cgatgcgaga	tcttgaatct	tccgggttag	gaggggtcaa	atgggctaat	aataagttca	600
ccctctctga	taaaagtctc	aaagaagagt	actctagtta	atccagtctc	aggattttga	660
gatcaaggtc	caagtcata	atggccgact	ctgaaaaaat	gtatatattg	tctgaagacg	720
aaagtgtctg	cccaacttgt	cttgaagaat	atcacatcga	gaaccocaa	attgtgacaa	780
aatgttcaca	ccatttccac	cttagttgca	tttatgatgt	gatggagaga	agtgtaaaact	840
gtccagctcg	cggaaaaggt	atggaaattca	acgaaacacc	gtgatcatcg	accattgatc	900
cggtctctgt	atctgaactg	aaaccgggga	agatgacaag	gcaatgcaag	gaatataatt	960
tgtaaatatt	gctttgtttg	tttgtgaata	ttttcattta	caatggtaaa	tatatgaagc	1020
agaaaaggag	aaactgtttc	tctgcacacg	tttaagttcc	tgagaaattt	taacttccat	1080
gaacaagaaa	gcaatgtttc	ttctttaagt	gactttttct	catgaaatgc	ctctgtgttt	1140
gtattctcta	gtcagtcata	aaaactctta	catcattgtc	gttatataaa	taaatttttc	1200
tttttttatg	tggttc					

(2) INFORMATION FOR SEQ ID NO:1416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..231
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416:

Met Gly Cys Val Ser Ser Cys Phe Arg Val Glu Asp Ile Asp Glu Tyr	
1	5 10 15
Met Asn Pro Asn Ser Ser Val Tyr Arg Asn Cys Pro Cys Ile Arg Cys	
	20 25 30
Leu Ala His Asn Phe Leu Asn Leu Tyr Ile Ser Val Phe Arg Arg Gly	
	35 40 45
Glu Thr Arg Ser Leu Pro Ser Ser Val Gln Ala Thr Ala Ser Ile Thr	

(2) INFORMATION FOR SEQ ID NO:1417:

(A) LENGTH: 215 amino acids

(A) LENGTH: 215 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..215

(D) OTHER INFORMATION: / Ceres Seq. ID 1569899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417:

Met	Asn	Pro	Asn	Ser	Ser	Val	Tyr	Arg	Asn	Cys	Pro	Cys	Ile	Arg	Cys
1			5					10						15	
Leu	Ala	His	Asn	Phe	Leu	Asn	Leu	Tyr	Ile	Ser	Val	Phe	Arg	Arg	Gly
			20					25					30		
Glu	Thr	Arg	Ser	Leu	Pro	Ser	Ser	Val	Gln	Ala	Thr	Ala	Ser	Ile	Thr
		35					40					45			
Ser	Ser	Ser	Ser	His	Asp	Asn	Phe	Leu	Ser	Glu	Ala	Phe	Arg	Ser	Thr
		50				55					60				
Pro	Arg	Pro	Leu	Pro	Tyr	Asp	Ala	Asp	Pro	Arg	Tyr	Phe	Arg	Ser	Leu
65					70					75					80
Val	Ser	Arg	Arg	Glu	Lys	Gly	Ser	Ser	His	Ser	His	Glu	Glu	Val	Glu
				85										95	
Pro	Leu	Arg	Ser	Asp	Ser	Asp	Ala	Asp	Ser	Glu	Ser	Phe	Gly	Val	Gly
				100				105					110		
Gly	Cys	Lys	Trp	Ala	Asn	Asn	Lys	Ser	Thr	Leu	Ser	Asp	Lys	Asp	Ser
		115					120					125			
Lys	Glu	Glu	Tyr	Ser	Ser	Lys	Ser	Ser	Leu	Arg	Ile	Leu	Arg	Ser	Arg
		130				135					140				
Ser	Lys	Ser	Ile	Met	Ala	Asp	Ser	Glu	Asn	Met	Tyr	Ile	Leu	Ser	Glu
145					150					155					160
Asp	Glu	Asp	Val	Cys	Pro	Thr	Cys	Leu	Glu	Glu	Tyr	Thr	Ser	Glu	Asn
				165					170					175	
Pro	Lys	Ile	Val	Thr	Lys	Cys	Ser	His	His	Phe	His	Leu	Ser	Cys	Ile
			180					185					190		
Tyr	Glu	Trp	Met	Glu	Arg	Ser	Glu	Asn	Cys	Pro	Val	Cys	Gly	Lys	Val
		195					200					205			

Met Glu Phe Asn Glu Thr Pro
210 215

(2) INFORMATION FOR SEQ ID NO:1418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1253
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418:

aaacacatga	cccttaaatc	gagaggcttc	gttaggagaa	ggagaagcag	aagagtgttg	60
gttctcgatt	gtcgaatctca	acaatggcgt	agtcctccca	aaatgcgtca	acctcgagct	120
tctctcgccg	cgtatgttaa	ggatgggtctg	atcattgtga	ttggaggttg	caggtcccaa	180
aatatcgaga	cttggggaga	gatttatgat	ctaaagacca	atacttgggg	gcgaataactg	240
ctccaatcac	atgatcccac	agttcaaaat	gcttacttga	atcgctttaa	acctaaactgt	300
cagacgaatg	cttgctatgt	agagattgac	aaggtgtcgt	gctgtatatt	tttatccgat	360
gggaagactat	tttggcgtga	aacaaagcaa	ggttttgaga	ggtgtagtgt	tatatgtgga	420
gatgatgagc	aagtgtcctc	ttatcaactt	gtttcgggtg	caaacgcgcg	cggaggagga	480
agagtgcacg	tttggtgaaa	gtcgggggta	aaagtctctg	atctcttaag	tggcactgag	540
acttgggaat	gttacacaaa	tagtcgggtg	gcagagattt	cgtttgagag	aagaggttta	600
agagagcttt	ggggattcgt	tgaatggctc	agagaggtgt	ttaccgttga	tggatatgac	660
gataacttaag	atttcttttt	aaattctgct	attgtgacct	attgatcagt	gggactttat	720
cttaacttga	ctgtgggaat	tttgagtatg	attttaaatg	ataaataaat	gtgattttgt	780
aacaacatta	caacatagat	ctaagcatto	aaggtgtTtg	tggtgcctga	tggcttttga	840
tgaaggggag	gttttctact	ttgtatcaga	cttttgcctg	ctagtgaag	agagaataat	900
gggcacaaca	tttttggttac	tccatgggaa	agataatgta	gagtggtctc	aaggaaaaaa	960
tggtgtggag	agtggtcaag	ggacttggat	tgccaaacat	tgtgtttcag	tttgtgtgtg	1020
tacaatgttg	gatcacccct	atggctgtaa	agtgacagatt	tcgcagagct	ttccaaggga	1080
atcatagaat	cgtcaacgga	gttgtgtttc	gaaccaaagg	atgtatatatt	cgttccactt	1140
tctctettgca	cttgtctata	gtaacacatg	gattgtatg	ctctcatggg	agttgcacaaa	1200
tctctagtga	tcttctgtttt	tatttgcctt	ttggaatgct	taaagaatga	tat	

(2) INFORMATION FOR SEQ ID NO:1419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..234
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419:

Lys	His	Met	Thr	Pro	Lys	Ser	Arg	Gly	Phe	Val	Arg	Arg	Arg	Arg	Ser	
1					5			10						15		
Arg	Arg	Val	Leu	Val	Leu	Asp	Cys	Arg	Ser	Gln	Gln	Trp	Arg	Ser	Leu	
		20					25						30			
Pro	Lys	Met	Arg	Gln	Pro	Arg	Ala	Ser	Pro	Ala	Ala	Tyr	Val	Lys	Asp	
		35					40					45				
Gly	Leu	Ile	Ile	Val	Ile	Gly	Cys	Arg	Ser	Lys	Asn	Ile	Glu	Thr		
	50					55				60						
Trp	Gly	Glu	Ile	Tyr	Asp	Leu	Lys	Thr	Asn	Thr	Trp	Gly	Arg	Ile	Leu	
	65				70				75					80		
Leu	Gln	Ser	His	Asp	Pro	Thr	Val	Gln	Asn	Ala	Tyr	Leu	Asn	Arg	Phe	
			85						90				95			
Lys	Pro	Asn	Leu	Gln	Thr	Asn	Ala	Cys	Tyr	Val	Glu	Ile	Asp	Lys	Val	
		100					105						110			

Ser Cys Leu Ile Phe Leu Ser Asp Gly Lys Leu Phe Trp Arg Glu Thr
115 120 125
Lys Gln Gly Phe Glu Arg Cys Ser Val Ile Leu Gly Asp Asp Glu Gln
130 135 140
Val Ser Ser Tyr Gln Leu Val Ser Val Ala Asn Ala Ala Gly Gly Gly
145 150 155 160
Arg Val Thr Val Trp Trp Lys Ser Gly Leu Lys Val Leu Asp Leu Leu
165 170 175
Ser Gly Thr Glu Thr Trp Glu Cys Tyr Thr Asn Ser Arg Cys Ala Glu
180 185 190
Ile Ser Phe Glu Arg Arg Gly Leu Arg Glu Leu Trp Gly Phe Val Glu
195 200 205
Trp Ser Arg Glu Val Phe Thr Val Asp Gly Tyr Asp Asp Thr Tyr Asp
210 215 220
Phe Phe Leu Asn Ser Ala Ile Val Thr Tyr
225 230

(2) INFORMATION FOR SEQ ID NO:1420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..232
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:

Met Thr Pro Lys Ser Arg Gly Phe Val Arg Arg Arg Arg Ser Arg Arg
1 5 10 15
Val Leu Val Leu Asp Cys Arg Ser Gln Gln Trp Arg Ser Leu Pro Lys
20 25 30
Met Arg Gln Pro Arg Ala Ser Pro Ala Ala Tyr Val Lys Asp Gly Leu
35 40 45
Ile Ile Val Ile Gly Gly Cys Arg Ser Lys Asn Ile Glu Thr Trp Gly
50 55 60
Glu Ile Tyr Asp Leu Lys Thr Asn Thr Trp Gly Arg Ile Leu Leu Gln
65 70 75 80
Ser His Asp Pro Thr Val Gln Asn Ala Tyr Leu Asn Arg Phe Lys Pro
85 90 95
Asn Leu Gln Thr Asn Ala Cys Tyr Val Glu Ile Asp Lys Val Ser Cys
100 105 110
Leu Ile Phe Leu Ser Asp Gly Lys Leu Phe Trp Arg Glu Thr Lys Gln
115 120 125
Gly Phe Glu Arg Cys Ser Val Ile Leu Gly Asp Asp Glu Gln Val Ser
130 135 140
Ser Tyr Gln Leu Val Ser Val Ala Asn Ala Ala Gly Gly Gly Arg Val
145 150 155 160
Thr Val Trp Trp Lys Ser Gly Leu Lys Val Leu Asp Leu Leu Ser Gly
165 170 175
Thr Glu Thr Trp Glu Cys Tyr Thr Asn Ser Arg Cys Ala Glu Ile Ser
180 185 190
Phe Glu Arg Arg Gly Leu Arg Glu Leu Trp Gly Phe Val Glu Trp Ser
195 200 205
Arg Glu Val Phe Thr Val Asp Gly Tyr Asp Asp Thr Tyr Asp Phe Phe
210 215 220
Leu Asn Ser Ala Ile Val Thr Tyr
225 230

(2) INFORMATION FOR SEQ ID NO:1421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:1421:															
Met	Arg	Gln	Pro	Arg	Ala	Ser	Pro	Ala	Ala	Tyr	Val	Lys	Asp	Gly	Leu
1				5				10						15	
Ile	Ile	Val	Ile	Gly	Gly	Cys	Arg	Ser	Lys	Asn	Ile	Glu	Thr	Trp	Gly
			20					25					30		
Glu	Ile	Tyr	Asp	Leu	Lys	Thr	Asn	Thr	Trp	Gly	Arg	Ile	Glu	Leu	Gln
		35					40					45			
Ser	His	Asp	Pro	Thr	Val	Gln	Asn	Ala	Tyr	Leu	Asn	Arg	Phe	Lys	Pro
	50					55					60				
Asn	Leu	Gln	Thr	Asn	Ala	Cys	Tyr	Val	Glu	Ile	Asp	Lys	Val	Ser	Cys
65				70						75				80	
Leu	Ile	Phe	Leu	Ser	Asp	Gly	Lys	Leu	Phe	Trp	Arg	Glu	Thr	Lys	Gln
				85				90						95	
Gly	Phe	Glu	Arg	Cys	Ser	Val	Ile	Leu	Gly	Asp	Asp	Glu	Gln	Val	Ser
			100					105					110		
Ser	Tyr	Gln	Leu	Val	Ser	Val	Ala	Asn	Ala	Ala	Gly	Gly	Gly	Arg	Val
		115					120					125			
Thr	Val	Trp	Trp	Lys	Ser	Gly	Leu	Lys	Val	Leu	Asp	Leu	Leu	Ser	Gly
		130				135					140				
Thr	Glu	Thr	Trp	Glu	Cys	Tyr	Thr	Asn	Ser	Arg	Cys	Ala	Glu	Ile	Ser
145				150						155				160	
Phe	Glu	Arg	Arg	Gly	Leu	Arg	Glu	Leu	Trp	Gly	Phe	Val	Glu	Trp	Ser
				165				170						175	
Arg	Glu	Val	Phe	Thr	Val	Asp	Gly	Tyr	Asp	Asp	Thr	Tyr	Asp	Phe	Phe
			180					185					190		
Leu	Asn	Ser	Ala	Ile	Val	Thr	Tyr								
		195				200									

(A) NAME/KEY: -
(B) LOCATION: 1..715
(D) OTHER INFORMATION: / Ceres Seq. ID 1569942

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..154
(D) OTHER INFORMATION: / Ceres Seq. ID 1569943
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:

Met	Asp	Tyr	Leu	Gly	Ile	Asp	Leu	Ser	Cys	Ala	Ile	Gly	Ser	Leu	Arg
1			5					10					15		
Asn	Gly	Glu	Phe	Pro	Ala	Lys	Asp	Cys	Leu	Leu	Pro	Leu	Ile	Ser	Lys
			20				25					30			
Leu	Leu	Gly	Tyr	Phe	Leu	Val	Ala	Ala	Ser	Met	Thr	Val	Lys	Leu	Pro
		35					40					45			
Gln	Ile	Met	Lys	Ile	Val	Asp	Asn	Lys	Ser	Val	Lys	Gly	Leu	Ser	Val
	50					55				60					
Val	Ala	Phe	Glu	Leu	Glu	Val	Ile	Gly	Tyr	Thr	Ile	Ser	Leu	Ala	Tyr
	65			70				75				80			
Cys	Leu	Asn	Lys	Asp	Leu	Pro	Phe	Ser	Ala	Phe	Gly	Glu	Leu	Ala	Phe
			85					90				95			
Leu	Leu	Ile	Gln	Ala	Leu	Ile	Leu	Val	Ala	Cys	Ile	Tyr	Tyr	Phe	Ser
		100					105					110			
Gln	Pro	Leu	Ser	Val	Thr	Thr	Trp	Val	Lys	Ala	Ile	Leu	Tyr	Phe	Ala
		115					120					125			
Ile	Ala	Pro	Thr	Val	Phe	Ala	Glu	Ser	Leu	Arg	Phe	Gly	Arg	Thr	Ser
	130				135					140					
Glu	Thr	Lys	Ala	Leu	Asp	Asn	Leu	Val	Ser						
	145				150										

(2) INFORMATION FOR SEQ ID NO:1424:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..112
(D) OTHER INFORMATION: / Ceres Seq. ID 1569945
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:

Met	Thr	Val	Lys	Leu	Pro	Gln	Ile	Met	Lys	Ile	Val	Asp	Asn	Lys	Ser
1			5					10					15		
Val	Lys	Gly	Leu	Ser	Val	Val	Ala	Phe	Glu	Leu	Glu	Val	Ile	Gly	Tyr
		20					25					30			
Thr	Ile	Ser	Leu	Ala	Tyr	Cys	Leu	Asn	Lys	Asp	Leu	Pro	Phe	Ser	Ala
		35				40					45				
Phe	Gly	Glu	Leu	Ala	Phe	Leu	Leu	Ile	Gln	Ala	Leu	Ile	Leu	Val	Ala
	50				55					60					
Cys	Ile	Tyr	Tyr	Phe	Ser	Gln	Pro	Leu	Ser	Val	Thr	Thr	Trp	Val	Lys
	65			70				75				80			
Ala	Ile	Leu	Tyr	Phe	Ala	Ile	Ala	Pro	Thr	Val	Phe	Ala	Glu	Ser	Leu
		85					90					95			
Arg	Phe	Gly	Arg	Thr	Ser	Glu	Thr	Lys	Ala	Leu	Asp	Asn	Leu	Val	Ser
		100					105					110			

(2) INFORMATION FOR SEQ ID NO:1425:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 496 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..496
(D) OTHER INFORMATION: / Ceres Seq. ID 1569946
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:
atgacgaaag cttcttggtc tctgttgctc tctcagtcgt gttagatctt cgtcttctca 60
cgtatcatat ggatagtgac attgtttcca cgttagatcg atctcagaca gcaatgcctg 120
atgtctttagc attcaagagt atcaatgato ctatcaagaa ccagatcaat agttgtgctg 180
caatctgtgt taagcaagat gatccatgcc atttcttgcc tgtcctgtat gagtctttga 240
taacaggagg gttagctggt gttgtgggtg aagctgctct gtatccaatt gatacaatca 300
aaactcgagt acaggttagca cgggatgggt gaaagataat gtgaaggagg ctatactctg 360
gtcttggtgc aaatcttgct ggtgtcttcc ctgcttcggc tctatttttt ggtgtatatg 420
aaccaccaa acagaagctg Gcactaagat tttctggtaa aaccttttagc agcttctggt 480
tggttggttc atatac

(2) INFORMATION FOR SEQ ID NO:1426:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..164
(D) OTHER INFORMATION: / Ceres Seq. ID 1569947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:

Asp Glu Ser Ser Leu Ala Ser Val Ala Leu Ser Val Trp Leu Asp Leu
1 5 10 15
Arg Leu Leu Thr Tyr His Met Asp Ser Asp Ile Val Ser Ser Val Asp
20 25 30
Arg Ser Gln Thr Ala Met Pro Asp Ala Leu Ala Phe Lys Ser Ile Asn
35 40 45
Asp Pro Ile Lys Asn Gln Ile Asn Ser Cys Ala Ala Ile Cys Val Lys
50 55 60
Gln Asp Asp Pro Cys His Phe Leu Arg Val Leu Tyr Glu Ser Leu Ile
65 70 75 80
Thr Gly Gly Leu Ala Gly Val Val Val Glu Ala Ala Leu Tyr Pro Ile
85 90 95
Asp Thr Ile Lys Thr Arg Val Gln Val Ala Arg Asp Gly Gly Lys Ile
100 105 110
Ile Trp Lys Gly Leu Tyr Ser Gly Leu Gly Ala Asn Leu Val Gly Val
115 120 125
Leu Pro Ala Ser Ala Leu Phe Phe Gly Val Tyr Glu Pro Thr Lys Gln
130 135 140
Lys Leu Ala Leu Arg Phe Ser Gly Lys Thr Phe Ser Ser Phe Cys Leu
145 150 155 160
Val Gly Ser Tyr

(2) INFORMATION FOR SEQ ID NO:1427:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1569948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:

Met Asp Ser Asp Ile Val Ser Ser Val Asp Arg Ser Gln Thr Ala Met
1 5 10 15
Pro Asp Ala Leu Ala Phe Lys Ser Ile Asn Asp Pro Ile Lys Asn Gln
20 25 30
Ile Asn Ser Cys Ala Ala Ile Cys Val Lys Gln Asp Asp Pro Cys His
35 40 45
Phe Leu Arg Val Leu Tyr Glu Ser Leu Ile Thr Gly Gly Leu Ala Gly
50 55 60
Val Val Val Glu Ala Ala Leu Tyr Pro Ile Asp Thr Ile Lys Thr Arg
65 70 75 80
Val Gln Val Ala Arg Asp Gly Gly Lys Ile Ile Trp Lys Gly Leu Tyr
85 90 95
Ser Gly Leu Gly Ala Asn Leu Val Gly Val Leu Pro Ala Ser Ala Leu
100 105 110
Phe Phe Gly Val Tyr Glu Pro Thr Lys Gln Lys Leu Ala Leu Arg Phe
115 120 125
Ser Gly Lys Thr Phe Ser Ser Phe Cys Leu Val Gly Ser Tyr
130 135 140

(2) INFORMATION FOR SEQ ID NO:1428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1569949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:

Met Pro Asp Ala Leu Ala Phe Lys Ser Ile Asn Asp Pro Ile Lys Asn
1 5 10 15
Gln Ile Asn Ser Cys Ala Ala Ile Cys Val Lys Gln Asp Asp Pro Cys
20 25 30
His Phe Leu Arg Val Leu Tyr Glu Ser Leu Ile Thr Gly Gly Leu Ala
35 40 45
Gly Val Val Val Glu Ala Ala Leu Tyr Pro Ile Asp Thr Ile Lys Thr
50 55 60
Arg Val Gln Val Ala Arg Asp Gly Gly Lys Ile Ile Trp Lys Gly Leu
65 70 75 80
Tyr Ser Gly Leu Gly Ala Asn Leu Val Gly Val Leu Pro Ala Ser Ala
85 90 95
Leu Phe Phe Gly Val Tyr Glu Pro Thr Lys Gln Lys Leu Ala Leu Arg
100 105 110
Phe Ser Gly Lys Thr Phe Ser Ser Phe Cys Leu Val Gly Ser Tyr
115 120 125

(2) INFORMATION FOR SEQ ID NO:1429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1368 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1368

(D) OTHER INFORMATION: / Ceres Seq. ID 1569950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:

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(1) SEQUENCE CHARACTERISTICS:

- ```

(17) (A) LENGTH: 397 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..397
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569951
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Ile | Leu | Asp | Thr | Gly | Ala | Arg | Phe | Ser | Ala | Val | Arg | Phe | Ser |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Pro | Val | Phe | Asn | Pro | Pro | Pro | Thr | Ser | Leu | Arg | Arg | Arg | Tyr | Phe | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Arg | Ala | Asn | Leu | Pro | Phe | Pro | Lys | His | Gln | Ala | Lys | Tyr | His | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Leu | Glu | Val | Ala | Ile | Asp | Ala | Val | Asp | Arg | Ala | Cys | Arg | Leu | Cys |
|     |     | 50  |     |     |     | 55  |     |     |     |     |     |     |     |     |     |
| Val | Asp | Val | Lys | Arg | Ser | Leu | Phe | Ser | Ser | Lys | Glu | Lys | Ile | Val | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Asn | Asp | Gln | Thr | Pro | Val | Thr | Ile | Ala | Asp | Phe | Gly | Val | Gln | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Val | Ser | Leu | Glu | Leu | Ser | Lys | Leu | Phe | Pro | Ser | Ile | Pro | Leu | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Glu | Glu | Asp | Ser | His | Phe | Val | Arg | Ala | Asn | Asn | Leu | Val | Ser | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Val | Ser | Glu | Val | Lys | Ser | Lys | Ala | Ser | Ile | Gly | Asp | Asn | His | Leu |
|     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Ser | Asp | Ala | Asp | Val | Leu | Glu | Ala | Ile | Asp | Arg | Gly | Gly | Lys | Asp | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Tyr | Thr | Phe | Cys | Asn | Lys | Pro | Ala | Thr | Tyr | Trp | Val | Leu | Asp | Pro | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asp | Gly | Thr | Arg | Gly | Phe | Leu | Lys | Gly | Asp | Glu | Ala | Leu | Tyr | Val | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Leu | Ala | Leu | Val | Val | Asp | Asn | Glu | Ile | Val | Leu | Gly | Val | Met | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

Cys Pro Asn Trp Pro Gly Asp Ser Ser Asp Gly Ser Thr Gly Thr Leu  
210 215 220  
Met Leu Ser His Ile Gly Cys Gly Thr Trp Thr Lys Lys Leu Gln Asn  
225 230 235 240  
Val Ser Gly Asn Val Ala Gly Asp Trp Ile Arg Cys Phe Val Asp Ala  
245 250 255  
Cys Val Leu Met Asn Lys Ala Arg Phe Cys Ile Gln Glu Ser Gln Thr  
260 265 270  
Trp Glu Ser Leu Pro Leu Ser Gly Phe Phe Asp Ala Ser Thr Val Ser  
275 280 285  
Glu Asp Leu Lys His Lys Glu Ile Leu Leu Leu Pro Thr Cys Cys Gly  
290 295 300  
Ser Leu Cys Lys Tyr Leu Met Val Ala Ser Gly Arg Ala Ser Val Phe  
305 310 315 320  
Leu Leu Arg Ala Lys Thr Gln Arg Thr Ile Lys Ser Trp Asp His Ala  
325 330 335  
Val Gly Ile Ile Cys Val His Glu Ala Gly Gly Lys Val Thr Asp Trp  
340 345 350  
Glu Gly Asp Glu Ile Asn Leu Glu Glu Asp Gln Ser Glu Arg Arg Leu  
355 360 365  
Ile Phe Pro Ala Gly Gly Val Val Val Ser Asn Gly Ser Leu His Asn  
370 375 380  
Gln Ile Leu Glu Met Ile Ser Ser Ala Ser Pro Thr Leu  
385 390 395

(2) INFORMATION FOR SEQ ID NO:1431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..976
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| acgtctgacg  | gaagtcggtt | cacttccacc | tgtgcgctgg  | ggatgttctg | tcgtcacagt | 60  |
| cggtcaagag  | atgtatgtaa | tgtgtggact | ccctagacata | agacgtttac | aggtaatgac | 120 |
| ttctatcgat  | tgcagaactc | acaaatttcc | ctcgtctccg  | agtatgaaaa | gaggtcggtt | 180 |
| caaacgagcc  | gccggagttg | tgcacggaaa | gatttacgta  | atcggaggtt | tcaggatgag | 240 |
| aaaaccggat  | gctgaatgga | ttgaagtgtt | tgatctaaag  | acacagattt | gggaatcttt | 300 |
| gccttggtccg | taccctaaaa | ctagttctgt | ttgcgagttg  | gacgcttatg | tgtgtatgga | 360 |
| agagaagtta  | tacatgtgtg | gttctaaatt | ttgttttggt  | tacgaaccac | aaagaaacgg | 420 |
| tgaatggGac  | gcacccgtcg | gagcaacccc | attaaaaaat  | ttgtgggaca | agactttgtt | 480 |
| tgtgtgatag  | gatatgttgt | atacagactg | tctctggcgt  | actcttggac | atccaaatag | 540 |
| cgtgtatcat  | ccaaaggaca | agacttggag | accttgtaaa  | ggtgaatcct | tggggagttt | 600 |
| gcctagtatt  | ttcttttcta | agtcctgaaa | tggcgaaatt  | tgttgggaaa | ttggtgattt | 660 |
| tgggcagaaa  | caagagctat | gttactgggt | attgcattgg  | agaaaaagtt | attttggtgc | 720 |
| taatgatcga  | gttggaaaaa | cgtgaaggag | gtgagatttg  | ggggaaggtt | gaatcactcg | 780 |
| actgtgtgtt  | tggatacata | gacattgtgt | cggttgggct  | ttgtcgatct | ctgaccattt | 840 |
| gatgatacat  | gggatgttat | cttgacagta | cggtgatgtg  | aatgagtatg | acttttttgt | 900 |
| tgtttatgcc  | ttttctttag | cctcaagact | tacttgttct  | tttcatgac  | ttattactac | 960 |
| acottaacct  | ttgtgc     |            |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..229  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:

Arg Leu Thr Glu Val Gly Ser Leu Pro Val Pro Trp Gly Cys Ser  
1 5 10 15  
Val Val Thr Val Gly Gln Glu Met Tyr Val Ile Gly Gly Leu Leu Asp  
20 25 30  
Ile Arg Arg Leu Gln Val Met Thr Leu Ile Asp Cys Arg Thr His Lys  
35 40 45  
Phe Arg Ser Leu Pro Ser Met Lys Arg Gly Arg Cys Lys Ala Ala Ala  
50 55 60  
Gly Val Val Asp Gly Lys Ile Tyr Val Ile Gly Gly Phe Arg Met Arg  
65 70 75 80  
Lys Pro Asp Ala Glu Trp Ile Glu Val Phe Asp Leu Lys Thr Gln Ile  
85 90 95  
Trp Glu Ser Leu Pro Gly Pro Tyr Pro Lys Thr Ser Ser Cys Cys Glu  
100 105 110  
Leu Asp Ala Tyr Val Val Met Glu Glu Lys Leu Tyr Met Leu Gly Ser  
115 120 125  
Lys Phe Cys Leu Val Tyr Glu Pro Lys Arg Asn Gly Glu Trp Asp Ala  
130 135 140  
Ser Val Gly Ala Thr Pro Leu Lys Asp Leu Trp Asp Lys Thr Cys Cys  
145 150 155 160  
Val Val Asp Asp Met Leu Tyr Thr Thr Asp Pro Arg Arg Thr Leu Gly  
165 170 175  
His Pro Ile Val Val Tyr His Pro Lys Asp Lys Thr Trp Arg Pro Val  
180 185 190  
Lys Gly Glu Ser Leu Gly Ser Leu Pro Ser Tyr Phe Phe Ser Lys Ser  
195 200 205  
Glu Asn Gly Glu Phe Trp Trp Lys Val Gly Asp Phe Gly Gln Lys Gln  
210 215 220  
Glu Leu Cys Tyr Trp  
225

(2) INFORMATION FOR SEQ ID NO:1433:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..206  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433:

Met Tyr Val Ile Gly Gly Leu Leu Asp Ile Arg Arg Leu Gln Val Met  
1 5 10 15  
Thr Leu Ile Asp Cys Arg Thr His Lys Phe Arg Ser Leu Pro Ser Met  
20 25 30  
Lys Arg Gly Arg Cys Lys Ala Ala Ala Gly Val Val Asp Gly Lys Ile  
35 40 45  
Tyr Val Ile Gly Gly Phe Arg Met Arg Lys Pro Asp Ala Glu Trp Ile  
50 55 60  
Glu Val Phe Asp Leu Lys Thr Gln Ile Trp Glu Ser Leu Pro Gly Pro  
65 70 75 80  
Tyr Pro Lys Thr Ser Ser Cys Cys Glu Leu Asp Ala Tyr Val Val Met  
85 90 95  
Glu Glu Lys Leu Tyr Met Leu Gly Ser Lys Phe Cys Leu Val Tyr Glu  
100 105 110  
Pro Lys Arg Asn Gly Glu Trp Asp Ala Ser Val Gly Ala Thr Pro Leu

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 115                                                             | 120 | 125 |
| Lys Asp Leu Trp Asp Lys Thr Cys Cys Val Val Asp Asp Met Leu Tyr |     |     |
| 130                                                             | 135 | 140 |
| Thr Thr Asp Pro Arg Arg Thr Leu Gly His Pro Ile Val Val Tyr His |     |     |
| 145                                                             | 150 | 155 |
| Pro Lys Asp Lys Thr Trp Arg Pro Val Lys Gly Glu Ser Leu Gly Ser |     |     |
| 165                                                             | 170 | 175 |
| Leu Pro Ser Tyr Phe Phe Ser Lys Ser Glu Asn Gly Glu Phe Trp Trp |     |     |
| 180                                                             | 185 | 190 |
| Lys Val Gly Asp Phe Gly Gln Lys Gln Glu Leu Cys Tyr Trp         |     |     |
| 195                                                             | 200 | 205 |

(2) INFORMATION FOR SEQ ID NO:1434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..191
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Thr Leu Ile Asp Cys Arg Thr His Lys Phe Arg Ser Leu Pro Ser |     |
| 1                                                               | 5   |
| Met Lys Arg Gly Arg Cys Lys Ala Ala Ala Gly Val Val Asp Gly Lys |     |
| 20                                                              | 25  |
| Ile Tyr Val Ile Gly Gly Phe Arg Met Arg Lys Pro Asp Ala Glu Trp |     |
| 35                                                              | 40  |
| Ile Glu Val Phe Asp Leu Lys Thr Gln Ile Trp Glu Ser Leu Pro Gly |     |
| 50                                                              | 55  |
| Pro Tyr Pro Lys Thr Ser Cys Cys Glu Leu Asp Ala Tyr Val Val     |     |
| 65                                                              | 70  |
| Met Glu Glu Lys Leu Tyr Met Leu Gly Ser Lys Phe Cys Leu Val Tyr |     |
| 85                                                              | 90  |
| Glu Pro Lys Arg Asn Gly Glu Trp Asp Ala Ser Val Gly Ala Thr Pro |     |
| 100                                                             | 105 |
| Leu Lys Asp Leu Trp Asp Lys Thr Cys Cys Val Val Asp Asp Met Leu |     |
| 115                                                             | 120 |
| Tyr Thr Thr Asp Pro Arg Arg Thr Leu Gly His Pro Ile Val Val Tyr |     |
| 130                                                             | 135 |
| His Pro Lys Asp Lys Thr Trp Arg Pro Val Lys Gly Glu Ser Leu Gly |     |
| 145                                                             | 150 |
| Ser Leu Pro Ser Tyr Phe Phe Ser Lys Ser Glu Asn Gly Glu Phe Trp |     |
| 165                                                             | 170 |
| Trp Lys Val Gly Asp Phe Gly Gln Lys Gln Glu Leu Cys Tyr Trp     |     |
| 180                                                             | 185 |
|                                                                 | 190 |

(2) INFORMATION FOR SEQ ID NO:1435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1663
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:

aagcaaaaat gctacaaatt aaaaagtgtc tccaacatgt gcatattcac acacaagttg  
gtgtcaacgc tcagacaaga aaggcgtgtg ttcattgttg aatcttccca ttctctcatc

60  
120

```

caaatccga cataactatc ctagccgcca ttgtttctcc acattacaaa accctcagca 180
gcttcaaaac tcttcgcgat tctccctcac gctcgcaatt ctctcgtctc ctttttaata 240
gtttttcttc tcggaactac aaactctcgg cttctgtgtc cttggcgtgt gtgtgtgtgt 300
ttgaatggct ctgtgtcagc ggattccaat tctctcctcc agtattcggg attggcaaca 360
agcggaggacc aatttgactc ctatttgttg tttaacattac aatactgcac ctctctcttc 420
ttcacccctt acagagaagc actctgtgga gagataccaa agggatcaat ggctgtacaa 480
agcgtgttaa ccaacgcgac catcgactcc atctccatcg ccatttgaag atgaagtctt 540
tgttaggaaa aacgacattg catcgagctt gacctgagct aagaagcttt tggcagtgct 600
gaaagagaag agagttaaag gatgcaaagg tgggtattgt ggaccaggag atgtgtatct 660
tgttgggaca gggccaggag atcctgagct ttgtactctt aaagctgtca gagtattca 720
aagtgccgat cttttgtctt acgacaggct tgtctccaat gatgtcttgg agttggtgtc 780
tctgtactgc agactcttt atgtcggcaa aactgctgtg tatcatagca gaactcaagg 840
agagattcat gaactactcc taaattttgc tgaagctgtg gccactgttg tcaggcttaa 900
aggtggagat cctctggtct ttggacgggg cggcgaaagaa atggactttc tgcaacagca 960
agggattcga gttcaagtta taccagggat aactgcggcg tcggggatag cagcagagtt 1020
ggggattcca ctaacacact gaggtgttgc aactagtgtg aggtttctca ctgtgcttc 1080
aaggaaagga gggacagacc ctctgtttgt tgcagagaaat gcagctgacc cggatataac 1140
actttgcgtt tataatgggt ttggaaacttt acctctctct gcacaaaaac taatggacca 1200
tggtctcctt tctgatacac cagctgttgc ggttgaacgt ggaaccactc ctctacagcg 1260
tacagttttt ctgtgataca aagattttgc aactgagatt cagtcagctg gattggtgtc 1320
accaacactc atcatcatag ggaaagtcgt tgagctctca cttttatggc cacattgcac 1380
gaaagaatcc tcttcgcttg tagagaccgg gtatgatatt cactcttatt ttacggggct 1440
gtggcttcca tcgacattac ggtgaagttt taggagctat ggagctatga aggttgagac 1500
ttgagagatg taataaacaa aaaggaaagc tgatagtttc ttatgacgtg tcttcaatt 1560
gttttgggac aatggtaatg gcaatgttaa tgtaataaac aagttAtcaa tcagtgccac 1620
tgtgactaat ttttccacca caagatgatg tctttaaaac ttt

```

(2) INFORMATION FOR SEQ ID NO:1436:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..369

(D) OTHER INFORMATION: / Ceres Seq. ID 1569987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:

```

Met Ala Leu Val Gln Arg Ile Pro Ile Ser Ser Ser Ile Arg Asn
1 5 10 15
Trp Gln Gln Ala Arg Thr Asn Leu Thr Pro Ile Cys Cys Leu His Tyr
20 25 30
Asn Thr Ala Ser Ser Ser Ser Pro Phe Thr Glu Lys His Ser Val
35 40 45
Glu Arg Tyr Gln Arg Asp Gln Trp Leu Tyr Lys Ala Val Glu Pro Thr
50 55 60
Pro Pro Ser Thr Pro Ser Pro Ser Pro Phe Glu Asp Glu Val Phe Val
65 70 75 80
Arg Glu Asn Asp Ile Ala Ser Gln Leu Pro Glu Leu Lys Lys Leu Leu
85 90 95
Ala Val Leu Lys Glu Lys Arg Val Lys Gly Cys Lys Gly Gly Asp Cys
100 105 110
Gly Pro Gly Asp Val Tyr Leu Val Gly Thr Gly Pro Gly Asp Pro Glu
115 120 125
Leu Leu Thr Leu Lys Ala Val Arg Val Ile Gln Ser Ala Asp Leu Leu
130 135 140
Leu Tyr Asp Arg Leu Val Ser Asn Asp Val Leu Glu Leu Val Ala Pro
145 150 155 160
Asp Ala Arg Leu Leu Tyr Val Gly Lys Thr Ala Gly Tyr His Ser Arg
165 170 175
Thr Gln Glu Glu Ile His Glu Leu Leu Asn Phe Ala Glu Ala Gly

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Thr | Val | Val | Arg | Leu | Lys | Gly | Gly | Asp | Pro | Leu | Val | Phe | Gly | Arg |
| 195 |     |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Gly | Glu | Glu | Met | Asp | Phe | Leu | Gln | Gln | Gln | Gly | Ile | Arg | Val | Gln |
| 210 |     |     |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Val | Ile | Pro | Gly | Ile | Thr | Ala | Ala | Ser | Gly | Ile | Ala | Ala | Glu | Leu | Gly |
| 225 |     |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Ile | Pro | Leu | Thr | His | Arg | Gly | Val | Ala | Thr | Ser | Val | Arg | Phe | Leu | Thr |
|     |     |     |     |     | 245 |     |     |     |     | 250 |     |     |     | 255 |     |
| Gly | His | Ser | Arg | Lys | Gly | Gly | Thr | Asp | Pro | Leu | Phe | Val | Ala | Glu | Asn |
|     |     |     |     |     | 260 |     |     |     |     | 265 |     |     |     | 270 |     |
| Ala | Ala | Asp | Pro | Asp | Thr | Thr | Leu | Val | Val | Tyr | Met | Gly | Leu | Gly | Thr |
|     |     |     |     |     | 275 |     |     |     |     | 280 |     |     |     | 285 |     |
| Leu | Pro | Ser | Leu | Ala | Gln | Lys | Leu | Met | Asp | His | Gly | Leu | Pro | Ser | Asp |
|     |     |     |     |     | 290 |     |     |     |     | 295 |     |     |     | 300 |     |
| Thr | Pro | Ala | Val | Ala | Val | Glu | Arg | Gly | Thr | Thr | Pro | Leu | Gln | Arg | Thr |
| 305 |     |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |
| Val | Phe | Ala | Glu | Leu | Lys | Asp | Phe | Ala | Thr | Glu | Ile | Gln | Ser | Ala | Gly |
|     |     |     |     |     | 325 |     |     |     |     | 330 |     |     |     | 335 |     |
| Leu | Val | Ser | Pro | Thr | Leu | Ile | Ile | Ile | Gly | Lys | Val | Val | Glu | Leu | Ser |
|     |     |     |     |     | 340 |     |     |     |     | 345 |     |     |     | 350 |     |
| Pro | Leu | Trp | Pro | His | Cys | Thr | Lys | Glu | Ser | Ser | Cys | Leu | Val | Glu | Thr |
|     |     |     |     |     | 355 |     |     |     |     | 360 |     |     |     | 365 |     |

(2) INFORMATION FOR SEQ ID NO:1437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1409
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:

|             |             |            |            |             |             |      |
|-------------|-------------|------------|------------|-------------|-------------|------|
| acgaatcaaa  | attcaattaa  | aaaaaacctt | togatctctc | tcatccaatc  | gaatcgaaaa  | 60   |
| tctttgttat  | tctttctctc  | taactctact | gcactcagaa | tctctctgta  | tagaaaaacc  | 120  |
| ctaaagttagt | tgtgatgttg  | cgagctttag | cacggcctct | cgaacgctgt  | ttgggaagca  | 180  |
| gagctagtgg  | tgatgttita  | ctctggcaat | cgaattgag  | acctcacgct  | ggcggtgatt  | 240  |
| attcgatcgc  | gggtgttcaa  | gccaatcca  | ggcttgaaga | tcagagtcag  | gttttcacat  | 300  |
| cttctctcgc  | tacttaacgc  | ggtgtatagc | atggtcatgg | tggacctgaa  | gctctagat   | 360  |
| tcgttaacag  | acatctcttt  | ccttatatgc | acaaatttgc | aagagacaat  | ggcggattat  | 420  |
| ctgtgatagt  | tatcaaaaag  | gcattcaaag | aaacagaaga | agagttttgt  | ggtagtggtta | 480  |
| aacgatccct  | tcccatgaaa  | cgcgaatagg | ctactgtag  | atctgtcgtg  | cttgttggtg  | 540  |
| caatctctaa  | tgacacactg  | tatgttgcga | atcttgggga | ctcgagagcc  | gttcttgtaa  | 600  |
| gcgttgtttc  | aggggttgat  | agtaataaag | gtgcctgagc | tgaacggtta  | tcactgac    | 660  |
| ataatgttgc  | tgttgaagaa  | gtgagaaagg | aggttaaggc | acttaaccct  | gatgactcac  | 720  |
| aaatcgtctt  | atacacacgt  | ggagtttggc | ggattaaagg | cattattcag  | gtatcgagat  | 780  |
| caattggggg  | tgtatatttg  | aaaaaacccg | agtattacag | ggaccocgat  | ttccagcgac  | 840  |
| atggaaatcc  | cattctcttg  | aggagaccgc | cgatgacagc | cgaacccctc  | attatagttaa | 900  |
| ggaagcttaa  | gccacagcag  | tgttttctga | tatttgcctc | agatggtctc  | tgggaacatc  | 960  |
| ttagtgatga  | aacgcgcgta  | gaatatcttc | tcaaaacacc | agaactggtg  | attgcacgaa  | 1020 |
| gacttgtaag  | agctgctctg  | gaagaagcgg | caaagaagag | agaatagaga  | tatggagata  | 1080 |
| taaaagaaat  | agccaaagga  | attcgcagac | attccatgat | cgcataaagc  | gttatgtgat  | 1140 |
| tttatctaga  | tcaaaaacaaa | accagttcat | cgaatagtaa | attggtgagta | caaggaggtta | 1200 |
| tcaccgcgtc  | accggatatt  | tactcattac | actctgatga | agcagagcaa  | cgacggtttac | 1260 |
| tcaatgtgtt  | atactgactg  | tgtgattatg | gtaaaaatgg | tgtctgggaa  | agatccgaat  | 1320 |
| agggagaaaa  | cttgtttaca  | tatttgttta | tttgttttct | tacgaagaac  | tgtttttttt  | 1380 |
| ttttttttca  | atattggagt  | tggatttggc |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..380

(D) OTHER INFORMATION: / Ceres Seq. ID 1570001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:

```
Met Leu Arg Ala Leu Ala Arg Pro Leu Glu Arg Cys Leu Gly Ser Arg
1 5 10
Ala Ser Gly Asp Gly Leu Leu Trp Gln Ser Glu Leu Arg Pro His Ala
20 25 30
Gly Gly Asp Tyr Ser Ile Ala Val Val Gln Ala Asn Ser Arg Leu Glu
35 40 45
Asp Gln Ser Gln Val Phe Thr Ser Ser Ala Thr Tyr Val Gly Val
50 55 60
Tyr Asp Gly His Gly Gly Pro Glu Ala Ser Arg Phe Val Asn Arg His
65 70 75 80
Leu Phe Pro Tyr Met His Lys Phe Ala Arg Glu His Gly Gly Leu Ser
85 90 95
Val Asp Val Ile Lys Lys Ala Phe Lys Glu Thr Glu Glu Glu Phe Cys
100 105 110
Gly Met Val Lys Arg Ser Leu Pro Met Lys Pro Gln Met Ala Thr Val
115 120 125
Gly Ser Cys Cys Leu Val Gly Ala Ile Ser Asn Asp Thr Leu Tyr Val
130 135 140
Ala Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Ser Val Val Ser Gly
145 150 155 160
Val Asp Ser Asn Lys Gly Ala Val Ala Glu Arg Leu Ser Thr Asp His
165 170 175
Asn Val Ala Val Glu Glu Val Arg Lys Glu Val Lys Ala Leu Asn Pro
180 185 190
Asp Asp Ser Gln Ile Val Leu Tyr Thr Arg Gly Val Trp Arg Ile Lys
195 200 205
Gly Ile Ile Gln Val Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys Lys
210 215 220
Pro Glu Tyr Tyr Arg Asp Pro Ile Phe Gln Arg His Gly Asn Pro Ile
225 230 235 240
Pro Leu Arg Arg Pro Ala Met Thr Ala Glu Pro Ser Ile Ile Val Arg
245 250 255
Lys Leu Lys Pro Gln Asp Leu Phe Leu Ile Phe Ala Ser Asp Gly Leu
260 265 270
Trp Glu His Leu Ser Asp Glu Thr Ala Val Glu Ile Val Leu Lys His
275 280 285
Pro Arg Thr Gly Ile Ala Arg Arg Leu Val Arg Ala Ala Leu Glu Glu
290 295 300
Ala Ala Lys Lys Arg Glu Met Arg Tyr Gly Asp Ile Lys Lys Ile Ala
305 310 315 320
Lys Gly Ile Arg Arg His Phe His Asp Asp Ile Ser Val Ile Val Val
325 330 335
Tyr Leu Asp Gln Asn Lys Thr Ser Ser Ser Asn Ser Lys Leu Val Lys
340 345 350
Gln Gly Gly Ile Thr Ala Pro Pro Asp Ile Tyr Ser Leu His Ser Asp
355 360 365
Glu Ala Glu Gln Arg Arg Leu Leu Asn Val Leu Tyr
370 375 380
```

(2) INFORMATION FOR SEQ ID NO:1439:



(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 296 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..296  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570002  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Lys | Phe | Ala | Arg | Glu | His | Gly | Gly | Leu | Ser | Val | Asp | Val | Ile |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Lys | Ala | Phe | Lys | Glu | Thr | Glu | Glu | Glu | Phe | Cys | Gly | Met | Val | Lys |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ser | Leu | Pro | Met | Lys | Pro | Gln | Met | Ala | Thr | Val | Gly | Ser | Cys | Cys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Val | Gly | Ala | Ile | Ser | Asn | Asp | Thr | Leu | Tyr | Val | Ala | Asn | Leu | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Ser | Arg | Ala | Val | Leu | Gly | Ser | Val | Val | Ser | Gly | Val | Asp | Ser | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Gly | Ala | Val | Ala | Glu | Arg | Leu | Ser | Thr | Asp | His | Asn | Val | Ala | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Glu | Glu | Val | Arg | Lys | Glu | Val | Lys | Ala | Leu | Asn | Pro | Asp | Asp | Ser | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Val | Leu | Tyr | Thr | Arg | Gly | Val | Trp | Arg | Ile | Lys | Gly | Ile | Ile | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Ser | Arg | Ser | Ile | Gly | Asp | Val | Tyr | Leu | Lys | Lys | Pro | Glu | Tyr | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Asp | Pro | Ile | Phe | Gln | Arg | His | Gly | Asn | Pro | Ile | Pro | Leu | Arg | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Pro | Ala | Met | Thr | Ala | Glu | Pro | Ser | Ile | Ile | Val | Arg | Lys | Leu | Lys | Pro |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | Asp | Leu | Phe | Leu | Ile | Phe | Ala | Ser | Asp | Gly | Leu | Trp | Glu | His | Leu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Asp | Glu | Thr | Ala | Val | Glu | Ile | Val | Leu | Lys | His | Pro | Arg | Thr | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Ala | Arg | Arg | Leu | Val | Arg | Ala | Ala | Leu | Glu | Glu | Ala | Ala | Lys | Lys |
|     | 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Arg | Glu | Met | Arg | Tyr | Gly | Asp | Ile | Lys | Lys | Ile | Ala | Lys | Gly | Ile | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Arg | His | Phe | His | Asp | Asp | Ile | Ser | Val | Ile | Val | Val | Tyr | Leu | Asp | Gln |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asn | Lys | Thr | Ser | Ser | Ser | Asn | Ser | Lys | Leu | Val | Lys | Gln | Gly | Gly | Ile |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Thr | Ala | Pro | Pro | Asp | Ile | Tyr | Ser | Leu | His | Ser | Asp | Glu | Ala | Glu | Gln |
|     |     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |
| Arg | Arg | Leu | Leu | Asn | Val | Leu | Tyr |     |     |     |     |     |     |     |     |
|     | 290 |     |     |     |     |     | 295 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1440:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 267 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..267  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1570003  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:

```

Met Val Lys Arg Ser Leu Pro Met Lys Pro Gln Met Ala Thr Val Gly
1 5 10 15
Ser Cys Cys Leu Val Gly Ala Ile Ser Asn Asp Thr Leu Tyr Val Ala
20 25 30
Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Ser Val Val Ser Gly Val
35 40 45
Asp Ser Asn Lys Gly Ala Val Ala Glu Arg Leu Ser Thr Asp His Asn
50 55 60
Val Ala Val Glu Glu Val Arg Lys Glu Val Lys Ala Leu Asn Pro Asp
65 70 75 80
Asp Ser Gln Ile Val Leu Tyr Thr Arg Gly Val Trp Arg Ile Lys Gly
85 90 95
Ile Ile Gln Val Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys Lys Pro
100 105 110
Glu Tyr Tyr Arg Asp Pro Ile Phe Gln Arg His Gly Asn Pro Ile Pro
115 120 125
Leu Arg Arg Pro Ala Met Thr Ala Glu Pro Ser Ile Ile Val Arg Lys
130 135 140
Leu Lys Pro Gln Asp Leu Phe Leu Ile Phe Ala Ser Asp Gly Leu Trp
145 150 155 160
Glu His Leu Ser Asp Glu Thr Ala Val Glu Ile Val Leu Lys His Pro
165 170 175
Arg Thr Gly Ile Ala Arg Arg Leu Val Arg Ala Ala Leu Glu Ala
180 185 190
Ala Lys Lys Arg Glu Met Arg Tyr Gly Asp Ile Lys Lys Ile Ala Lys
195 200 205
Gly Ile Arg Arg His Phe His Asp Asp Ile Ser Val Ile Val Val Tyr
210 215 220
Leu Asp Gln Asn Lys Thr Ser Ser Ser Asn Ser Lys Leu Val Lys Gln
225 230 235 240
Gly Gly Ile Thr Ala Pro Pro Asp Ile Tyr Ser Leu His Ser Asp Glu
245 250 255
Ala Glu Gln Arg Arg Leu Leu Asn Val Leu Tyr
260 265

```

(2) INFORMATION FOR SEQ ID NO:1441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1649 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1649
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441:

```

aattttctctt gaaaaccctt aaatctccgg atttcgattc ccgaggctcg aaaaaaccct 60
aaatctcttc tcggttcaact catccaacgc aagatgcgtg agattcttca catccagggt 120
ggtcgaatgcg gtaaccagat cgggcgaacg ttctgggaag tggtttgcgc cgagcagcgc 180
atcgatccaa ccggaaggtg caccggagac tcagatctgc aacttgagcg catcaacggt 240
tactacaagt aagcgaggtg cggtagattc gttcctcgtg cagtgcctat ggatttgagg 300
ctcggggaact tggatagctc cagatctgga cgtacgggtc agacctttcg acctgataac 360
ttcgtctttg gccaatccgg tgctggttaac aactgggcca agggacacta caccgaagga 420
gtcgaaactaa tgcattccgt tctcgtattg gttcgttaagg aagctgGaga actgtgactg 480
ttccaagggt ttccagggtt gtcactcgtt gggaggagga actggatctg gtatgggaac 540
attgttgatc tetaagatcc gtgaagagta cccagatcgc atgatgctta cttctccggt 600
gttcctctca ccaaagggtt ctgatactgt ggttgagcct tacaacgcta cctctgtctgt 660
ccatcagctt gttgagaatg ctgatgagtg catggttctt gataatgagg ccttgtacga 720
tatttgcttc aggactctca aactcactac cccacgcttt ggtgatttga accacttgat 780
ttctgctact atgtctggtg tgacttgctg tctgaggttc cctggccaac tcaactctga 840
ctcccgaaag ctgtcgtgtg atctcatccc attccccggt cttcacttct tcatgggtgg 900

```

2025 RELEASE UNDER E.O. 14176

|            |            |            |            |             |             |      |
|------------|------------|------------|------------|-------------|-------------|------|
| ttttgctcct | ctcacctcaa | gaggttctca | gcagtagcgt | tcctctacag  | tccttgagct  | 960  |
| caccagcaca | atgtgggact | ccaagaacat | gatgtgtgct | gcagacccaa  | ggcagcgagc  | 1020 |
| ctacctcaca | gocctctgcc | tggtccgtgg | caagatgagc | acaaaggaag  | ttgacagaga  | 1080 |
| gatgctgaat | gtgcagaaac | agaactcgct | ctactttgtg | gagtgagatcc | ccaacaacgt  | 1140 |
| gaatcgaca  | gtctgtgaca | tcccacctac | tggtctgaag | atggcatcaa  | ctttctattgg | 1200 |
| aaactcaaca | tcaatccaag | agatgttcag | gcgagtgagt | gagcagttca  | cagctatgtt  | 1260 |
| caggagaaag | gottttcttg | attggtacac | agtgaggaga | atggacagaga | tggaaatcac  | 1320 |
| agaagcggag | agcaacatga | acgatcttgt | gtcagagtac | cagcaatacc  | aagatgcaac  | 1380 |
| tgccgatgaa | gaaggtgact | acgaggatga | ggaagaaggt | gaatatcaac  | aggaggaaga  | 1440 |
| gtactgagaa | taattttagt | ataactgctt | taaaaacaaa | aacaatttag  | tcgtttgcta  | 1500 |
| cttttctttt | ttttaaaagg | aacacctcaa | ctaccagttg | tagttttttt  | ctctgcttgt  | 1560 |
| atttgacata | tctggttgat | gtttctgtac | ttttgttctt | aatcttgta   | ttgcctgtga  | 1620 |
| gttttctatt | aatattttcc | agttgtact  |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..333

- (D) OTHER INFORMATION: / Ceres Seq. ID 1570005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Phe | Val | Arg | Lys | Leu | Glu | Asn | Cys | Asp | Cys | Leu | Gln | Gly | Phe |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Val | Cys | His | Ser | Leu | Gly | Gly | Gly | Thr | Gly | Ser | Gly | Met | Gly | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Leu | Ile | Ser | Lys | Ile | Arg | Glu | Glu | Tyr | Pro | Asp | Arg | Met | Met | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Phe | Ser | Val | Phe | Pro | Ser | Pro | Lys | Val | Ser | Asp | Thr | Val | Val | Glu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Pro | Tyr | Asn | Ala | Thr | Leu | Ser | Val | His | Gln | Leu | Val | Glu | Asn | Ala | Asp |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Glu | Cys | Met | Val | Leu | Asp | Asn | Glu | Ala | Leu | Tyr | Asp | Ile | Cys | Phe | Arg |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Leu | Lys | Leu | Thr | Thr | Pro | Ser | Phe | Gly | Asp | Leu | Asn | His | Leu | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Ala | Thr | Met | Ser | Gly | Val | Thr | Cys | Cys | Leu | Arg | Phe | Pro | Gly | Gln |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Asn | Ser | Asp | Leu | Arg | Lys | Leu | Ala | Val | Asn | Leu | Ile | Pro | Phe | Pro |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Arg | Leu | His | Phe | Phe | Met | Val | Gly | Phe | Ala | Pro | Leu | Thr | Ser | Arg | Gly |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     | 160 |     |
| Ser | Gln | Gln | Tyr | Arg | Ser | Leu | Thr | Val | Pro | Glu | Leu | Thr | Gln | Gln | Met |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Trp | Asp | Ser | Lys | Asn | Met | Met | Cys | Ala | Ala | Asp | Pro | Arg | His | Gly | Arg |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Tyr | Leu | Thr | Ala | Ser | Ala | Met | Phe | Arg | Gly | Lys | Met | Ser | Thr | Lys | Glu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Asp | Glu | Gln | Met | Leu | Asn | Val | Gln | Asn | Lys | Asn | Ser | Ser | Tyr | Phe |
|     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Val | Glu | Trp | Ile | Pro | Asn | Asn | Val | Lys | Ser | Thr | Val | Cys | Asp | Ile | Pro |
|     |     |     | 225 |     |     |     | 230 |     |     |     | 235 |     |     | 240 |     |
| Pro | Thr | Gly | Leu | Lys | Met | Ala | Ser | Thr | Phe | Ile | Gly | Asn | Ser | Thr | Ser |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ile | Gln | Glu | Met | Phe | Arg | Arg | Val | Ser | Glu | Gln | Phe | Thr | Ala | Met | Phe |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Arg | Arg | Lys | Ala | Phe | Leu | His | Trp | Tyr | Thr | Gly | Glu | Gly | Met | Asp | Glu |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

Met Glu Phe Thr Glu Ala Glu Ser Asn Met Asn Asp Leu Val Ser Glu  
290 295 300  
Tyr Gln Gln Tyr Gln Asp Ala Thr Ala Asp Glu Gly Asp Tyr Glu  
305 310 315 320  
Asp Glu Glu Glu Gly Glu Tyr Gln Gln Glu Glu Tyr  
325 330

(2) INFORMATION FOR SEQ ID NO:1443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..304

(D) OTHER INFORMATION: / Ceres Seq. ID 1570006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443:

Met Gly Thr Leu Leu Ile Ser Lys Ile Arg Glu Glu Tyr Pro Asp Arg  
1 5 10 15  
Met Met Leu Thr Phe Ser Val Phe Pro Ser Pro Lys Val Ser Asp Thr  
20 25 30  
Val Val Glu Pro Tyr Asn Ala Thr Leu Ser Val His Gln Leu Val Glu  
35 40 45  
Asn Ala Asp Glu Cys Met Val Leu Asp Asn Glu Ala Leu Tyr Asp Ile  
50 55 60  
Cys Phe Arg Thr Leu Lys Leu Thr Thr Pro Ser Phe Gly Asp Leu Asn  
65 70 75 80  
His Leu Ile Ser Ala Thr Met Ser Gly Val Thr Cys Cys Leu Arg Phe  
85 90 95  
Pro Gly Gln Leu Asn Ser Asp Leu Arg Lys Leu Ala Val Asn Leu Ile  
100 105 110  
Pro Phe Pro Arg Leu His Phe Phe Met Val Gly Phe Ala Pro Leu Thr  
115 120 125  
Ser Arg Gly Ser Gln Gln Tyr Arg Ser Leu Thr Val Pro Glu Leu Thr  
130 135 140  
Gln Gln Met Trp Asp Ser Lys Asn Met Met Cys Ala Ala Asp Pro Arg  
145 150 155 160  
His Gly Arg Tyr Leu Thr Ala Ser Ala Met Phe Arg Gly Lys Met Ser  
165 170 175  
Thr Lys Glu Val Asp Glu Gln Met Leu Asn Val Gln Asn Lys Asn Ser  
180 185 190  
Ser Tyr Phe Val Glu Trp Ile Pro Asn Asn Val Lys Ser Thr Val Cys  
195 200 205  
Asp Ile Pro Pro Thr Gly Leu Lys Met Ala Ser Thr Phe Ile Gly Asn  
210 215 220  
Ser Thr Ser Ile Gln Glu Met Phe Arg Arg Val Ser Glu Gln Phe Thr  
225 230 235 240  
Ala Met Phe Arg Arg Lys Ala Phe Leu His Trp Tyr Thr Gly Glu Gly  
245 250 255  
Met Asp Glu Met Glu Phe Thr Glu Ala Glu Ser Asn Met Asn Asp Leu  
260 265 270  
Val Ser Glu Tyr Gln Gln Tyr Gln Asp Ala Thr Ala Asp Glu Glu Gly  
275 280 285  
Asp Tyr Glu Asp Glu Glu Glu Gly Glu Tyr Gln Gln Glu Glu Glu Tyr  
290 295 300

(2) INFORMATION FOR SEQ ID NO:1444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..288  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570007  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Leu | Thr | Phe | Ser | Val | Phe | Pro | Ser | Pro | Lys | Val | Ser | Asp | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Val | Glu | Pro | Tyr | Asn | Ala | Thr | Leu | Ser | Val | His | Gln | Leu | Val | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Ala | Asp | Glu | Cys | Met | Val | Leu | Asp | Asn | Glu | Ala | Leu | Tyr | Asp | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Phe | Arg | Thr | Leu | Lys | Leu | Thr | Thr | Pro | Ser | Phe | Gly | Asp | Leu | Asn |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His | Leu | Ile | Ser | Ala | Thr | Met | Ser | Gly | Val | Thr | Cys | Cys | Leu | Arg | Phe |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Pro | Gly | Gln | Leu | Asn | Ser | Asp | Leu | Arg | Lys | Leu | Ala | Val | Asn | Leu | Ile |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Pro | Phe | Pro | Arg | Leu | His | Phe | Phe | Met | Val | Gly | Phe | Ala | Pro | Leu | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Arg | Gly | Ser | Gln | Gln | Tyr | Arg | Ser | Leu | Thr | Val | Pro | Glu | Leu | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Gln | Met | Trp | Asp | Ser | Lys | Asn | Met | Met | Cys | Ala | Ala | Asp | Pro | Arg |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| His | Gly | Arg | Tyr | Leu | Thr | Ala | Ser | Ala | Met | Phe | Arg | Gly | Lys | Met | Ser |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Thr | Lys | Glu | Val | Asp | Glu | Gln | Met | Leu | Asn | Val | Gln | Asn | Lys | Asn | Ser |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ser | Tyr | Phe | Val | Glu | Trp | Ile | Pro | Asn | Asn | Val | Lys | Ser | Thr | Val | Cys |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Asp | Ile | Pro | Pro | Thr | Gly | Leu | Lys | Met | Ala | Ser | Thr | Phe | Ile | Gly | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Thr | Ser | Ile | Gln | Glu | Met | Phe | Arg | Arg | Val | Ser | Glu | Gln | Phe | Thr |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Met | Phe | Arg | Arg | Lys | Ala | Phe | Leu | His | Trp | Tyr | Thr | Gly | Glu | Gly |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Met | Asp | Glu | Met | Glu | Phe | Thr | Glu | Ala | Glu | Ser | Asn | Met | Asn | Asp | Leu |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Val | Ser | Glu | Tyr | Gln | Gln | Tyr | Gln | Asp | Ala | Thr | Ala | Asp | Glu | Glu | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | Tyr | Glu | Asp | Glu | Glu | Glu | Gly | Glu | Tyr | Gln | Gln | Glu | Glu | Glu | Tyr |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1445:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 503 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..503  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:

attttttttt gaacagaaMH atcTCagaaa gatcaatcta gagagaccaa aaagagatcg  
gaagagatgg cttctacctc cgcgatgtca ttggtcacac cacttaacca gaccggttcg

60  
120

tctctcttcc tcaagccatt acctctgaaa ccattccaagg ctttgggtgc aactggaggc 180  
agagcacaga ggcttcaagt taaggccctc aagatggaca aggcctttgac cggtatctcc 240  
gcggctgctc ttactgtctc gatggtgatt ccggagatag ctgaagctgc tggttctgga 300  
atctctcctt cctccaagaa tttcttgctc agcattgctt ctggtggcct cgtctcact 360  
gtcatcattg gtgtcgtcgt cggtgtctcc aactttgacc ctgtcaagag aacctaagac 420  
ctataatct ttcttacatc attattgtaa tctgttctcc ttctgtgat togtttcaat 480  
gttgcaagaa tgaacttttg gat

(2) INFORMATION FOR SEQ ID NO:1446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:

Ile Xaa Phe Arg Asn Arg Xaa Ser Gln Lys Asp Gln Ser Arg Glu Thr  
1 5 10 15  
Lys Lys Arg Ser Glu Glu Met Ala Ser Thr Ser Ala Met Ser Leu Val  
20 25 30  
Thr Pro Leu Asn Gln Thr Arg Ser Ser Pro Phe Leu Lys Pro Leu Pro  
35 40 45  
Leu Lys Pro Ser Lys Ala Leu Val Ala Thr Gly Gly Arg Ala Gln Arg  
50 55 60  
Leu Gln Val Lys Ala Leu Lys Met Asp Lys Ala Leu Thr Gly Ile Ser  
65 70 75 80  
Ala Ala Ala Leu Thr Ala Ser Met Val Ile Pro Glu Ile Ala Glu Ala  
85 90 95  
Ala Gly Ser Gly Ile Ser Pro Ser Leu Lys Asn Phe Leu Leu Ser Ile  
100 105 110  
Ala Ser Gly Gly Leu Val Leu Thr Val Ile Ile Gly Val Val Val Gly  
115 120 125  
Val Ser Asn Phe Asp Pro Val Lys Arg Thr  
130 135

(2) INFORMATION FOR SEQ ID NO:1447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:

Met Ala Ser Thr Ser Ala Met Ser Leu Val Thr Pro Leu Asn Gln Thr  
1 5 10 15  
Arg Ser Ser Pro Phe Leu Lys Pro Leu Pro Leu Lys Pro Ser Lys Ala  
20 25 30  
Leu Val Ala Thr Gly Gly Arg Ala Gln Arg Leu Gln Val Lys Ala Leu  
35 40 45  
Lys Met Asp Lys Ala Leu Thr Gly Ile Ser Ala Ala Leu Thr Ala  
50 55 60  
Ser Met Val Ile Pro Glu Ile Ala Glu Ala Ala Gly Ser Gly Ile Ser  
65 70 75 80  
Pro Ser Leu Lys Asn Phe Leu Leu Ser Ile Ala Ser Gly Gly Leu Val  
85 90 95

Leu Thr Val Ile Ile Gly Val Val Val Gly Val Ser Asn Phe Asp Pro  
100 105 110  
Val Lys Arg Thr  
115

(2) INFORMATION FOR SEQ ID NO:1448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1570011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | Val | Thr | Pro | Leu | Asn | Gln | Thr | Arg | Ser | Ser | Pro | Phe | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Lys | Pro | Leu | Pro | Leu | Lys | Pro | Ser | Lys | Ala | Leu | Val | Ala | Thr | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ala | Gln | Arg | Leu | Gln | Val | Lys | Ala | Leu | Lys | Met | Asp | Lys | Ala | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Gly | Ile | Ser | Ala | Ala | Ala | Leu | Thr | Ala | Ser | Met | Val | Ile | Pro | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Ala | Glu | Ala | Ala | Gly | Ser | Gly | Ile | Ser | Pro | Ser | Leu | Lys | Asn | Phe |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Leu | Ser | Ile | Ala | Ser | Gly | Gly | Leu | Val | Leu | Thr | Val | Ile | Ile | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Val | Val | Val | Gly | Val | Ser | Asn | Phe | Asp | Pro | Val | Lys | Arg | Thr |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:1449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..691

(D) OTHER INFORMATION: / Ceres Seq. ID 1570036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:

|             |            |            |             |             |             |     |
|-------------|------------|------------|-------------|-------------|-------------|-----|
| aaccttattc  | tattgattaa | aattgttcgg | tctcgattat  | ctctgtgttt  | ttgggaactg  | 60  |
| agaagcatcc  | actcgacaat | ggagactcgc | atttgttgga  | gatttagctct | cgcaccatcc  | 120 |
| tctctcttca  | attctaaatc | aggggacaaa | catttagtct  | caaaaggacc  | atgtgtgaaat | 180 |
| cgtagcattc  | tcattgacct | gtctacatct | gctgcattgg  | gtaaaaggagg | tgtgtgtctta | 240 |
| gcacaaacaa  | ttatagagaa | aaccactcct | ggctgtgaaat | ccgagtttga  | tttaaggaaa  | 300 |
| tcaaaagaaga | tagctccacc | ttacagggtg | atactacaca  | atgacaactt  | caacaagagg  | 360 |
| gaatatgtgg  | ttcaggtggt | gatgaaggta | atacccccatg | actgtagaca  | acgcgggttaa | 420 |
| cattatgcaa  | gaagctcata | tcaacggttt | ggcagtttgt  | attgttttgt  | ctcaggctga  | 480 |
| tcgacagcaa  | cactgtatgc | agctgcgcgg | taacggcctt  | ctcagttctg  | ttgaacctga  | 540 |
| tgggtggagg  | tgctgaaact | aattaaactc | agtatagatt  | ttcccacctt  | ccaggactct  | 600 |
| ctatttagtc  | aaaaacatGt | tgttgtttta | atgtatatata | tatcagaaat  | ttggtacaag  | 660 |
| actgttacta  | tatgcaatga | acctgtcccc | c           |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..113  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450:

```
Met Glu Thr Ala Ile Cys Gly Arg Leu Ala Leu Ala Pro Ser Ser Leu
1 5 10 15
Phe Asn Ser Lys Ser Gly Asp Lys His Leu Val Ser Lys Gly Pro Cys
20 25 30
Val Asn Arg Ser Ile Leu Met Thr Leu Ser Thr Ser Ala Ala Leu Gly
35 40 45
Lys Gly Gly Gly Val Leu Asp Lys Pro Ile Ile Glu Lys Thr Thr Pro
50 55 60
Gly Arg Glu Ser Glu Phe Asp Leu Arg Lys Ser Lys Lys Ile Ala Pro
65 70 75 80
Pro Tyr Arg Val Ile Leu His Asn Asp Asn Phe Asn Lys Arg Glu Tyr
85 90 95
Val Val Gln Val Leu Met Lys Val Ile Pro His Asp Cys Arg Gln Arg
100 105 110
Gly
```

(2) INFORMATION FOR SEQ ID NO:1451:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 75 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..75  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451:

```
Met Thr Leu Ser Thr Ser Ala Ala Leu Gly Lys Gly Gly Gly Val Leu
1 5 10 15
Asp Lys Pro Ile Ile Glu Lys Thr Thr Pro Gly Arg Glu Ser Glu Phe
20 25 30
Asp Leu Arg Lys Ser Lys Lys Ile Ala Pro Pro Tyr Arg Val Ile Leu
35 40 45
His Asn Asp Asn Phe Asn Lys Arg Glu Tyr Val Val Gln Val Leu Met
50 55 60
Lys Val Ile Pro His Asp Cys Arg Gln Arg Gly
65 70 75
```

(2) INFORMATION FOR SEQ ID NO:1452:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 664 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..664  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452:

```
aacggccgat ttattaaaaa aaaactccga caaatgattc gccggccgat ctacgacttc 60
gcgcgcgttt ttgcgcactt aacttctccg ttatcgacat cctcggttt ttgtttctat 120
ttctcatctg aaacatgaagc tcgaaaaccg attgtctcga accctaatac cccaatcggtg 180
ttctcgactc ggggttcaaaa gctcatagct tcgcaatcgt atcctctcct cgccaaggag 240
attttcgatt atgctttcca acagcccaat ttccgccttt ctcatcttc tcatcctaac 300
ctcatttcca aactcggcgc tggtagatat ttcaatctta tcgacgacgt tctcgccaaa 360
```



cacagatcaa gtggttatcc attaacctga gaaattttca cttatctgat caaagtctac 420  
gcagaagcaa agttaccgga gaaagtctta agtacgtttt acaaaatgct ggagtccaat 480  
ttcaagccgc agccaaaaca tctgaatcgg attctagatg ttctcgtaag ccatagaggt 540  
tatctccaga aagctttttga gcttttcaag agtttcacgac ttcatggagt aatgcctaac 600  
acgagaaggt acaattttatt gatgcaagct ttttgtttga atgatgattt gaggatttga 660  
tacc

(2) INFORMATION FOR SEQ ID NO:1453:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1570040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Gly | Arg | Phe | Ile | Lys | Lys | Lys | Leu | Arg | Gln | Met | Ile | Arg | Arg | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Tyr | Asp | Phe | Ala | Ala | Val | Phe | Arg | His | Leu | Thr | Ser | Pro | Leu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ser | Ser | Arg | Phe | Leu | Phe | Tyr | Ser | Ser | Ser | Glu | His | Glu | Ala | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Pro | Ile | Val | Ser | Asn | Pro | Lys | Ser | Pro | Ile | Gly | Ser | Pro | Thr | Arg |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Val | Gln | Lys | Leu | Ile | Ala | Ser | Gln | Ser | Asp | Pro | Leu | Leu | Ala | Lys | Glu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Phe | Asp | Tyr | Ala | Ser | Gln | Gln | Pro | Asn | Phe | Arg | His | Ser | Arg | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Ser | His | Leu | Ile | Leu | Ile | Leu | Lys | Leu | Gly | Arg | Gly | Arg | Tyr | Phe | Asn |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Leu | Ile | Asp | Asp | Val | Leu | Ala | Lys | His | Arg | Ser | Ser | Gly | Tyr | Pro | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1454:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1570041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Arg | Arg | Pro | Ile | Tyr | Asp | Phe | Ala | Ala | Val | Phe | Arg | His | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Ser | Pro | Leu | Ser | Thr | Ser | Ser | Arg | Phe | Leu | Phe | Tyr | Ser | Ser | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | His | Glu | Ala | Arg | Lys | Pro | Ile | Val | Ser | Asn | Pro | Lys | Ser | Pro | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Ser | Pro | Thr | Arg | Val | Gln | Lys | Leu | Ile | Ala | Ser | Gln | Ser | Asp | Pro |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Leu | Leu | Ala | Lys | Glu | Ile | Phe | Asp | Tyr | Ala | Ser | Gln | Gln | Pro | Asn | Phe |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | His | Ser | Arg | Ser | Ser | His | Leu | Ile | Leu | Ile | Leu | Lys | Leu | Gly | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Gly | Arg | Tyr | Phe | Asn | Leu | Ile | Asp | Asp | Val | Leu | Ala | Lys | His | Arg | Ser |

100 105 110  
Ser Gly Tyr Pro Leu Thr  
115

(2) INFORMATION FOR SEQ ID NO:1455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Glu | Phe | Asn | Phe | Thr | Pro | Gln | Pro | Lys | His | Leu | Asn | Arg | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Leu | Asp | Val | Leu | Val | Ser | His | Arg | Gly | Tyr | Leu | Gln | Lys | Ala | Phe | Glu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Phe | Lys | Ser | Ser | Arg | Leu | His | Gly | Val | Met | Pro | Asn | Thr | Arg | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Asn | Leu | Leu | Met | Gln | Ala | Phe | Cys | Leu | Asn | Asp | Asp | Leu | Ser | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Tyr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..509
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| acatctccca | agatcatttg  | tcggttgatt | ccatacgate | tccaagtctt | gtcgttcgac | 60  |
| aatctctaag | aagctaacga  | aaatggctct | tcaaaacgat | attgatctgc | ttaaccctcc | 120 |
| tgctgagctc | gagaagagga  | agcacaagct | caagcgctct | gttcaatcac | ccaattcggt | 180 |
| tttcattgat | gtcaaagtgc  | aagcgtgctt | taacattacg | actgtgttca | gccactctca | 240 |
| gaccgtttgt | atgtgtggaa  | actgccagac | tttgctctgc | acacccacag | gagggaaggg | 300 |
| aaagctcact | gaaggatgct  | ctttcaggaa | aaagtgaagc | tgaagaagaa | gatatgactc | 360 |
| cattccattc | actcaccacc  | aaattttctt | ttcgtttatt | atgaattttt | gttgatattt | 420 |
| gagctagtag | taacccctct  | ttgtcgataa | tcctttgttt | taatacgcga | agCtcgttcc | 480 |
| tcctttatga | atgggttatgt | attttcttg  |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Leu | Gln | Asn | Asp | Ile | Asp | Leu | Leu | Asn | Pro | Pro | Ala | Glu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Glu | Lys | Arg | Lys | His | Lys | Leu | Lys | Arg | Leu | Val | Gln | Ser | Pro | Asn | Ser |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
|     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |     |  |  |  |  |
| Phe | Phe | Met | Asp | Val | Lys | Cys | Gln | Gly | Cys | Phe | Asn | Ile | Thr | Thr | Val |  |  |  |  |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |  |  |
| Phe | Ser | His | Ser | Gln | Thr | Val | Val | Met | Cys | Gly | Asn | Cys | Gln | Thr | Leu |  |  |  |  |
|     | 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |  |  |  |
| Leu | Cys | Thr | Pro | Thr | Gly | Gly | Lys | Ala | Lys | Leu | Thr | Glu | Gly | Cys | Ser |  |  |  |  |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |  |  |  |
| Phe | Arg | Lys | Lys |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:1458:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..50  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Met | Asp | Val | Lys | Cys | Gln | Gly | Cys | Phe | Asn | Ile | Thr | Thr | Val | Phe | Ser |  |  |  |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |  |  |
| His | Ser | Gln | Thr | Val | Val | Met | Cys | Gly | Asn | Cys | Gln | Thr | Leu | Leu | Cys |  |  |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |  |  |
| Thr | Pro | Thr | Gly | Gly | Lys | Ala | Lys | Leu | Thr | Glu | Gly | Cys | Ser | Phe | Arg |  |  |  |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |  |  |  |  |
| Lys | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|     | 50  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:1459:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 931 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..931  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459:

|            |             |             |             |            |             |     |
|------------|-------------|-------------|-------------|------------|-------------|-----|
| aaaaattctc | tgccggtgtt  | gacttcaaac  | tctcttgat   | tagatcggcg | ccaacttcta  | 60  |
| aacgcaaatg | ggaatcacga  | gaaacttgat  | cctgggtttg  | gcttgtttag | cctttgtctc  | 120 |
| cattgctaaa | gctctgcctc  | atgaaccaga  | acttggctcg  | gctcgtgtcg | tcttccagac  | 180 |
| tagttatgga | gatatcgaat  | ttgggttcta  | tcccactgtg  | gcacccaaga | cagtggatca  | 240 |
| catcttcaag | cttgttcggt  | taggaggata  | caacactaat  | cattttctca | gggttgataa  | 300 |
| aggttttgtt | gctcaagttg  | cggatgtggc  | gagtggaaga  | tcagctccaa | tgaatgagga  | 360 |
| gcaaaaggaa | gaagctgaga  | agaaaaattg  | gggagagttc  | agtgatgtta | agcatgtcag  | 420 |
| aggtactcTt | tccatgggaa  | gatatgacga  | tccaaacagt  | gcacaaactt | cattttcgat  | 480 |
| gcttcttgcc | aatgctctct  | atcttgatcg  | ccagtatgct  | gtgtttggta | aagtacttaa  | 540 |
| aggagatgaa | acattgagta  | agctagaaga  | agttcccact  | cgccgcgag  | ggatttttgt  | 600 |
| tatgcgcagc | gagcggatca  | cgattttgtc  | gacatactat  | tacgacacta | aaatggagag  | 660 |
| ctgtgaagaa | gagagatctg  | tcctgaaaag  | aaggcttcaa  | gcactctttg | tggagggtcga | 720 |
| aagacagaga | atgaaagtct  | tcctcgtgaat | gaagtttaaca | cataagaaca | tggttcaacaa | 780 |
| aagcctttaa | acgcccaggga | acacaaaggt  | aaatgtatgt  | ctagtaaaaa | aactcagaat  | 840 |
| gctagacagt | ttttgagtg   | tttatcagtg  | tgagagattg  | tagttaacag | tgtaaacagt  | 900 |
| ttgagacatt | gaatcatgga  | ttgttctctc  | c           |            |             |     |

(2) INFORMATION FOR SEQ ID NO:1460:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 226 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..226  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570070  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:  
Met Gly Ile Thr Arg Asn Leu Ile Leu Gly Leu Ala Cys Leu Ala Phe  
1 5 10 15  
Val Ser Ile Ala Lys Ala Leu Pro His Glu Pro Glu Leu Gly Ser Ala  
20 25 30  
Arg Val Val Phe Gln Thr Ser Tyr Gly Asp Ile Glu Phe Gly Phe Tyr  
35 40 45  
Pro Thr Val Ala Pro Lys Thr Val Asp His Ile Phe Lys Leu Val Arg  
50 55 60  
Leu Gly Gly Tyr Asn Thr Asn His Phe Phe Arg Val Asp Lys Gly Phe  
65 70 75 80  
Val Ala Gln Val Ala Asp Val Ala Ser Gly Arg Ser Ala Pro Met Asn  
85 90 95  
Glu Glu Gln Arg Lys Glu Ala Glu Lys Lys Ile Val Gly Glu Phe Ser  
100 105 110  
Asp Val Lys His Val Arg Gly Thr Leu Ser Met Gly Arg Tyr Asp Asp  
115 120 125  
Pro Asn Ser Ala Gln Ser Ser Phe Ser Met Leu Leu Gly Asn Ala Pro  
130 135 140  
His Leu Asp Arg Gln Tyr Ala Val Phe Gly Lys Val Thr Lys Gly Asp  
145 150 155 160  
Glu Thr Leu Ser Lys Leu Glu Glu Val Pro Thr Arg Arg Glu Gly Ile  
165 170 175  
Phe Val Met Pro Thr Glu Arg Ile Thr Ile Leu Ser Thr Tyr Tyr Tyr  
180 185 190  
Asp Thr Lys Met Glu Ser Cys Glu Glu Glu Arg Ser Val Leu Lys Arg  
195 200 205  
Arg Leu Gln Ala Ser Phe Val Glu Val Glu Arg Gln Arg Met Lys Cys  
210 215 220  
Phe Pro  
225

(2) INFORMATION FOR SEQ ID NO:1461:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 132 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..132  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461:  
Met Asn Glu Glu Gln Arg Lys Glu Ala Glu Lys Lys Ile Val Gly Glu  
1 5 10 15  
Phe Ser Asp Val Lys His Val Arg Gly Thr Leu Ser Met Gly Arg Tyr  
20 25 30  
Asp Asp Pro Asn Ser Ala Gln Ser Ser Phe Ser Met Leu Leu Gly Asn  
35 40 45  
Ala Pro His Leu Asp Arg Gln Tyr Ala Val Phe Gly Lys Val Thr Lys  
50 55 60  
Gly Asp Glu Thr Leu Ser Lys Leu Glu Glu Val Pro Thr Arg Arg Glu  
65 70 75 80  
Gly Ile Phe Val Met Pro Thr Glu Arg Ile Thr Ile Leu Ser Thr Tyr

|                                                                 |     |  |     |  |     |
|-----------------------------------------------------------------|-----|--|-----|--|-----|
|                                                                 | 85  |  | 90  |  | 95  |
| Tyr Tyr Asp Thr Lys Met Glu Ser Cys Glu Glu Glu Arg Ser Val Leu |     |  |     |  |     |
|                                                                 | 100 |  | 105 |  | 110 |
| Lys Arg Arg Leu Gln Ala Ser Phe Val Glu Val Glu Arg Gln Arg Met |     |  |     |  |     |
|                                                                 | 115 |  | 120 |  | 125 |
| Lys Cys Phe Pro                                                 |     |  |     |  |     |
|                                                                 | 130 |  |     |  |     |

(2) INFORMATION FOR SEQ ID NO:1462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1248

(D) OTHER INFORMATION: / Ceres Seq. ID 1570072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:

|             |             |            |            |             |            |      |
|-------------|-------------|------------|------------|-------------|------------|------|
| aatagccaca  | aagacttttt  | tctttcatcc | tctaaaaaaa | aatctttcta  | gtgagtaacg | 60   |
| aaaaaaatgt  | gtccggtgga  | gaacaaatgg | ttaaagggtg | gtcaaaaagg  | agctgggtcc | 120  |
| ggggctagaa  | gctcacatgc  | catgaccgtc | gttgggaaca | aaattttactg | ttttgggtgt | 180  |
| gagcttaagc  | caacgatcca  | tattgataac | gatctttacg | ttttcgatct  | tgggactcaa | 240  |
| gaatgggtga  | tagctcctgc  | gaccggagag | gctcctttcc | ccgtgttttg  | tgctcgtatg | 300  |
| gtaacgatcg  | gttcaacgat  | ctatgtctac | gggtggcctg | acgataaaag  | gagatacaac | 360  |
| ggctcttcatt | cgtatgatac  | tgagaccaat | gagtggaagt | tggtttgagg  | aa         | 420  |
| gggcttccgt  | ctcgtatgata | tcattcaaat | gctggtgatg | atcggaagag  | ttatgtgttt | 480  |
| cgtgggtgga  | ctgctaaagg  | acgtgtgaat | acgcttcatg | cgtagcatgt  | tggtgatcag | 540  |
| aaatgggttg  | agtatccggc  | ggctggggaa | gcttgttaag | gcagaggagc  | acctgggctt | 600  |
| gtggtttggg  | aaggagagaat | ttgggttttg | tttgggtttg | atggtaaatg  | atgggtgatg | 660  |
| attcattggt  | ttgacttgcc  | tagtgaacag | tggaaggctg | tggaagactac | cggggatgat | 720  |
| ccggcgccga  | gaagcgtgtt  | tcggcggttt | tottacggga | agtaacattg  | tatttatggt | 780  |
| ggggagggaag | agccgcgatg  | gcttatgcac | atgggagctg | ggaagatgtc  | tggaagaggt | 840  |
| tatcagcttg  | atacagaagc  | gttagtggtg | gagaggatgg | ttgtgtggga  | tgaagaggag | 900  |
| aagccgagcc  | aacgcgggtg  | gtgcgcgttt | acgaaagcgg | ttaaggatgg  | tgaggaaggt | 960  |
| ttgtgtgttc  | atggtgggaa  | ttctccgacc | aatgagcgcc | ttgatgattt  | gggtgttttg | 1020 |
| ggtttctctc  | actttaatgt  | caattaatga | ctagtgtgct | tggtctcttc  | gtgtttatga | 1080 |
| actgtttagt  | gtgtgttgtt  | tttaaggagt | ttaagtgtgt | atgatatgta  | actgcctaag | 1140 |
| gtctgctgtt  | aaggagctat  | gtgtgtgtaa | actttgctac | ctattccaaa  | tattttatta | 1200 |
| agtgtgtgtg  | tttgtaatt   | taataaaaaa | cttgttagtc | tgattctc    |            |      |

(2) INFORMATION FOR SEQ ID NO:1463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..326

(D) OTHER INFORMATION: / Ceres Seq. ID 1570073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:

|                                                                 |          |
|-----------------------------------------------------------------|----------|
| Met Cys Pro Val Glu Asn Lys Trp Leu Lys Val Gly Gln Lys Gly Ala |          |
| 1                                                               | 5 10 15  |
| Gly Pro Gly Ala Arg Ser Ser His Ala Met Thr Val Val Gly Asn Lys |          |
|                                                                 | 20 25 30 |
| Val Tyr Cys Phe Gly Gly Glu Leu Lys Pro Thr Ile His Ile Asp Asn |          |
|                                                                 | 35 40 45 |
| Asp Leu Tyr Val Phe Asp Leu Gly Thr Gln Glu Trp Ser Ile Ala Pro |          |
|                                                                 | 50 55 60 |
| Ala Thr Gly Glu Ala Pro Phe Pro Cys Phe Gly Val Ser Met Val Thr |          |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Gly | Ser | Thr | Ile | Tyr | Val | Tyr | Gly | Gly | Arg | Asp | Asp | Lys | Arg | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Asn | Gly | Leu | His | Ser | Tyr | Asp | Thr | Glu | Thr | Asn | Glu | Trp | Lys | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Ser | Pro | Val | Glu | Glu | Gly | Leu | Pro | Gly | Arg | Ser | Tyr | His | Ser | Met |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Gly | Asp | Asp | Arg | Lys | Val | Tyr | Val | Phe | Arg | Gly | Val | Thr | Ala | Lys |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Arg | Val | Asn | Thr | Leu | His | Ala | Tyr | Asp | Val | Val | Asp | Gln | Lys | Trp |
|     |     |     | 145 |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Val | Glu | Tyr | Pro | Ala | Ala | Gly | Glu | Ala | Cys | Lys | Gly | Arg | Gly | Ala | Pro |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Gly | Leu | Val | Val | Val | Glu | Gly | Arg | Ile | Trp | Val | Leu | Phe | Gly | Phe | Asp |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Gly | Asn | Glu | Leu | Gly | Asp | Ile | His | Cys | Phe | Asp | Leu | Ala | Ser | Glu | Gln |
|     |     |     | 195 |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Trp | Lys | Ala | Val | Glu | Thr | Thr | Gly | Asp | Val | Pro | Ala | Ala | Arg | Ser | Val |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Pro | Ala | Val | Ser | Tyr | Gly | Lys | Tyr | Ile | Val | Ile | Tyr | Gly | Gly | Glu |
|     |     |     | 225 |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Glu | Glu | Pro | His | Glu | Leu | Met | His | Met | Gly | Ala | Gly | Lys | Met | Ser | Gly |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Glu | Val | Tyr | Gln | Leu | Asp | Thr | Glu | Thr | Leu | Val | Trp | Glu | Arg | Ile | Val |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Cys | Gly | Asn | Glu | Glu | Glu | Lys | Pro | Ser | Gln | Arg | Gly | Trp | Cys | Ala | Phe |
|     |     |     | 275 |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Thr | Lys | Ala | Val | Lys | Asp | Gly | Glu | Glu | Gly | Leu | Leu | Val | His | Gly | Gly |
|     |     |     | 290 |     | 295 |     |     |     | 300 |     |     |     |     |     |     |
| Asn | Ser | Pro | Thr | Asn | Glu | Arg | Leu | Asp | Asp | Leu | Val | Phe | Trp | Gly | Phe |
|     |     |     | 305 |     | 310 |     |     | 315 |     |     |     |     |     | 320 |     |
| Ser | His | Leu | Asn | Val | Asn |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 325 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..301
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1464:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Val | Val | Gly | Asn | Lys | Val | Tyr | Cys | Phe | Gly | Gly | Glu | Leu | Lys |
|     |     |     |     |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Pro | Thr | Ile | His | Ile | Asp | Asn | Asp | Leu | Tyr | Val | Phe | Asp | Leu | Gly | Thr |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gln | Glu | Trp | Ser | Ile | Ala | Pro | Ala | Thr | Gly | Glu | Ala | Pro | Phe | Pro | Cys |
|     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |     |     |     |
| Phe | Gly | Val | Ser | Met | Val | Thr | Ile | Gly | Ser | Thr | Ile | Tyr | Val | Tyr | Gly |
|     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Gly | Arg | Asp | Asp | Lys | Arg | Arg | Tyr | Asn | Gly | Leu | His | Ser | Tyr | Asp | Thr |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Thr | Asn | Glu | Trp | Lys | Leu | Leu | Ser | Pro | Val | Glu | Glu | Gly | Leu | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Arg | Ser | Tyr | His | Ser | Met | Ala | Gly | Asp | Asp | Arg | Lys | Val | Tyr | Val |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Phe | Arg | Gly | Val | Thr | Ala | Lys | Gly | Arg | Val | Asn | Thr | Leu | His | Ala | Tyr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Val | Val | Asp | Gln | Lys | Trp | Val | Glu | Tyr | Pro | Ala | Ala | Gly | Glu | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Cys | Lys | Gly | Arg | Gly | Ala | Pro | Gly | Leu | Val | Val | Val | Glu | Gly | Arg | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Trp | Val | Leu | Phe | Gly | Phe | Asp | Gly | Asn | Glu | Leu | Gly | Asp | Ile | His | Cys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Asp | Leu | Ala | Ser | Glu | Gln | Trp | Lys | Ala | Val | Glu | Thr | Thr | Gly | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Pro | Ala | Ala | Arg | Ser | Val | Phe | Pro | Ala | Val | Ser | Tyr | Gly | Lys | Tyr |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Val | Ile | Tyr | Gly | Gly | Glu | Glu | Glu | Pro | His | Glu | Leu | Met | His | Met |
|     | 210 |     |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Gly | Ala | Gly | Lys | Met | Ser | Gly | Glu | Val | Tyr | Gln | Leu | Asp | Thr | Glu | Thr |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |
| Leu | Val | Trp | Glu | Arg | Ile | Val | Cys | Gly | Asn | Glu | Glu | Lys | Pro | Ser |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Gln | Arg | Gly | Trp | Cys | Ala | Phe | Thr | Lys | Ala | Val | Lys | Asp | Gly | Glu | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Leu | Leu | Val | His | Gly | Gly | Asn | Ser | Pro | Thr | Asn | Glu | Arg | Leu | Asp |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Asp | Leu | Val | Phe | Trp | Gly | Phe | Ser | His | Leu | Asn | Val | Asn |     |     |     |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..249

(D) OTHER INFORMATION: / Ceres Seq. ID 1570075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Thr | Ile | Gly | Ser | Thr | Ile | Tyr | Val | Tyr | Gly | Gly | Arg | Asp | Asp |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Lys | Arg | Arg | Tyr | Asn | Gly | Leu | His | Ser | Tyr | Asp | Thr | Glu | Thr | Asn | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp | Lys | Leu | Leu | Ser | Pro | Val | Glu | Glu | Gly | Leu | Pro | Gly | Arg | Ser | Tyr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Ser | Met | Ala | Gly | Asp | Asp | Arg | Lys | Val | Tyr | Val | Phe | Arg | Gly | Val |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Thr | Ala | Lys | Gly | Arg | Val | Asn | Thr | Leu | His | Ala | Tyr | Asp | Val | Val | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gln | Lys | Trp | Val | Glu | Tyr | Pro | Ala | Ala | Gly | Glu | Ala | Cys | Lys | Gly | Arg |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Ala | Pro | Gly | Leu | Val | Val | Val | Glu | Gly | Arg | Ile | Trp | Val | Leu | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Phe | Asp | Gly | Asn | Glu | Leu | Gly | Asp | Ile | His | Cys | Phe | Asp | Leu | Ala |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Ser | Glu | Gln | Trp | Lys | Ala | Val | Glu | Thr | Thr | Gly | Asp | Val | Pro | Ala | Ala |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Arg | Ser | Val | Phe | Pro | Ala | Val | Ser | Tyr | Gly | Lys | Tyr | Ile | Val | Ile | Tyr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Gly | Glu | Glu | Glu | Pro | His | Glu | Leu | Met | His | Met | Gly | Ala | Gly | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Met | Ser | Gly | Glu | Val | Tyr | Gln | Leu | Asp | Thr | Glu | Thr | Leu | Val | Trp | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Ile | Val | Cys | Gly | Asn | Glu | Glu | Glu | Lys | Pro | Ser | Gln | Arg | Gly | Trp |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Cys | Ala | Phe | Thr | Lys | Ala | Val | Lys | Asp | Gly | Glu | Glu | Gly | Leu | Leu | Val |

210 215 220  
His Gly Gly Asn Ser Pro Thr Asn Glu Arg Leu Asp Asp Leu Val Phe  
225 230 235 240  
Trp Gly Phe Ser His Leu Asn Val Asn

(2) INFORMATION FOR SEQ ID NO:1466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..276
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466:

ctctttcgac ttcagtgaggc gcgcattcag agattcaaac tcagagaaaa tgggtggcgac 60  
aggcttattc gtgggggctaa acaaaggaca cggtgttacc aaacgcgagc aacctctcgc 120  
ccctaacaac agaaaaagga aaacaagcaa aaggactatt ttatcaggga atctcatcaa 180  
ggaagtgtgc ggtcaagctc cctatgagaa gaggatcaat gataaaaaata gtccttttgc 240  
tcgtddtaat tttagttgt taggtacttc tggttc

(2) INFORMATION FOR SEQ ID NO:1467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467:

Ser Phe Asp Phe Ser Gly Gly Ala Phe Arg Asp Ser Asn Ser Glu Lys  
1 5 10 15  
Met Val Ala Thr Gly Leu Phe Val Gly Leu Asn Lys Gly His Val Val  
20 25 30  
Thr Lys Arg Glu Gln Pro Pro Arg Pro Asn Asn Arg Lys Gly Lys Thr  
35 40 45  
Ser Lys Arg Thr Ile Phe Ile Arg Asn Leu Ile Lys Glu Val Ala Gly  
50 55 60  
Gln Ala Pro Tyr Glu Lys Arg Ile Thr Asp Lys Asn Ser Pro Phe Ala  
65 70 75 80  
Arg Xaa Asn Phe Gln Leu Leu Gly Thr Ser Gly  
85 90

(2) INFORMATION FOR SEQ ID NO:1468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468:

Met Val Ala Thr Gly Leu Phe Val Gly Leu Asn Lys Gly His Val Val  
1 5 10 15  
Thr Lys Arg Glu Gln Pro Pro Arg Pro Asn Asn Arg Lys Gly Lys Thr



|     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|
|     | 20  |     | 25  |     | 30  |
| Ser | Lys | Arg | Thr | Ile | Phe |
|     | 35  |     | 40  |     | 45  |
| Gln | Ala | Pro | Tyr | Glu | Lys |
|     | 50  |     | 55  |     | 60  |
| Arg | Xaa | Asn | Phe | Gln | Leu |
|     | 65  |     | 70  |     | 75  |

(2) INFORMATION FOR SEQ ID NO:1469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 941 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..941
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| gacaaaccaa | aaaaaaagcc | taaaaaagccg | accttttttc | ttcttttttc | tccttacct  | 60  |
| ctcagctttc | gctggtcttc | tccagcagac  | acgatcttgc | tcggagagat | tcgtagggga | 120 |
| ccgatctatc | aagccttcaa | gggcaaacag  | aaatggacca | cgacaagaca | ggatgccaaa | 180 |
| gcccacctga | aggtcccaag | ctatgtacta  | acaactgcgg | ttcttttgaa | gcgctgccac | 240 |
| aatgaacatg | tgttctaagt | gtcacaagga  | tatgtgtgtc | caacagtagc | agggcgctaa | 300 |
| gtttgcattc | gcagtgctgc | gaacatcgtc  | atccagcaac | atcataaagg | aaacctttac | 360 |
| cgctgcgttg | gtcgatattg | aaaccaaact  | cgttgagcgc | atgactgttt | ctgtacagcc | 420 |
| atcctctgtc | caagtcgttg | cagaggtagt  | agccagcaga | aagsgtcgca | aaccaaaagg | 480 |
| accaagcoga | tgtactactt | gcaataaagc  | ggttggcctg | actggattca | aatgtcgcgt | 540 |
| tggggacgtc | ttctgcggaa | AACacaccgc  | tatgcagaca | tacatgactg | ctccttcaat | 600 |
| taccatgtgc | ctcgccaaga | gcgcgatagc  | aaggcaaac  | cggttgtaga | agcagagaag | 660 |
| cttgacaaaa | ttctgaaact | taagtaaaact | tctctgtgtt | catcaggtgg | ctggtgtttt | 720 |
| ctctctctgc | tctgtgtctg | gttcaagtat  | tctcatgtta | aaaaggtttt | atataaggtc | 780 |
| gaatgaaagc | gtgcttgatc | tttagcgtct  | tccatctctc | tgcaatattt | gtggtgtgga | 840 |
| actttctatt | atctgtgttt | gcaagcagag  | aaacgtgctc | ttaaaaaaa  | tgctttgtgt | 900 |
| gtttatcttt | ctactatttt | tgagcactgt  | gttattgttt | c          |            |     |

(2) INFORMATION FOR SEQ ID NO:1470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Lys | Pro | Lys | Lys | Pro | Lys | Lys | Pro | Thr | Phe | Phe | Leu | Ser | Phe |
|     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |     |     |
| Ser | Pro | Leu | Pro | Leu | Ser | Phe | Cys | Trp | Ile | Ser | Pro | Ala | Asp | Thr |
|     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |     |
| Leu | Phe | Gly | Glu | Ile | Arg | Arg | Gly | Pro | Ile | Tyr | Gln | Gly | Phe | Lys |
|     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |     |
| Lys | Gln | Lys | Trp | Thr | Thr | Thr | Arg | Gln | Asp | Ala | Lys | Ala | His | Leu |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Pro | Ser | Tyr | Val | Leu | Thr | Thr | Ala | Val | Ser | Leu | Lys | Arg | Cys |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |
| Asn | Glu | His | Val | Phe |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1471:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..62  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570109  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:  
Thr Asn Gln Lys Lys Ser Leu Lys Ser Arg Pro Phe Phe Phe Leu Ser  
1 5 10 15  
Leu Leu Tyr Leu Ser Ala Ser Ala Gly Ser Leu Gln Gln Thr Arg Ser  
20 25 30  
Cys Ser Glu Arg Phe Val Gly Asp Arg Ser Ile Lys Ala Ser Arg Ala  
35 40 45  
Asn Arg Asn Gly Pro Arg Gln Asp Arg Met Pro Lys Pro Thr  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1472:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 75 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..75  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570110  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:  
Met Thr Val Ser Val Gln Pro Ser Ser Val Gln Val Val Ala Glu Val  
1 5 10 15  
Val Ala Pro Glu Glu Xaa Ala Lys Pro Lys Gly Pro Ser Arg Cys Thr  
20 25 30  
Thr Cys Asn Lys Arg Val Gly Leu Thr Gly Phe Lys Cys Arg Cys Gly  
35 40 45  
Ser Leu Phe Cys Gly Lys His Thr Ala Met Gln Thr Tyr Met Thr Ala  
50 55 60  
Pro Ser Ile Thr Met Leu Leu Arg Lys Arg Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1473:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 601 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..601  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570111  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:  
aagacaaaagc gcagaaaatg gtgggagcga ctgtagttag taaatggact ccctatgtg 60  
tgGCttcgcc gccggagaga aactcggcaa gtctcaatcc acactgttct ccagccaggg 120  
ttaattttag aacagcggtg gccgcatttc gtctcagtt cgtctctttc tctcgcaatt 180  
cgcgctctcg ccgcccgtctt cgcgcttcca gctccgcgga atcgggcggg agacgcggat 240  
gctcaaggaa agtatccata cacaggtttc ctcgattgtg cgatgaaaac cttaaaagaa 300  
ggaggacctc tgaattttta ctcaggtttc ccagtttact gtgtcaggat tgccctcatc 360  
gtcatgatga catggatctt cctaaaccag attacgaaat ttcaaaagaa gatgggtgat 420  
tgaggaaacga agacagcagc aaaaaataa gatgagaaga acgaaaacac aattggaatt 480  
gtgttcattt actttttaat catatacata acctgcctta aaagcatatt attgtagctg 540

tttgaacttt aattttttgt ttcggtcggt gattggtccg gtgaatttta aattttcttc 600  
C

(2) INFORMATION FOR SEQ ID NO:1474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Lys | Ala | Gln | Lys | Met | Val | Gly | Ala | Thr | Val | Val | Ser | Lys | Trp | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Leu | Cys | Val | Ala | Ser | Pro | Pro | Glu | Arg | Asn | Ser | Ala | Ser | Leu | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | His | Cys | Ser | Pro | Ala | Arg | Val | Asn | Phe | Arg | Thr | Ala | Leu | Ala | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Arg | Pro | Gln | Phe | Arg | Leu | Phe | Ser | Arg | Asn | Ser | Ala | Ser | Arg | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Leu | Arg | Ala | Ser | Ser | Ser | Ala | Glu | Ser | Ala | Ala | Arg | Arg | Gly | Cys |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Arg | Lys | Val | Ser | Ile | His | Arg | Phe | Ala | Arg | Leu | Cys | Asp | Glu | Asn |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Lys | Arg | Arg | Arg | Thr | Ser | Glu | Ile | Leu | Leu | Arg | Phe | Pro | Ser | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Cys | Gln | Asp | Cys | Pro | Ser | Arg | His | Asp | Asp | Met | Asp | Leu | Pro | Lys |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Pro | Asp | Tyr | Glu | Ile | Ser | Lys | Glu | Asp | Trp | Tyr | Val | Arg | Asn | Glu | Asp |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Ser | Lys | Lys | Ile | Arg |     |     |     |     |     |     |     |     |     |     |
|     | 145 |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Gly | Ala | Thr | Val | Val | Ser | Lys | Trp | Thr | Pro | Leu | Cys | Val | Ala |
| 1   |     |     |     |     |     | 5   |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Pro | Pro | Glu | Arg | Asn | Ser | Ala | Ser | Leu | Asn | Pro | His | Cys | Ser | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Arg | Val | Asn | Phe | Arg | Thr | Ala | Leu | Ala | Ala | Phe | Arg | Pro | Gln | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Leu | Phe | Ser | Arg | Asn | Ser | Ala | Ser | Arg | Arg | Arg | Leu | Arg | Ala | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ser | Ala | Glu | Ser | Ala | Ala | Arg | Arg | Gly | Cys | Ser | Arg | Lys | Val | Ser |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | His | Arg | Phe | Ala | Arg | Leu | Cys | Asp | Glu | Asn | Leu | Lys | Arg | Arg | Arg |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Ser | Glu | Ile | Leu | Leu | Arg | Phe | Pro | Ser | Leu | Leu | Cys | Gln | Asp | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Ser | Arg | His | Asp | Asp | Met | Asp | Leu | Pro | Lys | Pro | Asp | Tyr | Glu | Ile |

115 120 125  
Ser Lys Glu Asp Trp Tyr Val Arg Asn Glu Asp Ser Ser Lys Lys Ile  
130 135 140

Arg  
145

(2) INFORMATION FOR SEQ ID NO:1476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..621
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476:

|             |             |             |             |            |             |     |
|-------------|-------------|-------------|-------------|------------|-------------|-----|
| accctaagcg  | tatataaatc  | atatagtttt  | catttttttcg | tactttctot | ccatcgccgt  | 60  |
| ctaaaaaaccc | taatctcact  | cgcctctctg  | cgagatccat  | caacacttac | gcaaaaaatga | 120 |
| agggttggtgc | tgcggtttttg | cttgccgctct | tgagcgggaa  | agcttcccca | accaactggcg | 180 |
| atatcaagga  | tattcttgga  | tcagttgggtg | ctgagacaga  | ggattctcag | attgagcttt  | 240 |
| tgttgaagga  | agtgaagg    | aaagacttgg  | ctgagcta    | tgctgctgga | agggagaagt  | 300 |
| tagcttcagt  | accatcagga  | ggtggtgggtg | gtgttcgggt  | tgctctgct  | acatctggag  | 360 |
| gtggaggagg  | tggttggtgct | cctgctgctg  | agtcgaagaa  | agaagagaag | aaagaagaga  | 420 |
| agaagaagac  | cgatgatgac  | atgggtttca  | gtttgttcga  | gtaatcggtg | atactggca   | 480 |
| tttggttttg  | ctgtaccctt  | tcgaaatctt  | tatgtcgttg  | tttagttgtg | tgatttcgac  | 540 |
| tatctcttta  | gactttgctg  | aaattctcaa  | gagatttttt  | Tactcaaca  | tcagtoCact  | 600 |
| tgtagttggc  | atttatattt  | c           |             |            |             |     |

(2) INFORMATION FOR SEQ ID NO:1477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Val | Val | Ala | Ala | Phe | Leu | Leu | Ala | Val | Leu | Ser | Gly | Lys | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Pro | Thr | Thr | Gly | Asp | Ile | Lys | Asp | Ile | Leu | Gly | Ser | Val | Gly | Ala |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Glu | Thr | Glu | Asp | Ser | Gln | Ile | Glu | Leu | Leu | Leu | Lys | Glu | Val | Lys | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Asp | Leu | Ala | Glu | Leu | Ile | Ala | Ala | Gly | Arg | Glu | Lys | Leu | Ala | Ser |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Val | Pro | Ser | Gly | Gly | Gly | Gly | Gly | Val | Ala | Val | Ala | Ser | Ala | Thr | Ser |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Gly | Gly | Gly | Gly | Gly | Gly | Gly | Ala | Pro | Ala | Ala | Glu | Ser | Lys | Lys | Glu |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |     |
| Glu | Lys | Lys | Glu | Glu | Lys | Glu | Glu | Ser | Asp | Asp | Asp | Met | Gly | Phe | Ser |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Leu | Phe | Glu |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..534

(D) OTHER INFORMATION: / Ceres Seq. ID 1570138

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478:

|            |             |             |            |             |            |     |
|------------|-------------|-------------|------------|-------------|------------|-----|
| atattcaaag | attagaaca   | ttcttgatag  | atacaaaaaa | cattttttca  | gacacaaatt | 60  |
| cataaaatct | ttgccttgag  | tagatcaaaag | ttctttacat | taatcgttag  | aagatgagcc | 120 |
| agtagcatca | caaccagttct | gcaggagcta  | accacccgcc | accgatgtct  | acctgtacat | 180 |
| caccaccacc | gccgatttggt | taccgcacta  | accaaccgac | tcattggttcg | gtagctcagg | 240 |
| gtaaaagtga | aaccaagtct  | aagggtgacg  | gattcttcaa | aggctgtctt  | gcggccatgt | 300 |
| gttgctgttg | tgccctggac  | atttgcttct  | aagccatttg | ggaattggga  | tggtctattt | 360 |
| atgacgagtt | tatgtgaagt  | tgatgtgaat  | tattattatt | attctctcca  | gccttatgtt | 420 |
| ataaaattct | tattttttgt  | tattattttt  | cttgtaatac | tttgtagac   | gaacatatta | 480 |
| tgttttgtat | ttgatctct   | actctctagt  | acttaaat   | atttgctttg  | cYtt       |     |

- (2) INFORMATION FOR SEQ ID NO:1479:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1570139

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gln | Tyr | Asp | His | Asn | Gln | Ser | Ala | Gly | Ala | Asn | Pro | Pro | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Pro | Met | Ser | Thr | Cys | Thr | Ser | Pro | Pro | Pro | Pro | Ile | Gly | Tyr | Pro | Thr |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Asn | Gln | Pro | Ser | His | Gly | Ser | Val | Ala | Gln | Gly | Lys | Val | Glu | Thr | Lys |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Ser | Lys | Gly | Asp | Gly | Phe | Phe | Lys | Gly | Cys | Leu | Ala | Ala | Met | Cys | Cys |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Cys | Cys | Ala | Leu | Asp | Ile | Cys | Phe |     |     |     |     |     |     |     |     |
|     |     |     |     | 65  |     |     | 70  |     |     |     |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:1480:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..55

(D) OTHER INFORMATION: / Ceres Seq. ID 1570140

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Thr | Cys | Thr | Ser | Pro | Pro | Pro | Pro | Ile | Gly | Tyr | Pro | Thr | Asn |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     | 15  |     |     |
| Gln | Pro | Ser | His | Gly | Ser | Val | Ala | Gln | Gly | Lys | Val | Glu | Thr | Lys | Ser |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Lys | Gly | Asp | Gly | Phe | Phe | Lys | Gly | Cys | Leu | Ala | Ala | Met | Cys | Cys | Cys |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Cys | Ala | Leu | Asp | Ile | Cys | Phe |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 50  |     | 55  |     |     |     |     |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:1481:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..51  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570141  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481:  
Met Thr Ser Leu Cys Glu Cys Asp Val Asn Tyr Tyr Tyr Ser Leu  
1 5 10 15  
Gln Pro Tyr Cys Ile Asn Ser Leu Phe Val Tyr Tyr Phe Leu Val  
20 25 30  
Ile Leu Cys Glu Thr Asn Ile Leu Cys Phe Val Phe Gly Ser Leu Leu  
35 40 45  
Ser Ser Thr  
50

(2) INFORMATION FOR SEQ ID NO:1482:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 689 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..689  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570142  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:  
aaccaatctc aaagcaaat aaatacacta ctactttctg agctttttaa ctacacaaac 60  
aaatggctcc aagaaccccc ctgcaactct tcgtttctct caacctctct ttcttcaact 120  
acactctcgc aaccacaggc acttgctcta aaaattccat agagatcggt acttgtgtca 180  
ctgtgctcaa tctagtggac ctaacattgg gaaaccacac tgtaaagcca tgttgctcgc 240  
tcatccaagg ctggctgac cttgaggctg cggcctgcct ctgcaactgcg ctcaaagcta 300  
gcattcttgg aattgtcaat attaaccttc ctatcaatct cagcgctact ctcaatgttt 360  
gtagtaggaa tgcctccaaag agtttccagt gcgcgtaaat tgaataccta tgacatacct 420  
atgaaacaaa cgaatcatac csmTgcttga acatgttttc ttacctactt gttgtgttct 480  
taagatgttt gttttttctt tctttcttgg attgttaata atgaacgtac gacgttctga 540  
tgcaaaaataa tggaaaaatg gggtgtgtgt acaatcgaca agtttgtata tactccttta 600  
ctttgtgttt cctttgtttt gttgttcttc ttcttgttaa ctgtgtattt caaatgtgct 660  
taataaaaaa ataaaattgat gttgtagcc

(2) INFORMATION FOR SEQ ID NO:1483:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 111 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..111  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570143  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:  
Met Ala Pro Arg Thr Pro Leu Ala Leu Phe Val Ser Leu Asn Leu Leu  
1 5 10 15  
Phe Phe Thr Tyr Thr Ser Ala Thr Thr Gly Thr Cys Pro Lys Asn Ser  
20 25 30  
Ile Glu Ile Gly Thr Cys Val Thr Val Leu Asn Leu Val Asp Leu Thr  
35 40 45  
Leu Gly Asn Pro Pro Val Lys Pro Cys Cys Ser Leu Ile Gln Gly Leu  
50 55 60

Ala Asp Leu Glu Ala Ala Ala Cys Leu Cys Thr Ala Leu Lys Ala Ser  
65 70 75 80  
Ile Leu Gly Ile Val Asn Ile Asn Leu Pro Ile Asn Leu Ser Val Leu  
85 90 95  
Leu Asn Val Cys Ser Arg Asn Ala Pro Lys Ser Phe Gln Cys Ala  
100 105 110

(2) INFORMATION FOR SEQ ID NO:1484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..716
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:

aatcaagcaa tccaaagcga ttaaacctac tcaatctcag atctcgtaa acctagaaac 60  
ctcgagaaaa accgtatcaa tggcgccgaa agcagagaag aagcccgctg agaagaaacc 120  
agcttcggag aagccggtgg aggagaaatc aaaagccgag aaagctccgg cggagaagaa 180  
accaaaggcc ggaagaagac tccgaagga agctggtgccc ggaggcgaca agaagaaaaa 240  
gatgaagaag aagagtgtgc agacttacaa gatctacatc tcaaggtgc ttaagcaagt 300  
tcattccgat atcggaatct ccagcaaaagc gatgggggac atgaacagtt tcattaacga 360  
tatcttcgag aagcttgctc aagaggcgtc gaagcttgctg aggtacaata agadacctac 420  
gatcacttct cggagagattc agactgctgt gagattgggtg cttccctggag agttggcgaa 480  
gcatcgcggtt tctgagggga ctaaacgcgt caccgaaatc accagctctt gaataattga 540  
gttagggttc ttatcatatg gatgttgctc tgctttaggg ttaatgggatc ttaagagatc 600  
tgagttaggg ttttagaatg tcctttaagt atctctggtt cgtttggaat ttctacgttt 660  
tgtaagtact gctgctattg ataattgttg gagtctatat ttgctctttg tgtccc

(2) INFORMATION FOR SEQ ID NO:1485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:

Ile Lys Gln Ser Lys Ala Ile Lys Pro Thr Gln Ser Gln Ile Ser Leu  
1 5 10 15  
Asn Leu Glu Thr Ser Arg Lys Thr Val Ser Met Ala Pro Lys Ala Glu  
20 25 30  
Lys Lys Pro Ala Glu Lys Lys Pro Ala Ser Glu Lys Pro Val Glu Glu  
35 40 45  
Lys Ser Lys Ala Glu Lys Ala Pro Ala Glu Lys Lys Pro Lys Ala Gly  
50 55 60  
Lys Lys Leu Pro Lys Glu Ala Gly Ala Gly Asp Lys Lys Lys Lys  
65 70 75 80  
Met Lys Lys Lys Ser Val Glu Thr Tyr Lys Ile Tyr Ile Phe Lys Val  
85 90 95  
Leu Lys Gln Val His Pro Asp Ile Gly Ile Ser Ser Lys Ala Met Gly  
100 105 110  
Ile Met Asn Ser Phe Ile Asn Asp Ile Phe Glu Lys Leu Ala Gln Glu  
115 120 125  
Ala Ser Lys Leu Ala Arg Tyr Asn Lys Xaa Pro Thr Ile Thr Ser Arg  
130 135 140  
Glu Ile Gln Thr Ala Val Arg Leu Val Leu Pro Gly Glu Leu Ala Lys

145                      150                      155                      160  
His Ala Val Ser Glu Gly Thr Lys Ala Val Thr Lys Phe Thr Ser Ser  
                              165                      170                      175

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1570161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1487:

### (i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1570162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Lys | Ser | Val | Glu | Thr | Tyr | Lys | Ile | Tyr | Ile | Phe | Lys | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Lys | Gln | Val | His | Pro | Asp | Ile | Gly | Ile | Ser | Ser | Lys | Ala | Met | Gly |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Met | Asn | Ser | Phe | Ile | Asn | Asp | Ile | Phe | Glu | Lys | Leu | Ala | Gln | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Ser | Lys | Leu | Ala | Arg | Tyr | Asn | Lys | Xaa | Pro | Thr | Ile | Thr | Ser | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Ile | Gln | Thr | Ala | Val | Arg | Leu | Val | Leu | Pro | Gly | Glu | Leu | Ala | Lys |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| His | Ala | Val | Ser | Glu | Gly | Thr | Lys | Ala | Val | Thr | Lys | Phe | Thr | Ser | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |



(2) INFORMATION FOR SEQ ID NO:1488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..936
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:

|             |             |             |             |             |            |     |
|-------------|-------------|-------------|-------------|-------------|------------|-----|
| aaccttatca  | cgctattctc  | aaacaagcaa  | agaaccttaa  | ccaaaagaaa  | aacgtctacg | 60  |
| gagacatatg  | gagaggaaac  | atcacttcgt  | gttagttcac  | aacgcttacc  | atggagcctg | 120 |
| gattctggtag | aaagctcaagc | ccctcccttga | atcagccggc  | caccgcgtta  | ctgctgtcga | 180 |
| actcgccgcc  | tccgggtagc  | acccacgacc  | aatccaggcc  | gttgaaacgc  | tcgacgaata | 240 |
| ctccaaacgc  | ttgatcgaaa  | ccctcaaatc  | tctccagag   | aacgaagagg  | taattctggt | 300 |
| tggattcagc  | tccggaggca  | tcaacatcgc  | tctccggccc  | gacatatctc  | cgcggaagat | 360 |
| taaggttctt  | gtgttctctc  | acgccttctt  | gcccgacaca  | acccacgtgc  | cttctcacgt | 420 |
| tctggacaag  | tatatggaga  | tgccctggagg | tttgggagat  | tgtgagtttt  | catctcatga | 480 |
| aaacaagaaa  | gggacgatga  | gtttattTga  | agatggggacc | aaaattcatg  | aaggcacgtc | 540 |
| ttaccacaaa  | tgtctccata  | gaggattacg  | agctggcaca  | aatgttgcat  | aggaacgggt | 600 |
| catctttcac  | agaggatcta  | tcaagaagaa  | aaaagttag   | cgaggaaagga | tatggttcgg | 660 |
| tgaacagagt  | ttacgttatg  | agttagtgaag | acaaagccat  | ccctcgcat   | ttcattcggt | 720 |
| ggatgattga  | taatttcaac  | gtctcgaaag  | tctacgagat  | cgatggcgga  | gatcacatgg | 780 |
| tgatgctctc  | caaaccccaa  | aaactctttg  | actctctctc  | tgctattgcc  | acgattata  | 840 |
| tgttaataatc | ttaagtcctg  | ttacttttt   | tctcatggt   | actaataaaa  | caaacccctt | 900 |
| tttcggcgca  | actttcatca  | aaaaacaaaa  | cttatg      |             |            |     |

(2) INFORMATION FOR SEQ ID NO:1489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Arg | Lys | His | His | Phe | Val | Leu | Val | His | Asn | Ala | Tyr | His | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Trp | Ile | Trp | Tyr | Lys | Leu | Lys | Pro | Leu | Leu | Glu | Ser | Ala | Gly | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Val | Thr | Ala | Val | Glu | Leu | Ala | Ala | Ser | Gly | Ile | Asp | Pro | Arg | Pro |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ile | Gln | Ala | Val | Glu | Thr | Val | Asp | Glu | Tyr | Ser | Lys | Pro | Leu | Ile | Glu |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Thr | Leu | Lys | Ser | Leu | Pro | Glu | Asn | Glu | Val | Ile | Leu | Val | Gly | Phe |     |
| 65  |     |     |     |     |     |     |     | 70  |     |     |     |     | 75  |     | 80  |
| Ser | Phe | Gly | Gly | Ile | Asn | Ile | Ala | Leu | Ala | Ala | Asp | Ile | Phe | Pro | Ala |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Ile | Lys | Val | Leu | Val | Phe | Leu | Asn | Ala | Phe | Leu | Pro | Asp | Thr | Thr |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Val | Pro | Ser | His | Val | Leu | Asp | Lys | Tyr | Met | Glu | Met | Pro | Gly | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Leu | Gly | Asp | Cys | Glu | Phe | Ser | Ser | His | Glu | Thr | Arg | Asn | Gly | Thr | Met |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |
| Ser | Leu | Phe | Glu | Asp | Gly | Thr | Lys | Ile | His | Glu | Gly | Thr | Ser | Leu | Pro |

(2) INFORMATION FOR SEO ID NO:1490:

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..110
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1570165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:

(2) INFORMATION FOR SEO ID NO:1491:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..105
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1570166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:

(2) INFORMATION FOR SEO ID NO:1492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1220 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1220

(D) OTHER INFORMATION: / Ceres Seq. ID 1570170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| attctaatca  | tcccttgtaa  | ttttccaagt | tttctctctt  | tgtctctctt  | aactattttc  | 60   |
| ccttaaaaata | aaaatccaat  | ttttctttgt | ttcagtcctc  | tctctctgctc | attgatcttt  | 120  |
| aaatataactt | tgattctctc  | cgtttatgga | ttaacatttt  | gatcgagata  | actctccaag  | 180  |
| aaatcgactgt | agttcgttaac | ttgtttgtgt | ctgatctttt  | aaagattcaa  | ctcttttttg  | 240  |
| tcgcgatcatg | ctctgttgctg | agaatgctgt | tgctaaaagt  | gactctcttg  | gtcagaatttt | 300  |
| agacaaacaac | aacactgctg  | cttcagctac | cgagacgaca  | aagccgcat   | gtcctgatga  | 360  |
| tgatcaaaagc | cctaatactg  | actcatccac | tcctcttacc  | atcgattoga  | ctcctgaaac  | 420  |
| tgacgatogg  | atcaatgaga  | ctgctcaaaa | gggttcagact | ttaaaatggg  | ttagtggaaa  | 480  |
| tggtgagaga  | gataacaatg  | gagagatcaa | agatttggtc  | gatgcgtttt  | ctaagcttaa  | 540  |
| tcgcgatgct  | caggagtgtg  | ttctctcttc | tcttgctcga  | agtcactctg  | gggttttgag  | 600  |
| aaatgggata  | gggttttacta | acaattttgc | agccccacct  | aaacttgctg  | atgggaaatga | 660  |
| tcattttctc  | agaaggagaa  | ggagttttgc | ccaagggaag  | cgaagaatga  | acaaaaggac  | 720  |
| aagcttggtc  | cagaaggatg  | atgtaatac  | gacaactgta  | tatgtctctg  | acatcgacca  | 780  |
| acaggttaca  | gaggagaacc  | tcgcaggtgt | ctttattaac  | ttgtgacagg  | ttgttgattg  | 840  |
| tcgtgtatgc  | gggtatccaa  | attctgtctc | tcgtttcgtc  | tcaattgaat  | ttaccaatga  | 900  |
| agaggagact  | agagctgctt  | tgagcatgtc | gggtactgtg  | ctaggttttt  | acctcttaa   | 960  |
| ggttctcttc  | tccaaaacag  | ctattgctcc | tgtaaaccg   | acctttcttc  | cacgatctga  | 1020 |
| ggatgagcgt  | gagatgtgcg  | ttaggactgt | ttactgtacc  | acatttgaca  | agcggtcac   | 1080 |
| tcacaaatgac | ttgaaaggct  | tccttgaaat | gctttcgagg  | gaggttcatc  | gtctgaggct  | 1140 |
| tggagactat  | caccacccaa  | cccgatttgc | tttggttgag  | tttgcatgag  | cggaaagcgc  | 1200 |

aaCttgCtgc gcttcactgc

(2) INFORMATION FOR SEQ ID NO:1493:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..324

(D) OTHER INFORMATION: / Ceres Seq. ID 1570171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Val | Ala | Glu | Asn | Ala | Gly | Val | Lys | Val | Asp | Ser | Ser | Gly | Gln |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Asn | Leu | Asp | Asn | Asn | Asn | Thr | Ala | Ala | Ser | Ala | Thr | Glu | Thr | Thr | Lys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Pro | Pro | Cys | Pro | Asp | Asp | Asp | Gln | Ser | Pro | Lys | Ser | Asp | Ser | Ser | Thr |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Pro | Leu | Thr | Ile | Asp | Ser | Thr | Pro | Glu | Thr | Asp | Asp | Arg | Ile | Asn | Glu |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |  |
| Thr | Ala | Gln | Lys | Val | Gln | Thr | Leu | Asn | Gly | Phe | Ser | Gly | Asn | Gly | Glu |  |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     | 80  |     |     |  |
| Arg | Gsp | Asn | Asn | Gly | Glu | Ile | Lys | Asp | Leu | Ala | Asp | Ala | Phe | Ser | Lys |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Leu | Asn | Pro | Met | Ala | Gln | Glu | Phe | Val | Pro | Pro | Ser | Leu | Ala | Arg | Ser |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Gln | Ser | Gly | Val | Leu | Arg | Asn | Gly | Leu | Gly | Phe | Thr | Asn | Asn | Phe | Ala |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ala | Pro | Pro | Lys | Leu | Ala | Asp | Gly | Asn | Asp | His | Phe | Pro | Arg | Arg | Arg |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |  |
| Arg | Ser | Phe | Gly | Gln | Gly | Lys | Arg | Arg | Met | Asn | Lys | Arg | Thr | Ser | Leu |  |
|     |     |     | 145 |     |     | 150 |     |     | 155 |     |     |     |     | 160 |     |  |
| Ala | Gln | Lys | Asp | Asp | Val | Ile | Arg | Thr | Thr | Val | Tyr | Val | Ser | Asp | Ile |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |

(2) INFORMATION FOR SEQ ID NO:1494:

(A) LENGTH: 225 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..225

(D) OTHER INFORMATION: / Ceres Seq. ID 1570172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494:

[illegible]

225

(2) INFORMATION FOR SEQ ID NO:1495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asn | Lys | Arg | Thr | Ser | Leu | Ala | Gln | Lys | Asp | Asp | Val | Ile | Arg | Thr |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Thr | Val | Tyr | Val | Ser | Asp | Ile | Asp | Gln | Gln | Val | Thr | Glu | Glu | Asn | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ala | Gly | Val | Phe | Ile | Asn | Cys | Gly | Gln | Val | Val | Asp | Cys | Arg | Val | Cys |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Gly | Asp | Pro | Asn | Ser | Val | Leu | Arg | Phe | Ala | Phe | Ile | Glu | Phe | Thr | Asn |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Glu | Glu | Gly | Ala | Arg | Ala | Ala | Leu | Ser | Met | Ser | Gly | Thr | Val | Leu | Gly |  |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Phe | Tyr | Pro | Leu | Lys | Val | Leu | Pro | Ser | Lys | Thr | Ala | Ile | Ala | Pro | Val |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Asn | Pro | Thr | Phe | Leu | Pro | Arg | Ser | Glu | Asp | Glu | Arg | Glu | Met | Cys | Val |  |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Arg | Thr | Val | Tyr | Cys | Thr | Asn | Ile | Asp | Lys | Arg | Ile | Thr | Gln | Ile | Asp |  |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |  |
| Leu | Lys | Gly | Phe | Phe | Glu | Met | Leu | Cys | Gly | Glu | Val | His | Arg | Leu | Arg |  |
|     |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Leu | Gly | Asp | Tyr | His | His | Gln | Thr | Arg | Ile | Ala | Phe | Val | Glu | Phe | Ala |  |
|     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Met | Ala | Glu | Ser | Ala | Thr | Cys | Cys | Ala | Ser | Leu |     |     |     |     |     |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1460
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496:

|             |             |            |            |             |             |     |
|-------------|-------------|------------|------------|-------------|-------------|-----|
| atttttgagt  | tctcagattt  | caaacacaaa | agtttcgtct | cogatttaat  | ctttctacgt  | 60  |
| cttggtttat  | gagctcaaa   | gagaagccca | ctctcggagg | tacgcggatt  | aagaccgccca | 120 |
| aaaggaatat  | tgtcgtcct   | ctcgaccctg | ctgcttttct | tgatgcacta  | gttcagattt  | 180 |
| atctggataa  | tgtcgttgat  | ctggaacttg | tgcgcaag   | tttagagtoa  | tctgatctta  | 240 |
| atttttcaag  | atacgttgat  | attttctttg | aggttggttt | cattggagga  | cgtaactcaa  | 300 |
| ctgggttcagt | gaatcttgat  | gaagggggac | gccaccctta | ctctataatc  | gactgtgaac  | 360 |
| caaaagcgtga | agctattttta | ccatcagttg | tatacataca | gaaaattttg  | cgagggaag   | 420 |
| ccttccttat  | taagaacctt  | gagaatgtta | cacggagatt | cttacagtaa  | ctggagcttt  | 480 |
| ttagggagaa  | tgagaggaag  | aagcttgcaa | tattcacagc | acttgcaatt  | tcacagaagc  | 540 |
| tctcaggatt  | acctgcagag  | actgtcttcc | agccattgtc | taaggataact | cttgttgcca  | 600 |
| aagggatagt  | tctcaatttt  | gtaacagact | tcttcaatga | atatttggtt  | gagaacagtc  | 660 |
| tgtgatcatt  | gatttctatt  | tgaggcgctg | gcaagatgga | tgacaaactc  | ttggagtctc  | 720 |
| tgccaccac   | aaagcgagct  | acagaaagtt | tgcgagca   | tttcaactaa  | gcaggattga  | 780 |
| cagctctggt  | agagtacaat  | gaaaggaaaa | tatttgaggt | gaagctgaag  | gaaatcaag   | 840 |

```

cggtccttac gagccaagt acagaggaaa taaacgtaga tgaagtgtact gaaatgtgtga 900
agcaacaggt gaagatgtca aagctgccag agAactgagg ttgtgcatgt gatctgggat 960
aggataatga atgctgttca atggctctgg aaaaaccagc agcagaattc gaatgctgta 1020
ttacgccaaag tgaaaacatg ggcacccctt ctgaacacgc ttgttagcac cgggaacatg 1080
gagatggaac tgatgtataa agtacagatg caatgctatg aggatgcaaa gctgatgaaa 1140
gtgtttcctg aggtagtgtg atctctGTmt gTatrmAyggt atgtgcttgc ggaagacacc 1200
attctgcact ggtatcgcaa agggaccaac cctaagggca ggcaaacggt tbtgaaggga 1260
ttggaaccgt ttgtgaattg gctcgaagag gccgaagaag aggagtgtgt gagacgctct 1320
gcttctgttt ttctcttttt actctcttct aataaaagaa agacaatatt ttacttctct 1380
taacgcaaaa ttacagatgt ctacattgtt gtgacttggg ttgtgatctct tttttgaatg 1440
aataagtact tctttagttg

```

(2) INFORMATION FOR SEQ ID NO:1497:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..289

(D) OTHER INFORMATION: / Ceres Seq. ID 1570184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:

```

Met Ser Ser Lys Glu Lys Pro Thr Leu Gly Gly Thr Arg Ile Lys Thr
1 5 10 15
Arg Lys Arg Asn Ile Ala Ala Pro Leu Asp Pro Ala Ala Phe Ser Asp
20 25 30
Ala Leu Val Gln Ile Tyr Leu Asp Asn Ala Gly Asp Leu Gly Leu Val
35 40 45
Ala Arg Ser Leu Glu Ser Ser Asp Leu Asn Phe Ser Arg Tyr Gly Asp
50 55 60
Ile Phe Phe Glu Val Val Phe Ile Gly Gly Arg Thr Gln Thr Gly Ser
65 70 75 80
Val Lys Ser Asp Glu Gly Glu Arg His Pro Tyr Ser Ile Ile Asp Cys
85 90 95
Glu Pro Lys Arg Glu Ala Ile Leu Pro Ser Val Val Tyr Ile Gln Lys
100 105 110
Ile Leu Arg Arg Lys Ala Phe Leu Ile Lys Asn Leu Glu Asn Val Thr
115 120 125
Arg Arg Phe Leu Gln Ser Leu Glu Leu Phe Glu Glu Asn Glu Arg Lys
130 135 140
Lys Leu Ala Ile Phe Thr Ala Leu Ala Phe Ser Gln Lys Leu Ser Gly
145 150 155 160
Leu Pro Ala Glu Thr Val Phe Gln Pro Leu Leu Lys Asp Thr Leu Val
165 170 175
Ala Lys Gly Ile Val Leu Asn Phe Val Thr Asp Phe Phe Asn Glu Tyr
180 185 190
Leu Val Glu Asn Ser Leu Asp Asp Leu Ile Ser Ile Leu Arg Arg Gly
195 200 205
Lys Met Asp Asp Lys Leu Leu Glu Phe Leu Pro Pro Thr Lys Arg Thr
210 215 220
Thr Glu Ser Phe Ala Glu His Phe Thr Lys Ala Gly Leu Thr Ala Leu
225 230 235 240
Val Glu Tyr Asn Glu Arg Lys Ile Phe Glu Val Lys Leu Lys Glu Ile
245 250 255
Lys Ala Val Leu Thr Ser Gln Val Thr Glu Glu Ile Asn Val Asp Glu
260 265 270
Val Thr Glu Met Val Lys Gln Glu Val Lys Asp Ala Lys Leu Pro Glu
275 280 285

```

Asn

(2) INFORMATION FOR SEQ ID NO:1498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..557
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| actttacttt | tcggaggaa   | tagaaaattg | ggggctaggg | ttcgcaattg | tagttttcga  | 60  |
| gcgaagaaga | tgatcgaggt  | ggttctcaac | gatcggttag | ggaaaaaagt | taggggtgaag | 120 |
| tgtaacRgAt | gatgacacga  | tcggtgatct | gaagaagctt | gtcgcgggac | aaaccggaac  | 180 |
| acgagccgag | aagatcagaa  | ttcagaagt  | gtacaacatc | tacaaggatc | acatcaactc  | 240 |
| caaggactat | gagatccatg  | acggcatggg | tcttgagctt | tactacaact | aggccaatcg  | 300 |
| aaggagctaa | gctgaaggag  | tggtgttgat | ttggacacct | acataaaact | atatcaacca  | 360 |
| tgttacatct | aaaaaagaca  | caagtatgtt | gtaagacgtg | ataacttcaa | attttgggta  | 420 |
| ataataatc  | attcaactgtc | aatggtttta | aacccttcca | aattgtcaga | ttgattttctg | 480 |
| gttatctcta | agtttgtagt  | atattagctt | ttttggtgtg | attgatgtgc | tcttttccca  | 540 |
| aatgttacc  | atcttcc     |            |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:1499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Leu | Leu | Phe | Arg | Arg | Asn | Arg | Lys | Leu | Gly | Ala | Arg | Val | Arg | Asn |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Cys | Ser | Phe | Arg | Ala | Lys | Lys | Met | Ile | Glu | Val | Val | Leu | Asn | Asp | Arg |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Leu | Gly | Lys | Lys | Val | Arg | Val | Lys | Cys | Asn | Xaa |     |     |     |     |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1625 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1625
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:

|             |             |             |             |            |             |     |
|-------------|-------------|-------------|-------------|------------|-------------|-----|
| gagtaacatc  | gagacaaaga  | agaaaaagcta | aaaaaagagaa | ccccaaagaa | tcgaatatatt | 60  |
| attattttgc  | cccgaaagatt | ctattttctga | tcattttacac | ccctaaaaag | agtagagctt  | 120 |
| tcgtgaagcc  | accatgtgtg  | gaggagctat  | aatctccgat  | ttcatacctc | cgccgaggtc  | 180 |
| ctctccgcgc  | actaacgagt  | ttatctggcc  | ggatctgaaa  | aacaaagtga | aagcttcaaa  | 240 |
| gaagagatcg  | aataagcgat  | cgatctttct  | cgatcttgac  | gatgatttcg | aagctgattt  | 300 |
| ccaaggggtt  | aaggatgact  | cggtttttga  | ctcggaagac  | gatgatgatg | tcttgcgtcaa | 360 |
| tgttaaagcct | ttcgctcttca | ccgcaactac  | taagcccgtga | gtcttcgctt | tcgtctccac  | 420 |
| tgtaggttca  | gcataatgcca | agaaaactgt  | agagtcgcgt  | gagcaagctg | agaaatcttc  | 480 |
| taagaggaag  | aggaagaatc  | agtaccgagg  | gattagcgac  | cgctcctggg | gaaatagggg  | 540 |

|            |             |            |             |             |            |      |
|------------|-------------|------------|-------------|-------------|------------|------|
| tgccgagatc | cgtgatccgA  | aaaaaggctc | cgcagaatgg  | cttggaacat  | tcgacactgc | 600  |
| tgaggaagca | gcaagagcgt  | atgatgctgc | agcagcgaga  | atccgtggca  | cgaagactaa | 660  |
| ggtgaatttt | cccgaggaga  | agaaccctag | cgtcgtatcc  | cagaaaacgtc | cttagtctaa | 720  |
| gactaataat | cttcagaaat  | cagtggctaa | accaaacaaa  | agcgtaactt  | tggttcagca | 780  |
| gccaacacat | ctgagtcagc  | agtactgcaa | caactccttt  | gacaactctt  | ttgggtgat  | 840  |
| gagtttcatg | gaagagaagc  | ctcagatgta | caacaatcag  | tttgggttaa  | caaaactcgt | 900  |
| cgatgctgga | ggtaacaatg  | gataccagta | tttcagttcc  | gatcagggca  | gtaaactcct | 960  |
| cgactgttct | gagttcgggt  | ggagtgatca | cgccctaaa   | acacccgaga  | tctcttcaat | 1020 |
| gctgttcaat | aacaacgaag  | catcatttgt | tgaagaaacc  | aatgcagcca  | agaagctcaa | 1080 |
| acctaaactc | gatgagtcag  | acgatctgat | ggcatacctt  | gacaacgctt  | tgtgggacac | 1140 |
| ccactagtaa | gtgaaagcca  | tgcttggcgc | agatgctggt  | gctgtgactc  | aggaagagga | 1200 |
| aaaccagttg | gagctatgga  | gcttagatga | gatcaatttc  | atgctggaag  | gagacttttg | 1260 |
| aatgtagtga | tggttccctta | gtttgtaaat | aaagctgtgt  | tggattttgc  | tgttggggga | 1320 |
| tggtacaagt | cacacctcaa  | gctctatgca | ttggtatctc  | atgagocctc  | cttccataga | 1380 |
| gagtttctct | tttaattttg  | tcgaaataaa | aaaaggtgtga | tgaagtataa  | agaggtataa | 1440 |
| taatatctat | ctattaagtc  | ttgtttttgt | ctttcatttt  | tgtatttctt  | ttctatttaa | 1500 |
| aagaccagtt | attagctctc  | tgagctctct | ttttgatctt  | tggtatagcg  | tatcatcacc | 1560 |
| ctcgaaagtg | taattgtttt  | tacccccaaa | cttggtttagc | attataataa  | agtctctttg | 1620 |

gaacc

(2) INFORMATION FOR SEQ ID NO:1501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 375 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..375

(D) OTHER INFORMATION: / Ceres Seq. ID 1570202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1501:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Gly | Gly | Ala | Ile | Ile | Ser | Asp | Phe | Ile | Pro | Pro | Arg | Ser |
| 1   |     |     | 5   |     |     |     |     |     |     | 10  |     |     | 15  |     |
| Leu | Arg | Val | Thr | Asn | Glu | Phe | Ile | Trp |     | Pro | Asp | Leu | Lys | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  | Lys |
| Lys | Ala | Ser | Lys | Lys | Arg | Ser | Asn | Lys | Arg | Ser | Asp | Phe | Phe | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     | Leu |
| Asp | Asp | Asp | Phe | Glu | Ala | Asp | Phe | Gln | Gly | Phe | Lys | Asp | Asp | Ser |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     | Ala |
| Phe | Asp | Cys | Glu | Asp | Asp | Asp | Asp | Val | Phe | Val | Asn | Val | Lys | Pro |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Phe | Thr | Ala | Thr | Thr | Lys | Pro | Val | Ala | Ser | Ala | Phe | Val | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  | Thr |
| Val | Gly | Ser | Ala | Tyr | Ala | Lys | Lys | Thr | Val | Glu | Ser | Ala | Glu | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 | Ala |
| Glu | Lys | Ser | Ser | Lys | Arg | Lys | Arg | Lys | Asn | Gln | Tyr | Arg | Gly | Ile |
|     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     | Arg |
| Gln | Arg | Pro | Trp | Gly | Lys | Trp | Ala | Ala | Glu | Ile | Arg | Asp | Pro | Arg |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     | Lys |
| Gly | Ser | Arg | Glu | Trp | Leu | Gly | Thr | Phe | Asp | Thr | Ala | Glu | Glu | Ala |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg | Ala | Tyr | Asp | Ala | Ala | Ala | Arg | Arg | Ile | Arg | Gly | Thr | Lys | Ala |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 | Lys |
| Val | Asn | Phe | Pro | Glu | Glu | Lys | Asn | Pro | Ser | Val | Val | Ser | Gln | Lys |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 | Arg |
| Pro | Ser | Ala | Lys | Thr | Asn | Asn | Leu | Gln | Lys | Ser | Val | Ala | Lys | Pro |
|     |     |     | 195 |     |     | 200 |     |     |     |     | 205 |     |     | Asn |
| Lys | Ser | Val | Thr | Leu | Val | Gln | Gln | Pro | Thr | His | Leu | Ser | Gln | Gln |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     | Tyr |
| Cys | Asn | Asn | Ser | Phe | Asp | Asn | Ser | Phe | Gly | Asp | Met | Ser | Phe | Met |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | Glu |



Glu Lys Pro Gln Met Tyr Asn Asn Gln Phe Gly Leu Thr Asn Ser Phe  
245 250 255  
Asp Ala Gly Gly Asn Asn Gly Tyr Gln Tyr Phe Ser Ser Asp Gln Gly  
260 265 270  
Ser Asn Ser Phe Asp Cys Ser Glu Phe Gly Trp Ser Asp His Gly Pro  
275 280 285  
Lys Thr Pro Glu Ile Ser Ser Met Leu Val Asn Asn Asn Glu Ala Ser  
290 295 300  
Phe Val Glu Glu Thr Asn Ala Ala Lys Lys Leu Lys Pro Asn Ser Asp  
305 310 315 320  
Glu Ser Asp Asp Leu Met Ala Tyr Leu Asp Asn Ala Leu Trp Asp Thr  
325 330 335  
Pro Leu Glu Val Lys Ala Met Leu Gly Ala Asp Ala Gly Ala Val Thr  
340 345 350  
Gln Glu Glu Glu Asn Pro Val Glu Leu Trp Ser Leu Asp Glu Ile Asn  
355 360 365  
Phe Met Leu Glu Gly Asp Phe  
370 375

(2) INFORMATION FOR SEQ ID NO:1502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 996 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..996
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1502:

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| aatcaaat   | tttgcatt    | tttcaaat    | tttgagaaaa | tggtgagaag | taccaaaagg | 60  |
| cgctcagaaa | tagagatgaa  | aaaaatggaa  | aacgaaagca | accttcagg  | tactttctca | 120 |
| aaaagaagat | tcggtctttt  | caaaaaagct  | agtgaacttt | gcacattaa  | tggtgcagag | 180 |
| attctgttga | ttgtgttctc  | tcctgtgtgg  | aaagtgtttt | cttttggcca | tccaagtgtt | 240 |
| caagaactca | ttcatcgctt  | ttcgaatcct  | aaccataatt | ctgccattgt | ccatcatcag | 300 |
| aacaacaatc | tccaacttgt  | tgaaccctgt  | ccggatagaa | atatccaata | tctcaacaat | 360 |
| atactcactg | aggtgctggc  | aaaccaggaa  | aaggagaaac | agaagagaat | ggttttggac | 420 |
| ctattgaaag | aatccagaga  | acaagtagga  | aactggtatg | aaaaagatgt | gaagatctct | 480 |
| gacatgaatg | aaaccaacca  | gctgatattc  | gctcttcaag | atgtgaaaaa | gaactgggta | 540 |
| agagaaatgt | ctcaatattc  | tcaagtaaat  | gtttcgacga | attacttttg | tcaaaagtct | 600 |
| ggcgtgattg | gtgtgtgttaa | tggttgccatt | gatctttttg | atcaagaaga | aaatgcattc | 660 |
| aactataatc | caaacatggt  | gtttcccaat  | cataccacc  | caatgttttg | atacaacaat | 720 |
| gatggagttc | tcgttccgat  | atccaacatg  | aactacatgt | caagttacaa | cttcaaccag | 780 |
| agctagagtc | tgaagctaga  | agaacatcct  | aatcaaatat | tgcgttattt | tgctcatggt | 840 |
| tactgttagg | attgtttttg  | tattgtgaga  | cttaagtttg | ttttttcttt | taatttgggt | 900 |
| cagctgggtg | gtttttcaat  | ttattcgctg  | ttgtttttcc | tttgKttttc | ggatatattt | 960 |
| gtatccagaa | taaatattat  | tatcctttaa  | ttttac     |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..261
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1503:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Gln | Ile | Cys | His | Leu | Phe | Ile | Gln | Ile | Phe | Glu | Lys | Met | Val | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Ser Thr Lys Gly Arg Gln Lys Ile Glu Met Lys Lys Met Glu Asn Glu  
20 25 30  
Ser Asn Leu Gln Val Thr Phe Ser Lys Arg Arg Phe Gly Leu Phe Lys  
35 40 45  
Lys Ala Ser Glu Leu Cys Thr Leu Ser Gly Ala Glu Ile Leu Leu Ile  
50 55 60  
Val Phe Ser Pro Gly Gly Lys Val Phe Ser Phe Gly His Pro Ser Val  
65 70 75 80  
Gln Glu Leu Ile His Arg Phe Ser Asn Pro Asn His Asn Ser Ala Ile  
85 90 95  
Val His His Gln Asn Asn Asn Leu Gln Leu Val Glu Thr Arg Pro Asp  
100 105 110  
Arg Asn Ile Gln Tyr Leu Asn Asn Ile Leu Thr Glu Val Leu Ala Asn  
115 120 125  
Gln Glu Lys Glu Lys Gln Lys Arg Met Val Leu Asp Leu Leu Lys Glu  
130 135 140  
Ser Arg Glu Gln Val Gly Asn Trp Tyr Glu Lys Asp Val Lys Asp Leu  
145 150 155 160  
Asp Met Asn Glu Thr Asn Gln Leu Ile Ser Ala Leu Gln Asp Val Lys  
165 170 175  
Lys Lys Leu Val Arg Glu Met Ser Gln Tyr Ser Gln Val Asn Val Ser  
180 185 190  
Gln Asn Tyr Phe Gly Gln Ser Ser Gly Val Ile Gly Gly Gly Asn Val  
195 200 205  
Gly Ile Asp Leu Phe Asp Gln Arg Arg Asn Ala Phe Asn Tyr Asn Pro  
210 215 220  
Asn Met Val Phe Pro Asn His Thr Pro Pro Met Phe Gly Tyr Asn Asn  
225 230 235 240  
Asp Gly Val Leu Val Pro Ile Ser Asn Met Asn Tyr Met Ser Ser Tyr  
245 250 255  
Asn Phe Asn Gln Ser  
260

(2) INFORMATION FOR SEQ ID NO:1504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..248

(D) OTHER INFORMATION: / Ceres Seq. ID 1570229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1504:

Met Val Arg Ser Thr Lys Gly Arg Gln Lys Ile Glu Met Lys Lys Met  
1 5 10 15  
Glu Asn Glu Ser Asn Leu Gln Val Thr Phe Ser Lys Arg Arg Phe Gly  
20 25 30  
Leu Phe Lys Lys Ala Ser Glu Leu Cys Thr Leu Ser Gly Ala Glu Ile  
35 40 45  
Leu Leu Ile Val Phe Ser Pro Gly Gly Lys Val Phe Ser Phe Gly His  
50 55 60  
Pro Ser Val Gln Glu Leu Ile His Arg Phe Ser Asn Pro Asn His Asn  
65 70 75 80  
Ser Ala Ile Val His His Gln Asn Asn Asn Leu Gln Leu Val Glu Thr  
85 90 95  
Arg Pro Asp Arg Asn Ile Gln Tyr Leu Asn Asn Ile Leu Thr Glu Val  
100 105 110  
Leu Ala Asn Gln Glu Lys Glu Lys Gln Lys Arg Met Val Leu Asp Leu  
115 120 125  
Leu Lys Glu Ser Arg Glu Gln Val Gly Asn Trp Tyr Glu Lys Asp Val

(2) INFORMATION FOR SEQ ID NO:1505:

(A) LENGTH: 236 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

## {A} NAM

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:1505:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   | Lys | Lys | Asn | 5   | Asn | Glu | Ser | Asn | 10  | Gln | Val | Thr | Phe | Ser | Lys |
| Arg | Arg | Phe | Gly | Leu | Phe | Lys | Lys | Ala | Ser | Glu | Leu | Cys | Thr | Leu | Ser |
| Gly | Ala | Glu | Ile | Leu | Leu | Ile | Val | Phe | Ser | Pro | Gly | Gly | Lys | Val | Phe |
| Ser | Phe | Gly | His | Pro | Ser | Val | Gln | Glu | Leu | Ile | His | Arg | Phe | Ser | Asn |
| Pro | Asn | His | Asn | Ser | Ala | Ile | Val | His | His | Gln | Asn | Asn | Asn | Leu | Gln |
| Leu | Val | Glu | Thr | Arg | Pro | Asp | Arg | Asn | Ile | Gln | Tyr | Leu | Asn | Asn | Ile |
| Leu | Thr | Glu | Val | Leu | Ala | Asn | Gln | Glu | Lys | Glu | Lys | Gln | Lys | Arg | Met |
| Val | Leu | Asp | Ile | Leu | Lys | Glu | Ser | Arg | Glu | Gln | Val | Gly | Asn | Trp | Tyr |
| Glu | Lys | Asp | Val | Lys | Asp | Leu | Asp | Met | Asn | Glu | Thr | Asn | Gln | Leu | Ile |
| Ser | Ala | Leu | Gln | Asp | Val | Lys | Lys | Lys | Leu | Val | Arg | Glu | Met | Ser | Gln |
| Tyr | Ser | Gln | Val | Asn | Val | Ser | Gln | Asn | Tyr | Phe | Gly | Gln | Ser | Ser | Gly |
| Val | Ile | Gly | Gly | Gly | Asn | Val | Gly | Ile | Asp | Leu | Phe | Asp | Gln | Arg | Arg |
| Asn | Ala | Phe | Asn | Tyr | Asn | Pro | Asn | Met | Val | Phe | Pro | Asn | His | Thr | Pro |
| Pro | Met | Phe | Gly | Tyr | Asn | Asn | Asp | Gly | Val | Leu | Val | Pro | Ile | Ser | Asn |
| Met | Asn | Tyr | Met | Ser | Ser | Tyr | Asn | Phe | Asn | Gln | Ser |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1506:

(A) LENGTH: 1062 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1062  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570235  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1506:  
aaaaaaattt gttcgtattct cattctctctt ctacacagtcg taaacccctaa aaaaaaaaca 60  
gagaaatcaa atttcaatct cgaaggatct acaaaagaagc atgacgacgc gagatctcgt 120  
taatatccat cctactgacg ttaaatctccc ctttgagttg aagaaaacaa gttcgtgttc 180  
gatgcaattg accaacaaga caactactca atgtgtcgtc ttaagagtta aaacaaccaa 240  
tcctcgcaaa tactgtgttc gtcctaacac tgggtgtgtc ttgcccggtg attctcgtca 300  
tgttacagtg acgatgcaag cccagaaaga ggcaccactt gatatgcaat gcaaaagaca 360  
gttccttgtt cagactgtgt ttgtctctga tggctactact tccaaagaag tctcgtctga 420  
aatgttcaac aaggaggctg gtatagatgt tgaggatttc aaactgcgag ttgtttacat 480  
tcctgtcta cctccttcac ctgtcctctga aggttctgaa gaaggcaact cctcatgtgc 540  
ttcctcaac gatattgcct ctcaatctgc ctcaactctt gatgacgtgt caaaaacgtt 600  
tgaagaaaca agtgagaaat cttcabaggc atggctctat atttccaaat tgacggagga 660  
gaagactctt gctactcaac aaagtacaga gctcgtctct gaactggaaa tgcgtaggaa 720  
agaaacAaag caagaacgag tcgggtgggtc attcctgtct cttgatgctg ctggtgggtc 780  
tgctcgtgtt cgtgatgtgc tactatttga accggatata aacgccatgg ggtagcttc 840  
atcatccttt taatcatcaa atcttgcaaa gttcttaaga tttttgacca gattttcgta 900  
aaayggcgtt ggtttttttt taaaagttc atatttaagc tgtaaaatca gtatcgttag 960  
cacaggaaca ggtgtgattt tgtggcaggt tctctgttat tgatttaaac acactttcga 1020  
(2) INFORMATION FOR SEQ ID NO:1507:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 250 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..250  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1570236  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1507:  
Met Thr Thr Gly Asp Leu Val Asn Ile His Pro Thr Glu Leu Lys Phe  
1 5 10 15  
Pro Phe Glu Leu Lys Lys Gln Ser Ser Cys Ser Met Gln Leu Thr Asn  
20 25 30  
Lys Thr Thr Thr Gln Cys Val Ala Phe Lys Val Lys Thr Thr Asn Pro  
35 40 45  
Arg Lys Tyr Cys Val Arg Pro Asn Thr Gly Val Val Leu Pro Gly Asp  
50 55 60  
Ser Cys Asn Val Thr Val Thr Met Gln Ala Gln Lys Glu Ala Pro Leu  
65 70 75 80  
Asp Met Gln Cys Lys Asp Lys Phe Leu Val Gln Thr Val Val Val Ser  
85 90 95  
Asp Gly Thr Thr Ser Lys Glu Val Leu Ala Glu Met Phe Asn Lys Glu  
100 105 110  
Ala Gly Arg Val Ile Glu Asp Phe Lys Leu Arg Val Val Tyr Ile Pro  
115 120 125  
Ala Asn Pro Pro Ser Pro Val Pro Glu Gly Ser Glu Gly Asn Ser  
130 135 140  
Pro Met Ala Ser Leu Asn Asp Ile Ala Ser Gln Ser Ala Ser Leu Phe  
145 150 155 160  
Asp Asp Val Ser Lys Thr Phe Glu Glu Thr Ser Glu Lys Ser Ser Xaa  
165 170 175  
Ala Trp Ser Met Ile Ser Lys Leu Thr Glu Lys Thr Ser Ala Thr

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 180 |     | 185 |     | 190 |     |     |     |     |     |     |     |     |     |     |
| Gln | Gln | Ser | Gln | Lys | Leu | Arg | Leu | Glu | Met | Leu | Arg | Lys | Glu |     |     |
|     | 195 |     | 200 |     | 205 |     |     |     |     |     |     |     |     |     |     |
| Thr | Lys | Gln | Glu | Ala | Val | Gly | Trp | Ser | Phe | Leu | Ala | Leu | Asp | Ala | Ala |
|     | 210 |     | 215 |     | 220 |     |     |     |     |     |     |     |     |     |     |
| Gly | Gly | Ser | Ala | Arg | Leu | Arg | Asp | Trp | Leu | Leu | Ile | Glu | Pro | Asp | Ile |
|     | 225 |     | 230 |     | 235 |     |     |     |     |     |     |     |     | 240 |     |
| Asn | Ala | Met | Gly | Leu | Ala | Ser | Ser | Ser | Phe |     |     |     |     |     |     |
|     |     |     | 245 |     | 250 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1570237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1508:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Leu | Thr | Asn | Lys | Thr | Thr | Thr | Gln | Cys | Val | Ala | Phe | Lys | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Thr | Thr | Asn | Pro | Arg | Lys | Tyr | Cys | Val | Arg | Pro | Asn | Thr | Gly | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Leu | Pro | Gly | Asp | Ser | Cys | Asn | Val | Thr | Val | Thr | Met | Gln | Ala | Gln |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Lys | Glu | Ala | Pro | Leu | Asp | Met | Gln | Cys | Lys | Asp | Lys | Phe | Leu | Val | Gln |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Thr | Val | Val | Val | Ser | Asp | Gly | Thr | Thr | Ser | Lys | Glu | Val | Leu | Ala | Glu |
|     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |     |
| Met | Phe | Asn | Lys | Glu | Ala | Gly | Arg | Val | Ile | Glu | Asp | Phe | Lys | Leu | Arg |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Val | Val | Tyr | Ile | Pro | Ala | Asn | Pro | Pro | Ser | Pro | Val | Pro | Glu | Gly | Ser |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Glu | Glu | Gly | Asn | Ser | Pro | Met | Ala | Ser | Leu | Asn | Asp | Ile | Ala | Ser | Gln |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ser | Ala | Ser | Leu | Phe | Asp | Asp | Val | Ser | Lys | Thr | Phe | Glu | Glu | Thr | Ser |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Glu | Lys | Ser | Ser | Xaa | Ala | Trp | Ser | Met | Ile | Ser | Lys | Leu | Thr | Glu | Glu |
|     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Lys | Thr | Ser | Ala | Thr | Gln | Gln | Ser | Gln | Lys | Leu | Arg | Leu | Glu | Leu | Glu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Met | Leu | Arg | Lys | Glu | Thr | Lys | Gln | Glu | Ala | Val | Gly | Trp | Ser | Phe | Leu |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ala | Leu | Asp | Ala | Ala | Gly | Gly | Ser | Ala | Arg | Leu | Arg | Asp | Trp | Leu | Leu |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ile | Glu | Pro | Asp | Ile | Asn | Ala | Met | Gly | Leu | Ala | Ser | Ser | Ser | Phe |     |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1509:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1570238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1509:

Met Gln Ala Gln Lys Glu Ala Pro Leu Asp Met Gln Cys Lys Asp Lys  
1 5 10 15  
Phe Leu Val Gln Thr Val Val Val Ser Asp Gly Thr Thr Ser Lys Glu  
20 25 30  
Val Leu Ala Glu Met Phe Asn Lys Glu Ala Gly Arg Val Ile Glu Asp  
35 40 45  
Phe Lys Leu Arg Val Val Tyr Ile Pro Ala Asn Pro Pro Ser Pro Val  
50 55 60  
Pro Glu Gly Ser Glu Glu Gly Asn Ser Pro Met Ala Ser Leu Asn Asp  
65 70 75 80  
Ile Ala Ser Gln Ser Ala Ser Leu Phe Asp Asp Val Ser Lys Thr Phe  
85 90 95  
Glu Glu Thr Ser Glu Lys Ser Ser Xaa Ala Trp Ser Met Ile Ser Lys  
100 105 110  
Leu Thr Glu Glu Lys Thr Ser Ala Thr Gln Gln Ser Gln Lys Leu Arg  
115 120 125  
Leu Glu Leu Glu Met Leu Arg Lys Glu Thr Lys Gln Glu Ala Val Gly  
130 135 140  
Trp Ser Phe Leu Ala Leu Asp Ala Ala Gly Gly Ser Ala Arg Leu Arg  
145 150 155 160  
Asp Trp Leu Leu Ile Glu Pro Asp Ile Asn Ala Met Gly Leu Ala Ser  
165 170 175  
Ser Ser Phe

(2) INFORMATION FOR SEQ ID NO:1510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1224
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1510:

|             |            |            |             |             |             |      |
|-------------|------------|------------|-------------|-------------|-------------|------|
| atcaagtttaa | aaaaaaaaa  | gaaggagaaa | tggcaataag  | ttttagaact  | ctagctcttt  | 60   |
| tgacctctc   | ggtgttacta | atttccatat | ctctcggcgt  | cgctcacagca | acagagtcgc  | 120  |
| agaggaatga  | aggggggggt | cttacaatgt | acgagcaatg  | gcttgtagag  | aatgggaagt  | 180  |
| aactataacg  | gtcttgagga | gaaggagaga | cggttcaaga  | tcttcгаааа  | caacttgaag  | 240  |
| cgcatcgaga  | aacacaattc | agatccaaac | cggaagttat  | aacgcgggtt  | gaacaagttt  | 300  |
| tcggatctaa  | cggctgatga | gtttcaagct | agttacttag  | gtgggaagat  | ggaaaagaaa  | 360  |
| agccatcag   | atgtagcggg | gaggtatcag | tacaaagaag  | gagatgtttt  | acctgatgaa  | 420  |
| gttgattgga  | gggagagagg | agcagttggt | ccaagagtca  | aaagacaagg  | agagtgtgga  | 480  |
| agttgtggg   | cgtttgcgcg | gactgagcgg | tggaaaggtat | aaaccagatc  | acaaccggag  | 540  |
| aattagtaac  | tttatcggaa | caagaactca | ttgactgcga  | tagagggaac  | gacaactttg  | 600  |
| gatgtgctgg  | tggttgagca | gtatgggcct | ttgagttcat  | taaggagaac  | ggtgtattg   | 660  |
| tatccatcag  | agtttatggt | tataccgggt | aagatactgc  | cgcatgcaag  | gccattgaga  | 720  |
| tgaaaaccac  | tcgggttggt | accattaatg | gtcatgaggt  | tgttccctga  | aacgatgaga  | 780  |
| gtcttttgaa  | gaagctggtt | gcttatcaac | ctattagtgt  | tatgatatac  | gctgaaacaa  | 840  |
| tgagcgaata  | caaatctggt | gtgtataaag | gagcatgtag  | taattttgtg  | ggagatcaca  | 900  |
| atgtgctaata | tggtgggtat | ggaacatcat | cagatgaagg  | agactactgg  | cttattcgtga | 960  |
| attctctggg  | vccagagtg  | ggagaaggcg | ggatccttag  | gcttcaacgt  | aacttccatg  | 1020 |
| aaccaaccgg  | gaatgtgca  | gtcgtgtgag | ctctgtgata  | cccaatacag  | tcgaactctt  | 1080 |
| catctcatit  | gttctctcca | agtgtgttta | aattggttgt  | tttattttgt  | tttcagttgt  | 1140 |
| ttagtttgcc  | cttgccttga | aataactttt | tatcgtgtgt  | caagttcgtt  | ggtttttggt  | 1200 |
| ttataaaagg  | aaacaagatt | cgctc      |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..126  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1513:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | Lys | Lys | Ala | Val | Ala | Tyr | Gln | Pro | Ile | Ile | Ser | Val | Met | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Ala | Ala | Asn | Met | Ser | Asp | Tyr | Lys | Ser | Gly | Val | Tyr | Lys | Gly | Ala |     |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |     |
| Cys | Ser | Asn | Leu | Trp | Gly | Asp | His | Asn | Val | Leu | Ile | Val | Gly | Tyr | Gly |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |     |
| Thr | Ser | Ser | Asp | Glu | Gly | Asp | Tyr | Trp | Leu | Ile | Arg | Asn | Ser | Trp | Xaa |     |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |     |
| Pro | Glu | Trp | Gly | Glu | Gly | Tyr | Leu | Arg | Leu | Gln | Arg | Asn | Phe | His |     |     |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |     |
| Glu | Pro | Thr | Gly | Lys | Cys | Ala | Val | Ala | Val | Ala | Pro | Val | Tyr | Pro | Ile |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |
| Lys | Ser | Asn | Ser | Ser | Ser | His | Leu | Leu | Ser | Pro | Ser | Val | Phe | Lys | Leu |     |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |     |
| Val | Val | Leu | Phe | Val | Phe | Gln | Leu | Ile | Ser | Leu | Ala | Leu | Leu |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1514:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1387 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
    (B) LOCATION: 1..1387  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1514:

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| acgttctcag  | agttagttac  | acagcttttca | acgatgaatc | agctcgcgct  | ttcaagatccc | 60   |
| ggttacaccg  | ccgcggtgag  | gtttctccct  | atgctttccg | cagctgttcc  | gaagatcttta | 120  |
| tcatctctcg  | ccgcgcgcac  | caccgtccgc  | aacttcagct | ctaccggaga  | tcctctcacc  | 180  |
| agctacaaaa  | tcaataaaac  | tgcgcgtca   | aaatccttca | cttccaggct  | ttccaccaa   | 240  |
| tcctctcccg  | ccggtactcc  | tccgcaacaa  | cttttcggcg | cccgtagctt  | ctcatctccc  | 300  |
| agcagtgaat  | tcaacagcta  | caacattaat  | ccgcggtcta | actggggaat  | ccgaatcgct  | 360  |
| ccggagagga  | aagcttgtgt  | gattgagcgg  | tttggtaaa  | tccacacgac  | ttgcccgcgc  | 420  |
| gggattcaact | tccttgttcc  | gtttgtggat  | cgtatcgctt | atgttcattc  | ttcaaaaggaa | 480  |
| gaagcgattc  | ctattgttaa  | tcagactcgc  | attacaaagg | ataacggttag | cattccacatc | 540  |
| gatgtgtttc  | tctacgttaa  | gattgtggat  | cctaagtgtg | cttcttatgg  | cggtgagaaat | 600  |
| ccgatctatg  | ctgttatgca  | gttggctcag  | actacaatgc | gtagtgcgct  | cggtaaaatt  | 660  |
| actctttgca  | agacttttga  | ggaacgggac  | actctcaatg | agaagattgt  | ggaagccatc  | 720  |
| aatgttgttg  | caaaaagattg | gggtcttcag  | tgccttagtt | atgagatcag  | ggatatcatg  | 780  |
| ctctcctaag  | gagtgagagt  | tgctatggaa  | atgcaagctg | aagctgaacg  | taaaaagaga  | 840  |
| gccacagattc | ttgagttctga | aggagaacctg | caagcccata | tcaatagagc  | tgatgtgaag  | 900  |
| aaaagtcttg  | taatcttgga  | atcagaagct  | gcaatgatgg | accaagtcaa  | tcgtgcacaa  | 960  |
| ggtgagctcg  | aagcaaatatt | agctagagca  | caagcaacag | ccaaRgggac  | tgccatgggt  | 1020 |
| atctcaatcc  | ctcaagggaag | ctgggtggaga | ggagcgctcg | agtttgagag  | ttcgggagcta | 1080 |
| atacattccaa | gcttttggca  | aaattgctaa  | ggagggtaca | acaatcgtcg  | ttYccgagta  | 1140 |
| atgtcgacaa  | tcctgctagc  | atgatcgctc  | aAgcttttag | aatgtacaaa  | ggcttgtcaa  | 1200 |
| caaaaggtccc | aacagtgggt  | tcagggaacc  | ttctggagta | gaatcctcta  | ctaacgtgggt | 1260 |
| tgttgccaaa  | cttgaaatga  | agctataatg  | tagctgaacc | tagggaacaa  | ctattctttt  | 1320 |
| gattgtgcc   | ggcttttagc  | cattttcagt  | ttgtttattt | cttcatatga  | gaaacagtta  | 1380 |
| ttttacc     |             |             |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1515:

- (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 369 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..369  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1515:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Ser | Glu | Leu | Val | Thr | Gln | Leu | Ser | Thr | Met | Asn | Gln | Leu | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Ser | Arg | Ser | Gly | Tyr | Thr | Ala | Ala | Val | Arg | Phe | Leu | Pro | Met | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ala | Ala | Val | Pro | Lys | Ile | Leu | Ser | Ser | Leu | Ala | Ala | Ala | Ser | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Arg | Asn | Phe | Ser | Ser | Thr | Gly | Ser | Pro | Leu | Thr | Ser | Tyr | Gln | Ile |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Asn | Lys | Pro | Ser | Pro | Ser | Lys | Ser | Phe | Thr | Ser | Arg | Leu | Leu | His | Gln |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Ser | Ser | Ala | Gly | Thr | Pro | Pro | Gln | Gln | Leu | Phe | Gly | Ala | Arg | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Ser | Ser | Pro | Ser | Ser | Asp | Phe | Asn | Ser | Tyr | His | Ile | Asn | Pro | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Asn | Trp | Gly | Ile | Arg | Ile | Val | Pro | Glu | Arg | Lys | Ala | Cys | Val | Ile |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Arg | Phe | Gly | Lys | Phe | His | Thr | Thr | Leu | Pro | Ala | Gly | Ile | His | Phe |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Leu | Val | Pro | Phe | Val | Asp | Arg | Ile | Ala | Tyr | Val | His | Ser | Leu | Lys | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Glu | Ala | Ile | Pro | Ile | Gly | Asn | Gln | Thr | Ala | Ile | Thr | Lys | Asp | Asn | Val |
|     |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |     |
| Ser | Ile | His | Ile | Asp | Gly | Phe | Leu | Tyr | Val | Lys | Ile | Val | Asp | Pro | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Ala | Ser | Tyr | Gly | Val | Glu | Asn | Pro | Ile | Tyr | Ala | Val | Met | Gln | Leu |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     | 205 |     |     |     |
| Ala | Gln | Thr | Thr | Met | Arg | Ser | Glu | Leu | Gly | Lys | Ile | Thr | Leu | Asp | Lys |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Thr | Phe | Glu | Glu | Arg | Asp | Thr | Leu | Asn | Glu | Lys | Ile | Val | Glu | Ala | Ile |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Asn | Val | Ala | Ala | Lys | Asp | Trp | Gly | Leu | Gln | Cys | Leu | Ser | Tyr | Glu | Ile |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Arg | Asp | Ile | Met | Pro | Pro | Asn | Gly | Val | Arg | Val | Ala | Met | Glu | Met | Gln |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Ala | Glu | Ala | Glu | Arg | Lys | Lys | Arg | Ala | Gln | Ile | Leu | Glu | Ser | Glu | Gly |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Glu | Arg | Gln | Ala | His | Ile | Asn | Arg | Ala | Asp | Gly | Lys | Lys | Ser | Ser | Val |
|     |     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |
| Ile | Leu | Glu | Ser | Glu | Ala | Ala | Met | Met | Asp | Gln | Val | Asn | Arg | Ala | Gln |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Gly | Glu | Ala | Glu | Ala | Ile | Leu | Ala | Arg | Ala | Gln | Ala | Thr | Ala | Xaa | Gly |
|     |     |     |     | 325 |     |     |     |     |     | 330 |     |     |     | 335 |     |
| Thr | Gly | His | Gly | Ile | Ser | Ile | Pro | Gln | Gly | Ser | Trp | Trp | Arg | Gly | Gly |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Cys | Glu | Phe | Glu | Ser | Cys | Gly | Ala | Ile | His | Ser | Ser | Phe | Trp | Gln | Asn |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |

Cys

(2) INFORMATION FOR SEQ ID NO:1516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..358  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570249  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1516:  
Met Asn Gln Leu Ala Leu Ser Arg Ser Gly Tyr Thr Ala Ala Val Arg  
1                  5                  10                  15  
Phe Leu Pro Met Leu Ser Ala Ala Val Pro Lys Ile Leu Ser Ser Leu  
                  20                  25                  30  
Ala Ala Ala Ser Thr Val Arg Asn Phe Ser Ser Thr Gly Ser Pro Leu  
                  35                  40                  45  
Thr Ser Tyr Gln Ile Asn Lys Pro Ser Pro Ser Lys Ser Phe Thr Ser  
                  50                  55                  60  
Arg Leu Leu His Gln Ser Ser Ser Ala Gly Thr Pro Pro Gln Gln Leu  
65                  70                  75                  80  
Phe Gly Ala Arg Ser Phe Ser Ser Pro Ser Ser Asp Phe Asn Ser Tyr  
                  85                  90                  95  
His Ile Asn Pro Pro Ser Asn Trp Gly Ile Arg Ile Val Pro Glu Arg  
                  100                 105                 110  
Lys Ala Cys Val Ile Glu Arg Phe Gly Lys Phe His Thr Thr Leu Pro  
                  115                 120                 125  
Ala Gly Ile His Phe Leu Val Pro Phe Val Asp Arg Ile Ala Tyr Val  
                  130                 135                 140  
His Ser Leu Lys Glu Glu Ala Ile Pro Ile Gly Asn Gln Thr Ala Ile  
145                 150                 155                 160  
Thr Lys Asp Asn Val Ser Ile His Ile Asp Gly Phe Leu Tyr Val Lys  
                  165                 170                 175  
Ile Val Asp Pro Lys Leu Ala Ser Tyr Gly Val Glu Asn Pro Ile Tyr  
                  180                 185                 190  
Ala Val Met Gln Leu Ala Gln Thr Thr Met Arg Ser Glu Leu Gly Lys  
                  195                 200                 205  
Ile Thr Leu Asp Lys Thr Phe Glu Glu Arg Asp Thr Leu Asn Glu Lys  
                  210                 215                 220  
Ile Val Glu Ala Ile Asn Val Ala Ala Lys Asp Trp Gly Leu Gln Cys  
225                 230                 235                 240  
Leu Ser Tyr Glu Ile Arg Asp Ile Met Pro Pro Asn Gly Val Arg Val  
                  245                 250                 255  
Ala Met Glu Met Gln Ala Glu Ala Glu Arg Lys Lys Arg Ala Gln Ile  
                  260                 265                 270  
Leu Glu Ser Glu Gly Glu Arg Gln Ala His Ile Asn Arg Ala Asp Gly  
                  275                 280                 285  
Lys Lys Ser Ser Val Ile Leu Glu Ser Glu Ala Ala Met Met Asp Gln  
                  290                 295                 300  
Val Asn Arg Ala Gln Gly Glu Ala Glu Ala Ile Leu Ala Arg Ala Gln  
305                 310                 315                 320  
Ala Thr Ala Xaa Gly Thr Gly His Gly Ile Ser Ile Pro Gln Gly Ser  
                  325                 330                 335  
Trp Trp Arg Gly Gly Cys Glu Phe Glu Ser Cys Gly Ala Ile His Ser  
                  340                 345                 350  
Ser Phe Trp Gln Asn Cys  
                  355  
(2) INFORMATION FOR SEQ ID NO:1517:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 339 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..339

(D) OTHER INFORMATION: / Ceres Seq. ID 1570250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1517:

Met Leu Ser Ala Ala Val Pro Lys Ile Leu Ser Ser Leu Ala Ala Ala  
1 5 10 15  
Ser Thr Val Arg Asn Phe Ser Ser Thr Gly Ser Pro Leu Thr Ser Tyr  
20 25 30  
Gln Ile Asn Lys Pro Ser Pro Ser Lys Ser Phe Thr Ser Arg Leu Leu  
35 40 45  
His Gln Ser Ser Ser Ala Gly Thr Pro Pro Gln Gln Leu Phe Gly Ala  
50 55 60  
Arg Ser Phe Ser Ser Pro Ser Ser Asp Phe Asn Ser Tyr His Ile Asn  
65 70 75 80  
Pro Pro Ser Asn Trp Gly Ile Arg Ile Val Pro Glu Arg Lys Ala Cys  
85 90 95  
Val Ile Glu Arg Phe Gly Lys Phe His Thr Thr Leu Pro Ala Gly Ile  
100 105 110  
His Phe Leu Val Pro Phe Val Asp Arg Ile Ala Tyr Val His Ser Leu  
115 120 125  
Lys Glu Glu Ala Ile Pro Ile Gly Asn Gln Thr Ala Ile Thr Lys Asp  
130 135 140  
Asn Val Ser Ile His Ile Asp Gly Phe Leu Tyr Val Lys Ile Val Asp  
145 150 155 160  
Pro Lys Leu Ala Ser Tyr Gly Val Glu Asn Pro Ile Tyr Ala Val Met  
165 170 175  
Gln Leu Ala Gln Thr Thr Met Arg Ser Glu Leu Gly Lys Ile Thr Leu  
180 185 190  
Asp Lys Thr Phe Glu Glu Arg Asp Thr Leu Asn Glu Lys Ile Val Glu  
195 200 205  
Ala Ile Asn Val Ala Ala Lys Asp Trp Gly Leu Gln Cys Leu Ser Tyr  
210 215 220  
Glu Ile Arg Asp Ile Met Pro Pro Asn Gly Val Arg Val Ala Met Glu  
225 230 235 240  
Met Gln Ala Glu Ala Glu Arg Lys Lys Arg Ala Gln Ile Leu Glu Ser  
245 250 255  
Glu Gly Glu Arg Gln Ala His Ile Asn Arg Ala Asp Gly Lys Lys Ser  
260 265 270  
Ser Val Ile Leu Glu Ser Glu Ala Ala Met Met Asp Gln Val Asn Arg  
275 280 285  
Ala Gln Gly Glu Ala Glu Ala Ile Leu Ala Arg Ala Gln Ala Thr Ala  
290 295 300  
Xaa Gly Thr Gly His Gly Ile Ser Ile Pro Gln Gly Ser Trp Trp Arg  
305 310 315 320  
Gly Gly Cys Glu Phe Glu Ser Cys Gly Ala Ile His Ser Ser Phe Thr  
325 330 335  
Gln Asn Cys

(2) INFORMATION FOR SEQ ID NO:1518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1412 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1412

(D) OTHER INFORMATION: / Ceres Seq. ID 1570265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1518:

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| actccgagcg  | tttctcttct  | cacaagccaa | tgggcgcaatt | tactaattcc  | atcaattatc  | 60   |
| tcttttctgt  | ttctctctta  | tattttgtat | cgttccactg  | cttatgtttt  | cggttttcat  | 120  |
| tggttgacgc  | ttgttcaaac  | tccaccgacg | accaacagat  | tcaacaccat  | caccaccgga  | 180  |
| aatgggttgg  | tccctcagcg  | cacaaagtca | tcaccgtctc  | acttaaccgc  | cacgctcagt  | 240  |
| ttcgctccgt  | ccaagacgct  | gtggattcca | taccaaaagv  | caataaacaag | agcatcaca   | 300  |
| tcaagattgc  | tcccggtatt  | tacagagaga | aagtgtgtgt  | tccagctaca  | aaaccgtaca  | 360  |
| tAaacgttca  | aaggagctgg  | tagggatgtg | accgctatag  | agtggcacga  | cagctgcgtcc | 420  |
| gaccttggcg  | ctaacggtca  | acagttaact | acctatcaaa  | ccgcttccgt  | caccgtctac  | 480  |
| gctaattatt  | tcaccgctag  | aaacattagc | ttcacgggtac | tctattcaat  | tctaacgcga  | 540  |
| tatatatat   | agggaaactt  | tacaaaaaat | gcgagtcott  | ctttatttta  | ttttaaattg  | 600  |
| tgaagaatac  | tgccgcggct  | ccattgcccg | ggatgcgaag  | gtggcgaagc  | gtggcgttta  | 660  |
| ggatctccgg  | cgacaaagct  | ttcttttccg | gctgcgggtt  | ttacggtgca  | caagacactt  | 720  |
| tatgcgacga  | tgctggccgt  | cattacttca | aggagtgtta  | cattgaagcg  | tctatcgact  | 780  |
| ttatctttgg  | taatggccgc  | tccatgtata | aagattgtga  | gttgcatcgc  | atagcggtcaa | 840  |
| gattcgggtg  | gatagccggc  | catggttaga | catgcccgga  | agagaaaaag  | ggtttcgcgt  | 900  |
| tcgtgggttg  | tcgggttaaca | ggtagcggtc | catgtacgt   | gggcccggcc  | atgggaCcaa  | 960  |
| tactcacgtca | tcgtttacgc  | ctacacttac | tttgatgctc  | tcgtcgcgtca | cggtgggttg  | 1020 |
| gacgattggg  | accacaactc  | caacaaaagc | aagacggcat  | ttttcggagt  | gtacaattgc  | 1080 |
| tatgggccaag | gagcagcgcg  | gacgagagcg | gtgtcttggg  | ctagagcttt  | ggactatgaa  | 1140 |
| tcggcccatc  | catttatcgc  | gttaagcttc | gttaatggga  | gacattggat  | cgcctcgtca  | 1200 |
| gatgctttaa  | caacttcaaa  | ccttggcggg | gtttcttttc  | ctaattctct  | ggttcctccc  | 1260 |
| agtcocaaag  | ctcaaaagct  | tactatatt  | ttatcattcg  | tttattcttt  | tattgtttta  | 1320 |
| ttttttccaa  | tttatttata  | cattgtgtga | tagtacaaca  | aagtattgct  | tcttcttcat  | 1380 |

ctgtatccat ttcagttaaa tgttttgagc tt

(2) INFORMATION FOR SEQ ID NO:1519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1570266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1519:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Glu | Arg | Phe | Leu | Ser | His | Lys | Pro | Met | Ala | Gln | Phe | Thr | Asn | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Asn | Tyr | Leu | Phe | Ser | Val | Ser | Leu | Leu | Phe | Val | Ser | Phe | His |     |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Leu | Cys | Phe | Arg | Phe | Ser | Leu | Val | Ala | Ala | Cys | Ser | Asn | Ser | Thr |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Asp | Asp | Gln | Gln | Ile | Gln | His | His | His | Arg | Lys | Trp | Val | Gly | Pro |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Gly | His | Lys | Val | Ile | Thr | Val | Ser | Leu | Asn | Gly | His | Ala | Gln | Phe |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| Arg | Ser | Val | Gln | Asp | Ala | Val | Asp | Ser | Ile | Pro | Lys | Xaa | Asn | Asn | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Ile | Thr | Ile | Lys | Ile | Ala | Pro | Gly | Phe | Tyr | Arg | Glu | Lys | Val | Val |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Val | Pro | Ala | Thr | Lys | Pro | Tyr | Ile | Asn | Val | Gln | Arg | Ser | Trp |     |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |

(2) INFORMATION FOR SEQ ID NO:1520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..175  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1520:

Met Pro Gly Arg Glu Asn Gly Phe Arg Val Arg Gly Leu Ser Gly Asn  
1 5 10 15  
Arg Tyr Gly Ser Ile Val Arg Gly Pro Gly His Gly Thr Asn Thr His  
20 25 30  
Val Ser Phe Thr Pro Thr Leu Thr Leu Met Leu Ser Ser Leu Thr Val  
35 40 45  
Val Gly Thr Ile Gly Thr Thr Asn Pro Thr Lys Ala Arg Arg His Phe  
50 55 60  
Ser Glu Cys Thr Ile Ala Met Gly Gln Glu Gln Arg Arg Glu Ala  
65 70 75 80  
Cys Leu Gly Leu Glu Leu Trp Thr Met Asn Arg Pro Ile His Leu Ser  
85 90 95  
Leu Arg Ala Ser Leu Met Gly Asp Ile Gly Ser Leu Leu Glu Met Leu  
100 105 110  
Asn Gln Leu Gln Thr Leu Ala Gly Phe Leu Phe Leu Ile Pro Arg Phe  
115 120 125  
Leu Pro Val Pro Ser Pro Lys Ser Leu Leu Tyr Phe Tyr His Ser Phe  
130 135 140  
Ile Ser Phe Ile Val Tyr Phe Phe Gln Phe Ile Tyr Thr Leu Cys Asp  
145 150 155 160  
Ser Thr Thr Lys Tyr Cys Phe Phe Phe Ile Cys Ile His Phe Ser  
165 170 175

(2) INFORMATION FOR SEQ ID NO:1521:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 134 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1570268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1521:

Met Leu Ser Ser Leu Thr Val Val Gly Thr Thr Asn Pro  
1 5 10 15  
Thr Lys Ala Arg Arg His Phe Ser Glu Cys Thr Ile Ala Met Gly Gln  
20 25 30  
Glu Gln Gln Arg Arg Glu Ala Cys Leu Gly Leu Glu Leu Trp Thr Met  
35 40 45  
Asn Arg Pro Ile His Leu Ser Leu Arg Ala Ser Leu Met Gly Asp Ile  
50 55 60  
Gly Ser Leu Leu Glu Met Leu Asn Gln Leu Gln Thr Leu Ala Gly Phe  
65 70 75 80  
Leu Phe Leu Ile Pro Arg Phe Leu Pro Val Pro Ser Pro Lys Ser Leu  
85 90 95  
Leu Tyr Phe Tyr His Ser Phe Ile Ser Phe Ile Val Tyr Phe Phe Gln  
100 105 110  
Phe Ile Tyr Thr Leu Cys Asp Ser Thr Thr Lys Tyr Cys Phe Phe Phe  
115 120 125  
Ile Cys Ile His Phe Ser  
130

(2) INFORMATION FOR SEQ ID NO:1522:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 973 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

000001-1000000000

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..973

(D) OTHER INFORMATION: / Ceres Seq. ID 1570289

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1522:

|            |            |             |             |             |             |     |
|------------|------------|-------------|-------------|-------------|-------------|-----|
| gaacaatatt | cacagagatt | ttcgatctta  | accgagaaaa  | ggaagaaatg  | gctgtgtccat | 60  |
| cgacaacttc | aaacgcacca | aagcagagga  | agagagtcga  | agcccgagact | agcagcaaca  | 120 |
| ctctactact | cttactgcgc | gctaaagacg  | gaagcgcttt  | cgctctctgt  | gaaggatgta  | 180 |
| acaagatgtg | agctgtagcg | cttaataaga  | tgcacaattg  | cagttctcgt  | gctaagatga  | 240 |
| gagtgaaatc | cgaagcaca  | gttggtgaga  | cacaagcaga  | ggctaagaag  | aagcctgcag  | 300 |
| agaagaagaa | gacaacatct | gatggaccta  | agccaaagag  | acttaagaaa  | accaatgatg  | 360 |
| agaagaagag | ctcttcaact | tcaaaacaagc | ccaagcgacc  | tctcactgcc  | ttctttatct  | 420 |
| tcatgagtga | tttccgtaaa | acgttttaagt | cagagcataa  | tggttcatta  | gctaagggatg | 480 |
| ctgcaaaagt | cggtggtgag | aagtggaaagt | ctttgactga  | ggaagagaag  | aaagtttatc  | 540 |
| tggtataaag | tgctgaactt | aaggcagagt  | ataAcaagtc  | actggaagc   | aatgatgctg  | 600 |
| atgaggaaga | ggaagatgag | gagaagcaat  | ctgatgatgt  | tgatgatgct  | gaggagaaac  | 660 |
| aagttgacga | tgatgatgaa | gttgaggaga  | aagaagttga  | gaacacagat  | gatgacaaga  | 720 |
| aagaagctga | aggttaagaa | gaggagggaag | aagagatgtt  | ggatgactac  | tagaaatggt  | 780 |
| atgtcgtctt | ttgtgggtct | agtcttactg  | aaatcggttt  | atctctaatc  | gttgcgatgc  | 840 |
| attgtaaatg | aagcctttat | tagtgaaggt  | agtttatattg | aagtttaagt  | gtgagcaagt  | 900 |
| ggtttttttg | tatttcactg | aaatggtaat  | gccttttgtt  | taaacaagta  | atgaagctta  | 960 |
| tgtttttcgt | ttt        |             |             |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1523:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1570290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1523:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ile | Phe | Thr | Glu | Ile | Phe | Asp | Leu | Asn | Arg | Glu | Lys | Glu | Glu | Met |
| 1   |     |     | 5   |     |     |     |     |     |     |     | 10  |     |     | 15  |     |
| Ala | Gly | Pro | Ser | Thr | Thr | Ser | Asn | Ala | Pro | Lys | Gln | Arg | Lys | Arg | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ala | Glu | Thr | Ser | Ser | Asn | Thr | Ser | Thr | Thr | Leu | Arg | Arg | Ala | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Gly | Ser | Ala | Phe | Ala | Leu | Cys | Glu | Gly | Cys | Asn | Lys | Ser | Val | Ala |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Val | Ala | Leu | Ile | Ser | Met | His | Asn | Cys | Ser | Leu | Asp | Ala | Lys | Ile | Arg |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Val | Asn | Leu | Glu | Ala | Gln | Val | Val | Glu | Thr | Gln | Ala | Glu | Ala | Lys | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Pro | Ala | Glu | Lys | Lys | Lys | Thr | Thr | Ser | Asp | Gly | Pro | Lys | Pro | Lys |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Arg | Leu | Lys | Lys | Thr | Asn | Asp | Glu | Lys | Lys | Ser | Ser | Ser | Thr | Ser | Asn |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Lys | Pro | Lys | Arg | Pro | Leu | Thr | Ala | Phe | Phe | Ile | Phe | Met | Ser | Asp | Phe |
|     |     |     | 130 |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Arg | Lys | Thr | Phe | Lys | Ser | Glu | His | Asn | Gly | Ser | Leu | Ala | Lys | Asp | Ala |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Ala | Lys | Ile | Gly | Gly | Glu | Lys | Trp | Lys | Ser | Leu | Thr | Glu | Glu | Glu | Lys |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Lys | Val | Tyr | Leu | Asp | Lys | Ala | Ala | Glu | Leu | Lys | Ala | Glu | Tyr | Asn | Lys |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Ser | Leu | Glu | Ser | Asn | Asp | Ala | Asp | Glu | Glu | Glu | Asp | Glu | Glu | Lys |     |

(2) INFORMATION FOR SEO ID NO:1524:

(A) LENGTH: 241 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(1x) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..241

(D) OTHER INFORMATION: / Ceres Seq. ID 1570291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1524:

(2) INFORMATION FOR SEQ ID NO:1525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1570292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1525:

```
Met His Asn Cys Ser Leu Asp Ala Lys Ile Arg Val Asn Leu Glu Ala
1 5 10 15
Gln Val Val Glu Thr Gln Ala Glu Ala Lys Lys Lys Pro Ala Glu Lys
20 25 30
Lys Lys Thr Thr Ser Asp Gly Pro Lys Pro Lys Arg Leu Lys Lys Thr
35 40 45
Asn Asp Glu Lys Lys Ser Ser Ser Thr Ser Asn Lys Pro Lys Arg Pro
50 55 60
Leu Thr Ala Phe Phe Ile Phe Met Ser Asp Phe Arg Lys Thr Phe Lys
65 70 75
Ser Glu His Asn Gly Ser Leu Ala Lys Asp Ala Ala Lys Ile Gly Gly
85 90 95
Glu Lys Trp Lys Ser Leu Thr Glu Glu Glu Lys Lys Val Tyr Leu Asp
100 105 110
Lys Ala Ala Glu Leu Lys Ala Glu Tyr Asn Lys Ser Leu Glu Ser Asn
115 120 125
Asp Ala Asp Glu Glu Glu Glu Asp Glu Glu Lys Gln Ser Asp Asp Val
130 135 140
Asp Asp Ala Glu Glu Lys Gln Val Asp Asp Asp Glu Val Glu Glu
145 150 155
Lys Glu Val Glu Asn Thr Asp Asp Asp Lys Lys Glu Ala Glu Gly Lys
165 170 175
Glu Glu Glu Glu Glu Glu Ile Leu Asp Asp Tyr
180 185
```

(2) INFORMATION FOR SEQ ID NO:1526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 795 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..795

(D) OTHER INFORMATION: / Ceres Seq. ID 1570301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1526:

```
gttcccaact ccttaacgcgc tctctctcta tctcttttagc ttctcttttc tagcggcgcaa 60
catTgggttta tccggtggggg tacactgagc tctctctccc aagaatcttc cttaactttac 120
tctctctcttt aggccttaata cgaacactca tagacacggg ttctcggata ttgggtctac 180
cgaactttct cgaatccgcac ccggttttat cgtcatcgtc atggctggaa ccacgtata 240
tgtccacggc ggcgcatacat caccaagaaa gctcattttt ctccccagtg gcggcgaggc 300
tagctggaga aatctttgcc cgtcatcagat tctcggaact aactcgacc ggattcggat 360
cggatccgga ttgctgcgcg gtgtgcctcc acgagttcga gaacgaagac gagatccgac 420
ggctgacgaa ttgtcaaacac atatctcacc ggagctgttt agaccgttgg atgatggggt 480
ataatcagat gaactgtcca cttgttagaa cgcgcgtttat ttctgatgag ttacaagttg 540
cttttaacca acgagtttgg tctgaatctg aacttctcgc agaatacaaat tagaatcttt 600
cttggttggg tggaaattagt ttctactaat gagaaaaatta atttctatct tttttttttt 660
tttgtttaat ctttagctga gtggttgata tatgtaaaaa taaaaattat aggtggtgat 720
gcttagtaaaa ttgaagaagt gaaatttgta ttatccgttg agggaaaaaa agaatgaat 780
ggaaatctta atttt
```

(2) INFORMATION FOR SEQ ID NO:1527:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(D) OTHER INFORMATION: / Ceres Seq. ID 1570302

|              |            |            |            |             |            |     |
|--------------|------------|------------|------------|-------------|------------|-----|
| cataaatctctc | aaaaatctca | actttatctc | ccaaaacaca | aaacaaaaaa  | aaatggcttc | 60  |
| cactgtctctc  | tcaagcgcca | tgttgggaac | ttcattcttc | cgctggtccc  | cagctccaat | 120 |
| cagctctcgtg  | tcctctccat | cagccaacac | acaatccctc | ttcaggtctca | aatcaggcac | 180 |
| cgctcgtgtgt  | ggaactgtca | cagcactggc | tactacaag  | gtcgagttca  | taccaccaga | 240 |

aggtgagcta gaggttgagt gtgacgacga cgtctacggt cttgatgctg ctgaggaagc 300  
tggaatcgat ttgccttact attgccgtgc tggttcttgt tcgagctgtg ctggtaaaagt 360  
tgtgtctgga tctgttgatc agtctgacca gagtttccct gatgatgaac agattggtga 420  
agggttttgt ctcacttgtg ctgcttacct tacctctgat gttaccattg aaaCccacaa 480  
agaagaagac attgtttaag cctcacctac tcaccagctt ttgatgggtt aaaaatcatg 540  
tctttataat tgagtttgtt gttacaaaac tattgttacc tgtgtgtatt gttcctgtgt 600  
gggtccacca tcaatcgatg acatttt

(2) INFORMATION FOR SEQ ID NO:1530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1570309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1530:

Ile Ile Leu Lys Asn Leu Asn Phe Ile Ser Gln Asn Thr Lys Gln Lys  
1 5 10 15  
Lys Met Ala Ser Thr Ala Leu Ser Ser Ala Ile Val Gly Thr Ser Phe  
20 25 30  
Ile Arg Arg Ser Pro Ala Pro Ile Ser Leu Arg Ser Leu Pro Ser Ala  
35 40 45  
Asn Thr Gln Ser Leu Phe Gly Leu Lys Ser Gly Thr Ala Arg Gly Gly  
50 55 60  
Arg Val Thr Ala Met Ala Thr Tyr Lys Val Lys Phe Ile Thr Pro Glu  
65 70 75 80  
Gly Glu Leu Glu Val Glu Cys Asp Asp Asp Val Tyr Val Leu Asp Ala  
85 90 95  
Ala Glu Glu Ala Gly Ile Asp Leu Pro Tyr Ser Cys Arg Ala Gly Ser  
100 105 110  
Cys Ser Ser Cys Ala Gly Lys Val Ser Gly Ser Val Asp Gln Ser  
115 120 125  
Asp Gln Ser Phe Leu Asp Asp Glu Gln Ile Gly Glu Gly Phe Val Leu  
130 135 140  
Thr Cys Ala Ala Tyr Pro Thr Ser Asp Val Thr Ile Glu Thr His Lys  
145 150 155 160  
Glu Glu Asp Ile Val  
165

(2) INFORMATION FOR SEQ ID NO:1531:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1570310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1531:

Met Ala Ser Thr Ala Leu Ser Ser Ala Ile Val Gly Thr Ser Phe Ile  
1 5 10 15  
Arg Arg Ser Pro Ala Pro Ile Ser Leu Arg Ser Leu Pro Ser Ala Asn  
20 25 30  
Thr Gln Ser Leu Phe Gly Leu Lys Ser Gly Thr Ala Arg Gly Gly Arg  
35 40 45  
Val Thr Ala Met Ala Thr Tyr Lys Val Lys Phe Ile Thr Pro Glu Gly  
50 55 60

Glu Leu Glu Val Glu Cys Asp Asp Asp Val Tyr Val Leu Asp Ala Ala  
65 70 75 80  
Glu Glu Ala Gly Ile Asp Leu Pro Tyr Ser Cys Arg Ala Gly Ser Cys  
85 90 95  
Ser Ser Cys Ala Gly Lys Val Val Ser Gly Ser Val Asp Gln Ser Asp  
100 105 110  
Gln Ser Phe Leu Asp Asp Glu Gln Ile Gly Glu Gly Phe Val Leu Thr  
115 120 125  
Cys Ala Ala Tyr Pro Thr Ser Asp Val Thr Ile Glu Thr His Lys Glu  
130 135 140  
Glu Asp Ile Val  
145

(2) INFORMATION FOR SEQ ID NO:1532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1532:

Met Ala Thr Tyr Lys Val Lys Phe Ile Thr Pro Glu Gly Glu Leu Glu  
1 5 10 15  
Val Glu Cys Asp Asp Asp Val Tyr Val Leu Asp Ala Ala Glu Glu Ala  
20 25 30  
Gly Ile Asp Leu Pro Tyr Ser Cys Arg Ala Gly Ser Cys Ser Ser Cys  
35 40 45  
Ala Gly Lys Val Val Ser Gly Ser Val Asp Gln Ser Asp Gln Ser Phe  
50 55 60  
Leu Asp Asp Glu Gln Ile Gly Glu Gly Phe Val Leu Thr Cys Ala Ala  
65 70 75 80  
Tyr Pro Thr Ser Asp Val Thr Ile Glu Thr Lys Glu Glu Asp Ile  
85 90 95  
Val

(2) INFORMATION FOR SEQ ID NO:1533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..637
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1533:

|             |             |            |             |            |             |     |
|-------------|-------------|------------|-------------|------------|-------------|-----|
| tyttctctct  | CtCtctcacac | acttcacact | ttaaatatac  | actctcatta | tgactaccga  | 60  |
| agagaagag   | atcctcgccg  | ccaaattgga | agaacagaag  | atcgatctcg | ataagccoga  | 120 |
| agttgaggac  | gatgatgata  | acgaagacga | tgactctgat  | gacgatgata | aggatgatga  | 180 |
| cgaggctgat  | ggactagatg  | gagaggcagg | aggtaagtca  | aaacaaagca | gaagtggagaa | 240 |
| gaagagtgc   | aaagccatgc  | tcaaagcttg | catgaaaccc  | atcacttggt | ttagccgagt  | 300 |
| caccgtcaaa  | aagagcaaga  | atatcttgtt | tgctcatatca | aagcctgatg | tgctcaagag  | 360 |
| tcacagcatca | gacacatatg  | tgatcttttg | agaggcggaag | atcgaggatt | tgactctcaa  | 420 |
| gatccagtcg  | caagcagcag  | agcaattcaa | ggcaccagat  | ctcagcaatg | tgatctctcaa | 480 |
| gggtgagtca  | tcgagccctg  | cagtggttca | ggatgatgag  | gaggttgacg | aggaaggtgt  | 540 |
| tgagccaaag  | gacattgagt  | tggtgatgac | tcaagcagga  | gtgtctagcg | caaatgtctgt | 600 |
| gaaggctctc  | aaggctcgag  | atggagatat | tgtctctc    |            |             |     |

(2) INFORMATION FOR SEQ ID NO:1534:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1570316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1534:

Xaa Leu Ser Leu Phe Thr His Phe Thr Leu Ser Ile Tyr Thr Leu Ile  
1 5 10 15  
Met Thr Thr Glu Glu Lys Glu Ile Leu Ala Ala Lys Leu Glu Glu Gln  
20 25 30  
Lys Ile Asp Leu Asp Lys Pro Glu Val Glu Asp Asp Asp Asn Glu  
35 40 45  
Asp Asp Asp Ser Asp Asp Asp Asp Lys Asp Asp Asp Glu Ala Asp Gly  
50 55 60  
Leu Asp Gly Glu Ala Gly Gly Lys Ser Lys Gln Ser Arg Ser Glu Lys  
65 70 75 80  
Lys Ser Arg Lys Ala Met Leu Lys Leu Gly Met Lys Pro Ile Thr Gly  
85 90 95  
Val Ser Arg Val Thr Val Lys Lys Ser Lys Asn Ile Leu Phe Val Ile  
100 105 110  
Ser Lys Pro Asp Val Phe Lys Ser Pro Ala Ser Asp Thr Tyr Val Ile  
115 120 125  
Phe Gly Glu Ala Lys Ile Glu Asp Leu Ser Ser Gln Ile Gln Ser Gln  
130 135 140  
Ala Ala Glu Gln Phe Lys Ala Pro Asp Leu Ser Asn Val Ile Ser Lys  
145 150 155 160  
Gly Glu Ser Ser Ser Ala Ala Val Val Gln Asp Asp Glu Glu Val Asp  
165 170 175  
Glu Glu Gly Val Glu Pro Lys Asp Ile Glu Leu Val Met Thr Gln Ala  
180 185 190  
Gly Val Ser Arg Pro Asn Ala Val Lys Ala Leu Lys Ala Ala Asp Gly  
195 200 205  
Asp Ile Val Ser  
210

(2) INFORMATION FOR SEQ ID NO:1535:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..196

(D) OTHER INFORMATION: / Ceres Seq. ID 1570317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1535:

Met Thr Thr Glu Glu Lys Glu Ile Leu Ala Ala Lys Leu Glu Glu Gln  
1 5 10 15  
Lys Ile Asp Leu Asp Lys Pro Glu Val Glu Asp Asp Asp Asp Asn Glu  
20 25 30  
Asp Asp Asp Ser Asp Asp Asp Asp Lys Asp Asp Asp Glu Ala Asp Gly  
35 40 45  
Leu Asp Gly Glu Ala Gly Gly Lys Ser Lys Gln Ser Arg Ser Glu Lys  
50 55 60  
Lys Ser Arg Lys Ala Met Leu Lys Leu Gly Met Lys Pro Ile Thr Gly

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Val | Ser | Arg | Val | Thr | Val | Lys | Lys | Ser | Lys | Asn | Ile | Leu | Phe | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |
| Ser | Lys | Pro | Asp | Val | Phe | Lys | Ser | Pro | Ala | Ser | Asp | Thr | Tyr | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Phe | Gly | Glu | Ala | Lys | Ile | Glu | Asp | Leu | Ser | Ser | Gln | Ile | Gln | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Ala | Ala | Glu | Gln | Phe | Lys | Ala | Pro | Asp | Leu | Ser | Asn | Val | Ile | Ser |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Gly | Glu | Ser | Ser | Ser | Ala | Ala | Val | Val | Gln | Asp | Asp | Glu | Glu | Val |
|     |     |     | 145 |     |     | 150 |     |     | 155 |     |     |     |     | 160 |
| Glu | Glu | Gly | Val | Glu | Pro | Lys | Asp | Ile | Glu | Leu | Val | Met | Thr | Gln |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |
| Gly | Val | Ser | Arg | Pro | Asn | Ala | Val | Lys | Ala | Leu | Lys | Ala | Ala | Asp |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Asp | Ile | Val | Ser |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 195 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1536:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1570318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1536:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Lys | Leu | Gly | Met | Lys | Pro | Ile | Thr | Gly | Val | Ser | Arg | Val | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Lys | Lys | Ser | Lys | Asn | Ile | Leu | Phe | Val | Ile | Ser | Lys | Pro | Asp | Val |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Phe | Lys | Ser | Pro | Ala | Ser | Asp | Thr | Tyr | Val | Ile | Phe | Gly | Glu | Ala | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Glu | Asp | Leu | Ser | Ser | Gln | Ile | Gln | Ser | Gln | Ala | Ala | Glu | Gln | Phe |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Ala | Pro | Asp | Leu | Ser | Asn | Val | Ile | Ser | Lys | Gly | Glu | Ser | Ser | Ser |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Ala | Val | Val | Gln | Asp | Asp | Glu | Glu | Val | Asp | Glu | Glu | Gly | Val | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Pro | Lys | Asp | Ile | Glu | Leu | Val | Met | Thr | Gln | Ala | Gly | Val | Ser | Arg | Pro |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Asn | Ala | Val | Lys | Ala | Leu | Lys | Ala | Ala | Asp | Gly | Asp | Ile | Val | Ser |     |
|     |     |     | 115 |     |     | 120 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1537:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1131 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1131

(D) OTHER INFORMATION: / Ceres Seq. ID 1570339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1537:

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| aaccaaatac | aaacccatgc  | cgccttatcc | gtctctctcg | tctctctagt | ttttctctcag | 60  |
| tctctgttct | tagatccctt  | gtagtttcca | aatcttccga | taaaaaatgc | gggtaaaagga | 120 |
| gaaggaccag | ctatccggtat | cgatcttggg | accacttact | cttgcgctcg | agtatggcaa  | 180 |
| cacgaccgtg | ttgagatcat  | tgctaataat | gaaggaagaa | gaaccacgcc | atcttactggt | 240 |

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gttttcaccg actccgagag gttgatcggt gacgcagcta agaatacagg cgccatgaac 300
cccgtaatac ccggttttccg cgctaagagg ttgatcggtc gtcggttttc tgacagctct 360
gttcagaggt acatgaaatt gtggccattc aaagattcaag cggagacctg cgataagcca 420
atgatctaac tcgaatacaa ggggtaagag aaagagttcg cagctgagga gattttcttc 480
atggttctta ttaagatgcg tgagattgct gaggtctacc ttatgtgtac aatcaagaac 540
gcccgttgta ccgttccagc ttacttcaac gactctcagc gtcagggtac aaaggatgct 600
gggtgcatcg ctggtttgaa cgttatgcga atcatcaacg agcctacagc cgccgctatt 660
gCctacgggtc ttgacaaaaa ggctaccagc gttggagaga agaattgtct tatcttcgat 720
cttggtgggt gcaacttttg tgtctctctt cttaccattg aagagggtat ctttgagggt 780
aaggcaactg ctggtgacac ccactttggt gggaagattt ttgacaacag aatggttaac 840
cactttgtcc aagagttcaa gaggaagagt aagaaggata tcaccggtaa cccaagagct 900
cttagagagt tgagaacttc ctgtgagaga gcgaagagga ctcttctctc caactgtcag 960
accaccatcg agattgactc tctatacagc ggtatcgact tctactccac catcaccctg 1020
gctagatttg aggagctcaa catggatctc ttcagggaagt gtatggagcc agttgagaag 1080
tgtctctgtg atgctaagat ggacaagagc actgttcgat atgttgctct t

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(2) INFORMATION FOR SEQ ID NO:1538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..342

(D) OTHER INFORMATION: / Ceres Seq. ID 1570340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1538:

```

Met Ser Gly Lys Gly Glu Gly Pro Ala Ile Gly Ile Asp Leu Gly Thr
1 5 10 15
Thr Tyr Ser Cys Val Gly Val Trp Gln His Asp Arg Val Glu Ile Ile
20 25 30
Ala Asn Asp Gln Gly Asn Arg Thr Thr Pro Ser Tyr Val Ala Phe Thr
35 40 45
Asp Ser Glu Arg Leu Ile Gly Asp Ala Ala Lys Asn Gln Val Ala Met
50 55 60
Asn Pro Val Asn Thr Val Phe Asp Ala Lys Asp Leu Ile Gly Arg Arg
65 70 75 80
Phe Ser Asp Ser Ser Val Gln Ser Asp Met Lys Leu Trp Pro Phe Lys
85 90 95
Ile Gln Ala Gly Pro Ala Asp Lys Pro Met Ile Tyr Val Glu Tyr Lys
100 105 110
Gly Glu Glu Lys Glu Phe Ala Ala Glu Glu Ile Ser Ser Met Val Leu
115 120 125
Ile Lys Met Arg Glu Ile Ala Glu Ala Tyr Leu Ser Val Thr Ile Lys
130 135 140
Asn Ala Val Val Thr Val Pro Ala Tyr Phe Asn Asp Ser Gln Arg Gln
145 150 155 160
Ala Thr Lys Asp Ala Gly Val Ile Ala Gly Leu Asn Val Met Arg Ile
165 170 175
Ile Asn Glu Pro Thr Ala Ala Ala Ile Ala Tyr Gly Leu Asp Lys Lys
180 185 190
Ala Thr Ser Val Gly Glu Lys Asn Val Leu Ile Phe Asp Leu Gly Gly
195 200 205
Gly Thr Phe Asp Val Ser Leu Leu Thr Ile Glu Glu Gly Ile Phe Glu
210 215 220
Val Lys Ala Thr Ala Gly Asp Thr His Leu Gly Gly Glu Asp Phe Asp
225 230 235 240
Asn Arg Met Val Asn His Phe Val Gln Glu Phe Lys Arg Lys Ser Lys
245 250 255
Lys Asp Ile Thr Gly Asn Pro Arg Ala Leu Arg Arg Leu Arg Thr Ser
260 265 270

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Cys Glu Arg Ala Lys Arg Thr Leu Ser Ser Thr Ala Gln Thr Thr Ile  
275 280 285  
Glu Ile Asp Ser Leu Tyr Glu Gly Ile Asp Phe Tyr Ser Thr Ile Thr  
290 295 300  
Arg Ala Arg Phe Glu Glu Leu Asn Met Asp Leu Phe Arg Lys Cys Met  
305 310 315 320  
Glu Pro Val Glu Lys Cys Leu Arg Asp Ala Lys Met Asp Lys Ser Thr  
325 330 335  
Val His Asp Val Val Leu  
340

(2) INFORMATION FOR SEQ ID NO:1539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..279

(D) OTHER INFORMATION: / Ceres Seq. ID 1570341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1539:

Met Asn Pro Val Asn Thr Val Phe Asp Ala Lys Arg Leu Ile Gly Arg  
1 5 10 15  
Arg Phe Ser Asp Ser Ser Val Gln Ser Asp Met Lys Leu Trp Pro Phe  
20 25 30  
Lys Ile Gln Ala Gly Pro Ala Asp Lys Pro Met Ile Tyr Val Glu Tyr  
35 40 45  
Lys Gly Glu Glu Lys Glu Phe Ala Ala Glu Glu Ile Ser Ser Met Val  
50 55 60  
Leu Ile Lys Met Arg Glu Ile Ala Glu Ala Tyr Leu Ser Val Thr Ile  
65 70 75 80  
Lys Asn Ala Val Val Thr Val Pro Ala Tyr Phe Asn Asp Ser Gln Arg  
85 90 95  
Gln Ala Thr Lys Asp Ala Gly Val Ile Ala Gly Leu Asn Val Met Arg  
100 105 110  
Ile Ile Asn Glu Pro Thr Ala Ala Ala Ile Ala Tyr Gly Leu Asp Lys  
115 120 125  
Lys Ala Thr Ser Val Gly Glu Lys Asn Val Leu Ile Phe Asp Leu Gly  
130 135 140  
Gly Gly Thr Phe Asp Val Ser Leu Leu Thr Ile Glu Glu Gly Ile Phe  
145 150 155 160  
Glu Val Lys Ala Thr Ala Gly Asp Thr His Leu Gly Gly Glu Asp Phe  
165 170 175  
Asp Asn Arg Met Val Asn His Phe Val Gln Glu Phe Lys Arg Lys Ser  
180 185 190  
Lys Lys Asp Ile Thr Gly Asn Pro Arg Ala Leu Arg Arg Leu Arg Thr  
195 200 205  
Ser Cys Glu Arg Ala Lys Arg Thr Leu Ser Ser Thr Ala Gln Thr Thr  
210 215 220  
Ile Glu Ile Asp Ser Leu Tyr Glu Gly Ile Asp Phe Tyr Ser Thr Ile  
225 230 235 240  
Thr Arg Ala Arg Phe Glu Glu Leu Asn Met Asp Leu Phe Arg Lys Cys  
245 250 255  
Met Glu Pro Val Glu Lys Cys Leu Arg Asp Ala Lys Met Asp Lys Ser  
260 265 270  
Thr Val His Asp Val Val Leu  
275

(2) INFORMATION FOR SEQ ID NO:1540:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1540: |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|--------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met                                        | Lys | Leu | Trp | Pro | Phe | Lys | Ile | Gln | Ala | Gly | Pro | Ala | Asp | Lys | Pro | 15  |  |
| Met                                        | Ile | Tyr | Val | Glu | Tyr | Lys | Gly | Glu | Glu | Lys | Glu | Phe | Ala | Ala | Glu | 20  |  |
| Glu                                        | Ile | Ser | Ser | Met | Val | Leu | Ile | Lys | Met | Arg | Glu | Ile | Ala | Glu | Ala | 25  |  |
| Tyr                                        | Leu | Ser | Val | Thr | Ile | Lys | Asn | Ala | Val | Val | Thr | Val | Pro | Ala | Tyr | 30  |  |
| Phe                                        | Asn | Asp | Ser | Gln | Arg | Gln | Ala | Thr | Lys | Asp | Ala | Gly | Val | Ile | Ala | 35  |  |
| 65                                         |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Gly                                        | Leu | Asn | Val | Met | Arg | Ile | Ile | Asn | Glu | Pro | Thr | Ala | Ala | Ala | Ile | 85  |  |
| Ala                                        | Tyr | Gly | Leu | Asp | Lys | Lys | Ala | Thr | Ser | Val | Gly | Glu | Lys | Asn | Val | 90  |  |
| Leu                                        | Ile | Phe | Asp | Leu | Gly | Gly | Gly | Thr | Phe | Asp | Val | Ser | Leu | Leu | Thr | 100 |  |
| Ile                                        | Glu | Gly | Gly | Ile | Phe | Glu | Val | Lys | Ala | Thr | Ala | Gly | Asp | Thr | His | 105 |  |
| 130                                        |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     | 145 |  |
| Leu                                        | Gly | Gly | Glu | Asp | Phe | Asn | Arg | Met | Val | Asn | His | Phe | Val | Gln |     | 150 |  |
| 145                                        |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |  |
| Glu                                        | Phe | Lys | Arg | Lys | Ser | Lys | Lys | Asp | Ile | Thr | Gly | Asn | Pro | Arg | Ala | 165 |  |
| Leu                                        | Arg | Arg | Leu | Arg | Thr | Ser | Cys | Glu | Arg | Ala | Lys | Arg | Thr | Leu | Ser | 170 |  |
| Ser                                        | Thr | Ala | Gln | Thr | Thr | Ile | Glu | Ile | Asp | Ser | Leu | Tyr | Glu | Gly | Ile | 180 |  |
| Asp                                        | Phe | Tyr | Ser | Thr | Ile | Thr | Arg | Ala | Arg | Phe | Glu | Glu | Leu | Asn | Met | 190 |  |
| 210                                        |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     | 225 |  |
| Asp                                        | Leu | Phe | Arg | Lys | Cys | Met | Glu | Pro | Val | Glu | Lys | Cys | Leu | Arg | Ala | 230 |  |
| 225                                        |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     | 240 |  |
| Ala                                        | Lys | Met | Asp | Lys | Ser | Thr | Val | His | Asp | Val | Val | Leu |     |     |     | 245 |  |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1541:

|             |             |             |             |            |              |     |
|-------------|-------------|-------------|-------------|------------|--------------|-----|
| gaaatcattca | tatcctcttc  | catgattgttt | tgtcttctctt | tctcaacttc | aattcctcttc  | 60  |
| gaatatattca | tcgcgaattcg | tatcoggtttt | aagtataatga | gcgaatggag | tgtggaaagta  | 120 |
| caagctcatca | gatgagcaag  | agaaagaatt  | tcatgtgtttt | ccaggaggtg | gacattaccc   | 180 |
| acacgtctcaa | ggaggtttacc | ctccacaagg  | tatccaccca  | caacacaggt | atctctccag   | 240 |
| tggaggtctac | ccactgcgcg  | gatatacttc  | tgggtgttacc | ctctgtcgcg | ccgggttggtta | 300 |
| tctctctcgca | ctctgaggttt | acccctctcc  | tggctattctc | gcacctggag | ctcaaccttc   | 360 |
| aggacattctc | ggtgtgtggac | ctcgaggcat  | gatagcaggt  | gcagctgggt | gacccgcgac   | 420 |
| agcttatgga  | gtctcaccatg | ttgtgcacgc  | ctctcacagt  | ctctacggac | atgcctgtagg  | 480 |



acatggaggagg tatggccatg cccctgctca tggctttggc catggtgggc atggtaaaatt 540  
caagcacgga aagcatggag gcaaaattcaa gcacggaaag catggaaagc acggggaaca 600  
tggcatgttt ggaggaggag gcaaaattcaa gaagtggag taatctcaaa aacccacact 660  
ttgatctctc cctccagatg agtctcatta cctgaccgat gttttctaata atcccccttc 720  
aaacataatt cattttaact atgtcggttt agagattact ggttgaggaa ataattggag 780  
agtgtctagta taaaccttat ggtatctgca gcagagggtt ctttaacttc tcaatagtag 840  
atgctttgaa acttatctat aattttNggt ttgtaatgac agtttgtgtt tggGtttttt 900  
cttcagatc tctcttgttt g

(2) INFORMATION FOR SEQ ID NO:1542:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1570344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1542:

Met Gly Gly Lys Asp Lys His His Asp Glu Lys Gly Phe  
1 5 10 15  
His Gly Phe Pro Gly Gly Gly His Tyr Pro Pro Ala Gln Gly Tyr  
20 25 30  
Pro Pro Lys Gly Tyr Pro Pro Lys Gly Tyr Pro Pro Ala Gly Gly  
35 40 45  
Tyr Pro Pro Ala Gly Tyr Pro Pro Gly Ala Tyr Pro Ala Ala Pro Gly  
50 55 60  
Gly Tyr Pro Pro Ala Pro Gly Gly Tyr Pro Pro Ala Gly Tyr Pro Ala  
65 70 75 80  
Pro Gly Ala His His Ser Gly His Ser Gly Gly Gly Leu Gly Gly Met  
85 90 95  
Ile Ala Gly Ala Ala Gly Ala Ala Ala Ala Tyr Gly Ala His His  
100 105 110  
Val Gly His Ala Ser His Asn Pro Tyr Gly His Ala Val Gly His Gly  
115 120 125  
Gly Tyr Gly His Ala Pro Ala His Gly Phe Gly His Gly Gly His Gly  
130 135 140  
Lys Phe Lys His Gly Lys His Gly Gly Lys Phe Lys His Gly Lys His  
145 150 155 160  
Gly Lys His Gly Lys His Gly Met Phe Gly Gly Gly Lys Phe Lys  
165 170 175  
Lys Trp Lys

(2) INFORMATION FOR SEQ ID NO:1543:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2432 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2432

(D) OTHER INFORMATION: / Ceres Seq. ID 1570349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1543:

acctattctc actaacaac tctgaacaaa ccaaaaaaaa cttctttttt ttctatcttt 60  
cacgggttga agattcttga ttttctttct tctctcttct tacacgacca ctgatgtgt 120  
tcggtagctg aaaccatctg ttctcttttg cctctgattt atcgatatgt tttaaagaaa 180  
aacgggtgtt gaaacttttg taatttaagg ttcatcaaat actcagatct tgtctgagaa 240  
attaagctga aatctgataa atgggtttgt ttaaattcat cttcttgtaa tctcttctat 300

```

ggagttttcta cagtttaggc tcatctcagc tacaagcttc acaagcacia gttcttcttc 360
agctgaaaaa acacttagaa tatccacaac agctagaatc ttggtatgat cacagaacca 420
attcttgcta tctacaagca accactatga tgaacatcac ttgtttctct aatcagctct 480
cagagctaaa catcttcggt gataagtcac cagaaaaagc caaaagcttt gatggttttg 540
ctatctcttaa tgttacttta tctgatggat tctccattga atcattttgc actacactgt 600
caaggctaaa attctcttagg gtctcttact tggctttctc agggatttgg ggtcgtctcc 660
ctgagaaact tcatcggttta tctctcacttg agtattttga tttagaccaat aactttctgt 720
ttggttcagt accacctaa tttgtctaaa tggtaaaagt tgaacctttH cagattttgat 780
cataactctt tcaatggcac attacctagc tgggtttgatt cgtatttgta tctcaaaagt 840
cttagcttta aaagtaataa gactatcagg gagctacatt ctctactact ctggttgta 900
acaatcgagt atatcgattt gagagcaaat tctctgagtg gttcactttcc ggatgatctg 960
aaatgtgaaa gcaaaactct gtttatcgac atttccgaca ataagttaac cggaaaaactt 1020
ctctggttct taagcagcaa gcaagatatt gcgttgagat tcaatggaaa ctgtttatct 1080
ctagagaaac agcaacatct agaactcttt tgtgttaaa aagttcgcgc tgcggctaaa 1140
gctgaagcaa aagcagaagc agaggctgca aatgaatcag gaaaaagaaa atgggaagaa 1200
ggagctttta tcggttaaat cgttggtata tcaatggcgg tattggtttt agtctgctgt 1260
gtatttatct tgcctcagaag aaaaggagta acaaaagaac atgtccacca taatactgtc 1320
caagataatc atccaactac tggattttct tccgagatac tctcaaacgc aaggtacatt 1380
tctgaacctc caaagtttgg ttcagaggac ttacgggtat gtgacagtt tagcttagaa 1440
gagatagtta aagctacaaa gaactctgat aagactatga tactcgggta aagctcctta 1500
tatggcacgc tttacaagg aaatcttgag aatggaaaca aagtggaact aagatgctta 1560
ctctcatcga agaaatactc gataaggaa cttaaacctg ggttgattt gctccgaaa 1620
cttagaaccc cgaattctgt ctgcttgggt ggtcattgca tagattgtgg aggaataag 1680
gattacagcg ttgagaaagt ctttttgatt tattgagtaca ttccaaatgg aaacttccaa 1740
tctgttctct cagataaatg ttcaggtaag ggtatgaatt ggtcagagag gcttaagtgt 1800
ctcacaggtg ttgcaaaagc tgttctattt ctccacactg gagttatttc tggatttctc 1860
agcaatagac tcaagactaa caacgttttg cttaaccaac atcgggtttg gaaactaggt 1920
gttatgttgt tghccattgt ctctgaagca accagaaaat acacagaaaat cgcgaaaata 1980
tggcaaatgt caaggctaga agacagtggt tacagctttg gattgattct tctacaatca 2040
atcgtttggc catctgtatc cgcgaagaaa gaagcatttc taccgagaga actgctcatcg 2100
ttggagagcg aagaaggagg gagaagaatg gtgaatccga cagtacaagc cactgtgtca 2160
aacggatcac tgataaagt gataactctg atgaacaaat gtgttttcc tgaattctta 2220
agccgacctg ccttcgaaga tatctgttgg aatttacagt atgcttctca gtgccaagt 2280
gctctgatg gtgaccagtg ttaatatatt catagcttct tcttctctta gtaaaaaatt 2340
caaacgaact ttttaatgt ttaaagattc gtgtaatggt tgtgtaacaa aatccccctg 2400
tatttatgta acgattggga aaaatggaaa tt

```

(2) INFORMATION FOR SEQ ID NO:1544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..356
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1544:

```

Met Ala Val Leu Val Leu Val Cys Cys Val Phe Ile Leu Leu Arg Arg
1 5 10 15
Lys Gly Val Thr Lys Lys His Val His Asn Thr Val Gln Asp Asn
20 25 30
His Pro Thr Thr Gly Phe Ser Ser Glu Ile Leu Ser Asn Ala Arg Tyr
35 40 45 50
Ile Ser Glu Thr Ser Lys Phe Gly Ser Glu Asp Leu Pro Val Cys Arg
55 60
Gln Phe Ser Leu Glu Glu Ile Val Lys Ala Thr Lys Asn Phe Asp Lys
65 70 75 80
Thr Met Ile Leu Gly Glu Ser Ser Leu Tyr Gly Thr Leu Tyr Lys Gly
85 90 95
Asn Leu Glu Asn Gly Thr Lys Val Ala Ile Arg Cys Leu Pro Ser Ser

```

100 105 110  
Lys Lys Tyr Ser Ile Arg Asn Leu Lys Leu Arg Leu Asp Leu Leu Ala  
115 120 125  
Lys Leu Arg His Pro Asn Leu Val Cys Leu Leu Gly His Cys Ile Asp  
130 135 140  
Cys Gly Gly Lys Asp Asp Tyr Ser Val Glu Lys Val Phe Leu Ile Tyr  
145 150 155 160  
Glu Tyr Ile Pro Asn Gly Asn Phe Gln Ser Cys Leu Ser Asp Asn Ser  
165 170 175  
Ser Gly Lys Gly Met Asn Trp Ser Glu Arg Leu Asn Val Leu Thr Gly  
180 185 190  
Val Ala Lys Ala Val His Phe Leu His Thr Gly Val Ile Pro Gly Phe  
195 200 205  
Phe Ser Asn Arg Leu Lys Thr Asn Asn Val Leu Leu Asn Gln His Arg  
210 215 220  
Phe Val Lys Leu Ser Asp Tyr Gly Leu Xaa Ile Val Ser Glu Ala Thr  
225 230 235 240  
Arg His Asn Thr Glu Ile Ala Lys Ser Trp Gln Met Ser Arg Leu Glu  
245 250 255  
Asp Asp Val Tyr Ser Phe Gly Leu Ile Leu Leu Gln Ser Ile Val Gly  
260 265 270  
Pro Ser Val Ser Ala Arg Glu Glu Ala Phe Leu Arg Asp Glu Leu Ala  
275 280 285  
Ser Leu Glu Ser Glu Glu Gly Arg Arg Arg Met Val Asn Pro Thr Val  
290 295 300  
Gln Ala Thr Cys Arg Asn Gly Ser Leu Ile Arg Val Ile Thr Leu Met  
305 310 315 320  
Asn Lys Cys Val Ser Pro Glu Ser Leu Ser Arg Pro Ser Phe Glu Asp  
325 330 335  
Ile Leu Trp Asn Leu Gln Tyr Ala Ser Gln Leu Gln Ala Ala Ser Asp  
340 345 350  
Gly Asp Gln Cys  
355

(2) INFORMATION FOR SEQ ID NO:1545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..275
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1545:

Met Ile Leu Gly Glu Ser Ser Leu Tyr Gly Thr Leu Tyr Lys Gly Asn  
1 5 10 15  
Leu Glu Asn Gly Thr Lys Val Ala Ile Arg Cys Leu Pro Ser Ser Lys  
20 25 30  
Lys Tyr Ser Ile Arg Asn Leu Lys Leu Arg Leu Asp Leu Leu Ala Lys  
35 40 45  
Leu Arg His Pro Asn Leu Val Cys Leu Leu Gly His Cys Ile Asp Cys  
50 55 60  
Gly Gly Lys Asp Asp Tyr Ser Val Glu Lys Val Phe Leu Ile Tyr Glu  
65 70 75 80  
Tyr Ile Pro Asn Gly Asn Phe Gln Ser Cys Leu Ser Asp Asn Ser Ser  
85 90 95  
Gly Lys Gly Met Asn Trp Ser Glu Arg Leu Asn Val Leu Thr Gly Val  
100 105 110  
Ala Lys Ala Val His Phe Leu His Thr Gly Val Ile Pro Gly Phe Phe  
115 120 125

Ser Asn Arg Leu Lys Thr Asn Asn Val Leu Leu Asn Gln His Arg Phe  
130 135 140  
Val Lys Leu Ser Asp Tyr Gly Leu Xaa Ile Val Ser Glu Ala Thr Arg  
145 150 155 160  
His Asn Thr Glu Ile Ala Lys Ser Trp Gln Met Ser Arg Leu Glu Asp  
165 170 175  
Asp Val Tyr Ser Phe Gly Leu Ile Leu Leu Gln Ser Ile Val Gly Pro  
180 185 190  
Ser Val Ser Ala Arg Glu Glu Ala Phe Leu Arg Asp Glu Leu Ala Ser  
195 200 205  
Leu Glu Ser Glu Glu Gly Arg Arg Arg Met Val Asn Pro Thr Val Gln  
210 215 220  
Ala Thr Cys Arg Asn Gly Ser Leu Ile Arg Val Ile Thr Leu Met Asn  
225 230 235 240  
Lys Cys Val Ser Pro Glu Ser Leu Ser Arg Pro Ser Phe Glu Asp Ile  
245 250 255  
Leu Trp Asn Leu Gln Tyr Ala Ser Gln Leu Gln Ala Ala Ser Asp Gly  
260 265 270  
Asp Gln Cys  
275

(2) INFORMATION FOR SEQ ID NO:1546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..780
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1546:

|             |            |            |             |            |             |     |
|-------------|------------|------------|-------------|------------|-------------|-----|
| acagtaataa  | tcaagtcaga | gccggcgaas | ttgccgtttc  | cgccgttgga | gaggaattat  | 60  |
| agtcgatgaag | cttatttcac | ttgtcagaaa | cggttcgtttc | cgccaatgac | aaccggaagt  | 120 |
| tatctgggtct | ttgcaagttc | gtttcttgca | gcaagattct  | gtctcgaaag | ctaaacccaa  | 180 |
| gaaatacaaa  | taccgcgcag | tttatgatcc | gtatggtctc  | agaccccagc | cttcaagcaa  | 240 |
| aatcatggag  | ctagctgagc | gtatagctgc | tttatctcca  | gaagaaagaa | aacagattgg  | 300 |
| tcctgcactc  | aatgaacacc | tgaggcttcc | aaaaacaacg  | atgatttcat | cggacggcat  | 360 |
| tggaacaaaa  | caagataccg | gagctgggaa | agtagaggag  | aagaaggaga | agacggcttt  | 420 |
| cgatgtgaag  | ttggagaagt | ttaatgcac  | tgataagatc  | aaagtataa  | aagaagtgg   | 480 |
| aacgtttaca  | agtttgggct | tgaaggaagc | gaaagagctt  | gtggagaaag | tcccgctcat  | 540 |
| tccttaacaa  | ggtgtgcaca | aggaagaagc | taatgaaatc  | atagccaaga | tcaaaagctgt | 600 |
| tggtggagtc  | gcagttatgg | agtaggtgac | ttttgacact  | tcaattgttt | ttttgtttga  | 660 |
| ttcaactattt | ggtattgtga | tcacatcttg | gtacttaagg  | tagatgtttt | gtaataacaa  | 720 |
| atcgattact  | tgacattgag | ttttcaagaa | ctttggDtca  | attgtttgcc | ttctctttgc  | 780 |

(2) INFORMATION FOR SEQ ID NO:1547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1547:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Lys Leu Ile Ser Leu Val Arg Asn Val Arg Ser Arg Gln Cys Gln |  |
| 1 5 10 15                                                       |  |
| Pro Glu Val Ile Trp Ser Leu Gln Val Arg Phe Leu Gln Gln Asp Ser |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|
| 20  |     |     |     |     |     |     |     |     |     | 25  |     |     |     |     |     |     |     |     |     | 30  |  |  |  |  |  |  |  |  |  |
| Val | Ser | Lys | Ala | Lys | Pro | Lys | Lys | Tyr | Lys | Tyr | Pro | Ser | Lys | Ile | Met | Glu | Leu | Ala | Asp |     |  |  |  |  |  |  |  |  |  |
| 35  |     |     |     |     |     |     |     |     |     | 40  |     |     |     |     |     |     |     |     |     | 45  |  |  |  |  |  |  |  |  |  |
| Pro | Tyr | Gly | Pro | Arg | Pro | Gln | Pro | Ser | Ser | Lys | Ile | Met | Glu | Leu | Ala |     |     |     |     |     |  |  |  |  |  |  |  |  |  |
| 50  |     |     |     |     |     |     |     |     |     | 55  |     |     |     |     |     |     |     |     |     | 60  |  |  |  |  |  |  |  |  |  |
| Glu | Arg | Ile | Ala | Ala | Leu | Ser | Pro | Glu | Glu | Arg | Lys | Gln | Ile | Gly | Pro |     |     |     |     |     |  |  |  |  |  |  |  |  |  |
| 65  |     |     |     |     |     |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     | 75  |  |  |  |  |  |  |  |  |  |
| Ala | Leu | Asn | Glu | His | Leu | Arg | Leu | Pro | Lys | Gln | Gln | Met | Ile | Ser | Ser |     |     |     |     |     |  |  |  |  |  |  |  |  |  |
| 85  |     |     |     |     |     |     |     |     |     | 90  |     |     |     |     |     |     |     |     |     | 95  |  |  |  |  |  |  |  |  |  |
| Asp | Gly | Ile | Gly | Ala | Lys | Gln | Asp | Thr | Gly | Ala | Gly | Lys | Val | Glu | Glu |     |     |     |     |     |  |  |  |  |  |  |  |  |  |
| 100 |     |     |     |     |     |     |     |     |     | 105 |     |     |     |     |     |     |     |     |     | 110 |  |  |  |  |  |  |  |  |  |
| Lys | Lys | Glu | Lys | Thr | Ala | Phe | Asp | Val | Lys | Leu | Glu | Lys | Phe | Asn | Ala |     |     |     |     |     |  |  |  |  |  |  |  |  |  |
| 115 |     |     |     |     |     |     |     |     |     | 120 |     |     |     |     |     |     |     |     |     | 125 |  |  |  |  |  |  |  |  |  |
| Ser | Asp | Lys | Ile | Lys | Val | Ile | Lys | Glu | Val | Arg | Thr | Phe | Thr | Ser | Leu |     |     |     |     |     |  |  |  |  |  |  |  |  |  |
| 130 |     |     |     |     |     |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     | 140 |  |  |  |  |  |  |  |  |  |
| Gly | Leu | Lys | Glu | Ala | Lys | Glu | Leu | Val | Glu | Lys | Val | Pro | Ala | Ile | Leu |     |     |     |     |     |  |  |  |  |  |  |  |  |  |
| 145 |     |     |     |     |     |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     | 155 |  |  |  |  |  |  |  |  |  |
| Lys | Gln | Gly | Val | Thr | Lys | Glu | Glu | Ala | Asn | Glu | Ile | Ile | Ala | Lys | Ile |     |     |     |     |     |  |  |  |  |  |  |  |  |  |
| 165 |     |     |     |     |     |     |     |     |     | 170 |     |     |     |     |     |     |     |     |     | 175 |  |  |  |  |  |  |  |  |  |
| Lys | Ala | Val | Gly | Gly | Val | Ala | Val | Met | Glu |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |
| 180 |     |     |     |     |     |     |     |     |     | 185 |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:1548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1570358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1548:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Ala | Glu | Arg | Ile | Ala | Ala | Leu | Ser | Pro | Glu | Glu | Arg | Lys |
| 1   | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |     |     |
| Gln | Ile | Gly | Pro | Ala | Leu | Asn | Glu | His | Leu | Arg | Leu | Pro | Lys | Gln | Gln |
| 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |     |     |
| Met | Ile | Ser | Ser | Asp | Gly | Ile | Gly | Ala | Lys | Gln | Asp | Thr | Gly | Ala | Gly |
| 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
| Lys | Val | Glu | Glu | Lys | Lys | Glu | Lys | Thr | Ala | Phe | Asp | Val | Lys | Leu | Glu |
| 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Lys | Phe | Asn | Ala | Ser | Asp | Lys | Ile | Lys | Val | Ile | Lys | Glu | Val | Arg | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |
| Phe | Thr | Ser | Leu | Gly | Leu | Lys | Glu | Ala | Lys | Glu | Leu | Val | Glu | Lys | Val |
| 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |     |     |
| Pro | Ala | Ile | Leu | Lys | Gln | Gly | Val | Thr | Lys | Glu | Glu | Ala | Asn | Glu | Ile |
| 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |     |     |
| Ile | Ala | Lys | Ile | Lys | Ala | Val | Gly | Gly | Val | Ala | Val | Met | Glu |     |     |
| 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1570359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1549:

Met Ile Ser Ser Asp Gly Ile Gly Ala Lys Gln Asp Thr Gly Ala Gly  
1 5 10 15  
Lys Val Glu Glu Lys Lys Glu Lys Thr Ala Phe Asp Val Lys Leu Glu  
20 25 30  
Lys Phe Asn Ala Ser Asp Lys Ile Lys Val Ile Lys Glu Val Arg Thr  
35 40 45  
Phe Thr Ser Leu Gly Leu Lys Glu Ala Lys Glu Leu Val Glu Lys Val  
50 55 60  
Pro Ala Ile Leu Lys Gln Gly Val Thr Lys Glu Glu Ala Asn Glu Ile  
65 70 75 80  
Ile Ala Lys Ile Lys Ala Val Gly Gly Val Ala Val Met Glu  
85 90

(2) INFORMATION FOR SEQ ID NO:1550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1550:

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| ctttttctct  | ttcacatcgt  | tctttctctc | gcaaaacccaa | attctctcag  | cgccgggtcaa | 60   |
| atactgtgct  | ctctctctct  | ctctctttca | ctcttgttct  | gtctctcttg  | aagctgtgttg | 120  |
| ttctgttaaga | aagatgggaag | caggtggcgc | gtaccaatcca | cgcactgttg  | aagaggtgtt  | 180  |
| tagggattttt | aagggtcgta  | gagctggcat | gattaaggct  | ttaaccaactg | atgttcaagga | 240  |
| gttttttcoga | ctttgtgatc  | ccgaaaagga | gaaccttttg  | ctttacggac  | atccaaatga  | 300  |
| gcactgggaaa | gtgaatttgc  | cagctgaaga | ggttctctct  | gagctccacg  | agcctgtctt  | 360  |
| gggtatcaat  | tttgcagag   | acgggatggc | ggaaaaggat  | tggtttgcc   | ttgttgctgt  | 420  |
| ccacagtgtat | gcttggcttc  | ttgtgtttgc | tttctttttt  | ggagccagggt | ttggatttga  | 480  |
| caaaagctgat | aggaagaggg  | ttttcaatat | ggtgaatgac  | ctcccaacaa  | cttttgaggt  | 540  |
| tgtagtggc   | actgctaaga  | aacaaggaaa | agataagfcc  | cttgtttcca  | acaacagcag  | 600  |
| caacagatcc  | aaatcaagct  | ccaagcgagg | atctgaatcc  | cgtgccagt   | tctcaaaagcc | 660  |
| ggagccgaaa  | gatgatgagg  | aggaggaaga | ggaaggtgtg  | gaagaggagg  | atgaggatga  | 720  |
| gcaaggtgaa  | acacagtggt  | gagcatgtgg | tgagagctat  | gcagctgatg  | agttctggat  | 780  |
| ttgtctgtac  | ctctgtgaga  | tgtgttttca | tggaaaagtgt | gttaagataa  | caccagcaag  | 840  |
| agctgagcac  | atcaagcaat  | acaagtgccc | ttctgtcagc  | aaAcaaaagg  | gctcgtttctt | 900  |
| aaatttgggt  | accgctcgct  | tctgtgtatc | tacctttgca  | tatgatgatg  | aacagcttaa  | 960  |
| ctgttttggt  | tagatcagat  | tgttcatatg | gatttggtaa  | ttttaggaag  | acatttttat  | 1020 |
| tttttcattg  | ttacattttg  | gcgattgaag | ggataactct  | ttgtttaggg  | gtaatgatct  | 1080 |
| ttgtctctgt  | tttatgtttg  | tttattaaca | ttcttcaaac  | tcaatcaaaa  | gtattttggt  | 1140 |

tagtctt

(2) INFORMATION FOR SEQ ID NO:1551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..323
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1551:

Phe Phe Ser Phe Thr Ser Phe Phe Leu Ser Gln Thr Gln Ile Leu Ser  
1 5 10 15  
Ala Pro Val Lys Tyr Leu Ser Leu Ser Leu Ser Leu Phe His Ser Cys  
20 25 30  
Leu Val Ser Phe Glu Ala Val Cys Ser Val Arg Lys Met Glu Ala Gly

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ala | Gly | Gly | Ala | Tyr | Asn | Pro | Arg | Thr | Val | Glu | Glu | Val | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Asp | Phe | Lys | Gly | Arg | Arg | Ala | Gly | Met | Ile | Lys | Ala | Leu | Thr | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Val | Gln | Glu | Phe | Phe | Arg | Leu | Cys | Asp | Pro | Glu | Lys | Glu | Asn | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Leu | Tyr | Gly | His | Pro | Asn | Glu | His | Trp | Glu | Val | Asn | Leu | Pro | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Glu | Val | Pro | Pro | Glu | Leu | Pro | Glu | Pro | Val | Leu | Gly | Ile | Asn | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Arg | Asp | Gly | Met | Ala | Glu | Lys | Asp | Trp | Leu | Ser | Leu | Val | Ala | Val |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |

His Ser Asp Ala Trp Leu Leu Ala Val Ala Phe Phe Phe Gly Ala Arg  
100 105 110  
Phe Gly Phe Asp Lys Ala Asp Arg Lys Arg Leu Phe Asn Met Val Asn  
115 120 125  
Asp Leu Pro Thr Ile Phe Glu Val Val Ala Gly Thr Ala Lys Lys Gln  
130 135 140  
Gly Lys Asp Lys Ser Ser Val Ser Asn Asn Ser Ser Asn Arg Ser Lys  
145 150 155 160  
Ser Ser Ser Lys Arg Gly Ser Glu Ser Arg Ala Lys Phe Ser Lys Pro  
165 170 175  
Glu Pro Lys Asp Asp Glu Glu Glu Glu Glu Gly Val Glu Glu Glu  
180 185 190  
Asp Glu Asp Glu Gln Gly Glu Thr Gln Cys Gly Ala Cys Gly Glu Ser  
195 200 205  
Tyr Ala Ala Asp Glu Phe Trp Ile Cys Cys Asp Leu Cys Glu Met Trp  
210 215 220  
Phe His Gly Lys Cys Val Lys Ile Thr Pro Ala Arg Ala Glu His Ile  
225 230 235 240  
Lys Gln Tyr Lys Cys Pro Ser Cys Ser Lys Gln Lys Gly Ser Phe Leu  
245 250 255  
Asn Leu Leu Thr Ala Arg Phe Cys Val Ser Thr Phe Ala Tyr Asp Asp  
260 265 270  
Glu Gln Leu Asn Cys Leu Val  
275

(2) INFORMATION FOR SEQ ID NO:1553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1570369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1553:

Met Ile Lys Ala Leu Thr Thr Asp Val Gln Glu Phe Phe Arg Leu Cys  
1 5 10 15  
Asp Pro Glu Lys Glu Asn Leu Cys Leu Tyr Gly His Pro Asn Glu His  
20 25 30  
Trp Glu Val Asn Leu Pro Ala Glu Glu Val Pro Pro Glu Leu Pro Glu  
35 40 45  
Pro Val Leu Gly Ile Asn Phe Ala Arg Asp Gly Met Ala Glu Lys Asp  
50 55 60  
Trp Leu Ser Leu Val Ala Val His Ser Asp Ala Trp Leu Leu Ala Val  
65 70 75 80  
Ala Phe Phe Phe Gly Ala Arg Phe Gly Phe Asp Lys Ala Asp Arg Lys  
85 90 95  
Arg Leu Phe Asn Met Val Asn Asp Leu Pro Thr Ile Phe Glu Val Val  
100 105 110  
Ala Gly Thr Ala Lys Lys Gln Gly Lys Asp Lys Ser Ser Val Ser Asn  
115 120 125  
Asn Ser Ser Asn Arg Ser Lys Ser Ser Ser Lys Arg Gly Ser Glu Ser  
130 135 140  
Arg Ala Lys Phe Ser Lys Pro Glu Pro Lys Asp Asp Glu Glu Glu Glu  
145 150 155 160  
Glu Glu Gly Val Glu Glu Glu Asp Glu Asp Glu Gln Gly Glu Thr Gln  
165 170 175  
Cys Gly Ala Cys Gly Glu Ser Tyr Ala Ala Asp Glu Phe Trp Ile Cys  
180 185 190  
Cys Asp Leu Cys Glu Met Trp Phe His Gly Lys Cys Val Lys Ile Thr



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 195                                                             | 200 | 205 |
| Pro Ala Arg Ala Glu His Ile Lys Gln Tyr Lys Cys Pro Ser Cys Ser |     |     |
| 210                                                             | 215 | 220 |
| Lys Gln Lys Gly Ser Phe Leu Asn Leu Leu Thr Ala Arg Phe Cys Val |     |     |
| 225                                                             | 230 | 235 |
| Ser Thr Phe Ala Tyr Asp Asp Glu Gln Leu Asn Cys Leu Val         |     |     |
| 245                                                             | 250 |     |

(2) INFORMATION FOR SEQ ID NO:1554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1386
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1554:

|             |            |            |             |             |             |      |
|-------------|------------|------------|-------------|-------------|-------------|------|
| gtaattttctt | aggaagtgca | ttttgataga | gcgcacgata  | aacacagcac  | cgcaaaaagc  | 60   |
| acagagacag  | agaaagcga  | agacaaaaca | aaaaagcttc  | ccccaagaac  | aaaaagttag  | 120  |
| catagatgaa  | gagttctcgg | gtttttgtat | ttttgtaaaa  | cagaaaaaaa  | aaaaagagaa  | 180  |
| gaagagatgg  | gaggtttgct | ttgttttctt | tcttcacgaa  | gagctgatgt  | agataatgga  | 240  |
| cctgcgtact  | actactacc  | aagggcaaca | gaagagcgtg  | tgccctttatc | ttccgcctcat | 300  |
| aacaggactt  | cctctgcaat | ctctactggt | gtttgtagtag | tagacmcaaa  | cttagagacaa | 360  |
| tcatctctct  | atgctttat  | accaccgcc  | ctgcctaccc  | ctttcgatgt  | gcctataggg  | 420  |
| attctctaaa  | caccagctag | tggtgaagag | gctacttggt  | ttgatataag  | agaggtttcg  | 480  |
| gtggactctg  | ctaataccga | gtctgctcaa | gaacacagttg | atggtattac  | tctcgggggtt | 540  |
| ccaactacat  | gctcacatca | agagacagat | agcaaaaatcc | aaacagagat  | tgatcttgaa  | 600  |
| tctactgaag  | aaatagacc  | gaagctatca | aaagctgttt  | ttataccaat  | agaggaagag  | 660  |
| gaggatttgc  | ccatattgtt | ggaagaatat | gatatcgaga  | accgaaaact  | tgtagccaaa  | 720  |
| tgtgatcacc  | attttcacct | tgcatgcatt | ctagaatgga  | tggagagaga  | tgaacacctg  | 780  |
| cccgctctga  | acaaggaaat | ggtatttgac | tctactcttg  | actagcaacc  | cgcaaatgcc  | 840  |
| gcactcttaga | aggtctcaat | ctctctgtat | cagaagaaag  | aaattggagw  | acaagagaaaa | 900  |
| aacttaaaaa  | gaaaaaatgg | gtaagaatac | actaatagct  | gatcacaaag  | tgggattttac | 960  |
| gaaacatgct  | agtgttgata | tatatatgtt | tgtgtacaga  | cgttttcaaat | cgtctacaaa  | 1020 |
| aaaaacggga  | ttaagaatta | gagttttgtc | tttagattca  | ctctcttgtaa | taaaaaacga  | 1080 |
| gacaaaactg  | ataatttttc | ttctagatgt | tttaattttg  | gtaattcttg  | tttataggtt  | 1140 |
| atttttagag  | tggttttaag | ctgggggttc | aattttgggtt | tgatttcagt  | ttttcttgag  | 1200 |
| tttaagaaaa  | atattaatca | aactgaaatt | gagagtttgt  | tatgtatgga  | tgggttttat  | 1260 |
| tacgggttga  | tttttagttg | tttttagtct | tattttattt  | ctttatattt  | ttttgtgata  | 1320 |
| tgtaatatga  | aaattgttta | tacttactag | tttgtagtgt  | ttatgtttta  | gattttottag | 1380 |
| ttcttc      |            |            |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..212
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1555:

|                                                                 |    |
|-----------------------------------------------------------------|----|
| Met Gly Gly Cys Cys Cys Ser Ser Ser Arg Arg Ala Asp Val Asp     |    |
| 1                                                               | 10 |
| Asn Gly Pro Ala Tyr Tyr Tyr Tyr Pro Arg Ala Thr Glu Glu Arg Val |    |
| 20                                                              | 30 |
| Pro Leu Ser Ser Ala His Asn Arg Thr Ser Ser Ala Ile Ser Thr Gly |    |
| 35                                                              | 45 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Val | Val | Asp | Xaa | Asn | Leu | Glu | Thr | Ser | Ser | Pro | Asp | Ala | Tyr |
| 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Ile | Pro | Pro | Pro | Leu | Pro | Thr | Pro | Phe | Asp | Val | Pro | Ile | Gly | Ile | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gln | Thr | Pro | Ala | Ser | Gly | Glu | Glu | Ala | Thr | Cys | Val | Asp | Ile | Arg | Glu |
|     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |
| Val | Ser | Val | Asp | Ser | Ala | Asn | Thr | Glu | Ser | Ala | Gln | Glu | Thr | Val | Asp |
|     |     |     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |
| Gly | Ile | Thr | Leu | Gly | Val | Pro | Thr | Thr | Cys | Ser | His | Lys | Glu | Thr | Asp |
|     |     |     |     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |
| Ser | Lys | Ile | Gln | Thr | Glu | Ile | Asp | Leu | Glu | Ser | Thr | Glu | Glu | Ile | Asp |
|     |     |     |     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |
| Pro | Lys | Leu | Ser | Lys | Ala | Val | Phe | Ile | Pro | Ile | Glu | Glu | Glu | Glu | Asp |
|     |     |     |     | 145 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Cys | Pro | Ile | Cys | Leu | Glu | Glu | Tyr | Asp | Ile | Glu | Asn | Pro | Lys | Leu | Val |
|     |     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |
| Ala | Lys | Cys | Asp | His | His | Phe | His | Leu | Ala | Cys | Ile | Leu | Glu | Trp | Met |
|     |     |     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |
| Glu | Arg | Ser | Glu | Thr | Cys | Pro | Val | Cys | Asn | Lys | Glu | Met | Val | Phe | Asp |
|     |     |     |     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |
| Ser | Thr | Leu | Asp |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 210 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1247
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1556:

|            |             |             |            |             |            |      |
|------------|-------------|-------------|------------|-------------|------------|------|
| ctcttgcttc | tcttcactca  | caatctcaca  | gcaaaagctc | tcgttgctag  | aggaatcaaa | 60   |
| caatgtgtgt | tgtgaagtcc  | accaagtcca  | atgcttactt | caagagggtac | caagtgaagt | 120  |
| tcaggagaag | aagagatgga  | aagactgact  | acagggcaag | gatccgtctt  | atcaaccaag | 180  |
| acaagaacaa | gtacaatata  | cctaagtatc  | gttttggtgt | ccggtttacc  | aacaagaaca | 240  |
| tagtggcaca | gattgtatct  | gcaagcattg  | ctgttgacat | tgttaaatgt  | tctgtctaac | 300  |
| cacatgaact | gcctcagtat  | ggctctcactg | ttggtcttac | aaactatgct  | gcagcttaac | 360  |
| gtactggcct | tctttttgct  | cgccgtgtgt  | taaaagatgt | ggaaatggat  | gacgagtatg | 420  |
| agggaacgt  | tgaggccact  | ggagaggact  | tttccgttga | gccaaactgat | tcaaggagac | 480  |
| ctttccgtgc | tcttcttgat  | tttggaacta  | tcaggaccac | aacaggaaac  | cgtgtgttgc | 540  |
| gtgctcttaa | gggtgctttg  | gatggtgtgt  | ttgatatacc | tcacagtgc   | aagagatttg | 600  |
| ctgggttcca | caaggagaac  | aagcaacttg  | atgctgaaat | ccacaggaaac | tacatctatg | 660  |
| gtggccatgt | ctcaaaactac | atgaagctgt  | tgggagaaga | tgagccagag  | aagttacaaa | 720  |
| ctcacttcag | tgtttacatc  | aagaaaaggag | ttgaagtgtg | gagcattgag  | gagttgtaca | 780  |
| agaaggttca | cgcagctatt  | ctgtgctgrc  | ccaaCcsaag | gaaaaccctg  | aaacctgctc | 840  |
| ccaagcaaca | caagagggtac | aacttgaaga  | aaactactta | cgaggagagg  | aagaacaagt | 900  |
| tgatcgagag | agtcaggcat  | tgaatggagc  | aggtggtgat | gatgatgatg  | aggacgatga | 960  |
| asagtaaatc | agtcacagct  | tctttatctc  | atgcctcttg | tagttttttt  | tcttttgagc | 1020 |
| taaagtcctc | aaattttctg  | ttttcagact  | aaaaactcoa | gcttttgggt  | tcacatttta | 1080 |
| attgtgttgc | aggattttga  | tattgaggat  | acattttctt | tgaagtatca  | ttatcttatt | 1140 |
| attacctcca | tcataatttt  | caagaatttt  | tatgacaata | gtttgatgat  | ttgattttat | 1200 |
| ctgtagtttg | ctattgttaa  | gttaagaac   | tgtagactt  | catctat     |            |      |

(2) INFORMATION FOR SEQ ID NO:1557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..286

(D) OTHER INFORMATION: / Ceres Seq. ID 1570373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1557:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Phe | Val | Lys | Ser | Thr | Lys | Ser | Asn | Ala | Tyr | Phe | Lys | Arg | Tyr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gln | Val | Lys | Phe | Arg | Arg | Arg | Arg | Asp | Gly | Lys | Thr | Asp | Tyr | Arg | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ile | Arg | Leu | Ile | Asn | Gln | Asp | Lys | Asn | Lys | Tyr | Asn | Thr | Pro | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Arg | Phe | Val | Val | Arg | Phe | Thr | Asn | Lys | Asp | Ile | Val | Ala | Gln | Ile |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Ser | Ala | Ser | Ile | Ala | Gly | Asp | Ile | Val | Lys | Ala | Ser | Ala | Tyr | Ala |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| His | Glu | Leu | Pro | Gln | Tyr | Gly | Leu | Thr | Val | Gly | Leu | Thr | Asn | Tyr | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Ala | Ala | Tyr | Cys | Thr | Gly | Leu | Leu | Leu | Ala | Arg | Arg | Val | Leu | Lys | Met |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Glu | Met | Asp | Asp | Glu | Tyr | Glu | Gly | Asn | Val | Glu | Ala | Thr | Gly | Glu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Phe | Ser | Val | Glu | Pro | Thr | Asp | Ser | Arg | Arg | Pro | Phe | Arg | Ala | Leu |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Asp | Val | Gly | Leu | Ile | Arg | Thr | Thr | Gly | Asn | Arg | Val | Phe | Gly |     |
|     |     |     | 145 |     |     | 150 |     |     | 155 |     |     |     | 160 |     |     |
| Ala | Leu | Lys | Gly | Ala | Leu | Asp | Gly | Gly | Leu | Asp | Ile | Pro | His | Ser | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Lys | Arg | Phe | Ala | Gly | Phe | His | Lys | Glu | Asn | Lys | Gln | Leu | Asp | Ala | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | His | Arg | Asn | Tyr | Ile | Tyr | Gly | Gly | His | Val | Ser | Asn | Tyr | Met | Lys |
|     |     |     | 195 |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Leu | Leu | Gly | Glu | Asp | Glu | Pro | Glu | Lys | Leu | Gln | Thr | His | Phe | Ser | Ala |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Tyr | Ile | Lys | Lys | Gly | Val | Glu | Ala | Glu | Ser | Ile | Glu | Glu | Leu | Tyr | Lys |
|     |     |     | 225 |     |     | 230 |     |     | 235 |     |     |     | 240 |     |     |
| Lys | Val | His | Ala | Ala | Ile | Arg | Ala | Xaa | Pro | Asn | Xaa | Arg | Lys | Thr | Val |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Lys | Pro | Ala | Pro | Lys | Gln | His | Lys | Arg | Tyr | Asn | Leu | Lys | Lys | Leu | Thr |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Tyr | Glu | Glu | Arg | Lys | Asn | Lys | Leu | Ile | Glu | Arg | Val | Arg | His |     |     |
|     |     |     | 275 |     |     | 280 |     |     |     |     |     | 285 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1570374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1558:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Glu | Met | Asp | Asp | Glu | Tyr | Glu | Gly | Asn | Val | Glu | Ala | Thr | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Asp | Phe | Ser | Val | Glu | Pro | Thr | Asp | Ser | Arg | Arg | Pro | Phe | Arg | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Leu | Asp | Val | Gly | Leu | Ile | Arg | Thr | Thr | Gly | Asn | Arg | Val | Phe |     |
|     |     |     | 35  |     |     | 40  |     |     |     | 45  |     |     |     |     |     |
| Gly | Ala | Leu | Lys | Gly | Ala | Leu | Asp | Gly | Gly | Leu | Asp | Ile | Pro | His | Ser |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 50                                                              | 55  | 60  |
| Asp Lys Arg Phe Ala Gly Phe His Lys Glu Asn Lys Gln Leu Asp Ala |     |     |
| 65                                                              | 70  | 75  |
| Glu Ile His Arg Asn Tyr Ile Tyr Gly Gly His Val Ser Asn Tyr Met |     |     |
|                                                                 | 85  | 90  |
| Lys Leu Leu Gly Glu Asp Glu Pro Glu Lys Leu Gln Thr His Phe Ser |     |     |
|                                                                 | 100 | 105 |
| Ala Tyr Ile Lys Lys Gly Val Glu Ala Glu Ser Ile Glu Glu Leu Tyr |     |     |
|                                                                 | 115 | 120 |
| Lys Lys Val His Ala Ala Ile Arg Ala Xaa Pro Asn Xaa Arg Lys Thr |     |     |
|                                                                 | 130 | 135 |
| Val Lys Pro Ala Pro Lys Gln His Lys Arg Tyr Asn Leu Lys Lys Leu |     |     |
| 145                                                             | 150 | 155 |
| Thr Tyr Glu Glu Arg Lys Asn Lys Leu Ile Glu Arg Val Arg His     |     |     |
|                                                                 | 165 | 170 |
|                                                                 |     | 175 |

(2) INFORMATION FOR SEQ ID NO:1559:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..172

(D) OTHER INFORMATION: / Ceres Seq. ID 1570375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1559:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Asp Asp Glu Tyr Glu Gly Asn Val Glu Ala Thr Gly Glu Asp Phe |     |     |
| 1                                                               | 5   | 10  |
| Ser Val Glu Pro Thr Asp Ser Arg Arg Pro Phe Arg Ala Leu Leu Asp |     |     |
|                                                                 | 20  | 25  |
| Val Gly Leu Ile Arg Thr Thr Thr Gly Asn Arg Val Phe Gly Ala Leu |     |     |
|                                                                 | 35  | 40  |
| Lys Gly Ala Leu Asp Gly Gly Leu Asp Ile Pro His Ser Asp Lys Arg |     |     |
|                                                                 | 50  | 55  |
| Phe Ala Gly Phe His Lys Glu Asn Lys Gln Leu Asp Ala Glu Ile His |     |     |
| 65                                                              | 70  | 75  |
| Arg Asn Tyr Ile Tyr Gly Gly His Val Ser Asn Tyr Met Lys Leu Leu |     |     |
|                                                                 | 85  | 90  |
| Gly Glu Asp Glu Pro Glu Lys Leu Gln Thr His Phe Ser Ala Tyr Ile |     |     |
|                                                                 | 100 | 105 |
| Lys Lys Gly Val Glu Ala Glu Ser Ile Glu Glu Leu Tyr Lys Lys Val |     |     |
|                                                                 | 115 | 120 |
| His Ala Ala Ile Arg Ala Xaa Pro Asn Xaa Arg Lys Thr Val Lys Pro |     |     |
|                                                                 | 130 | 135 |
| Ala Pro Lys Gln His Lys Arg Tyr Asn Leu Lys Lys Leu Thr Tyr Glu |     |     |
| 145                                                             | 150 | 155 |
| Glu Arg Lys Asn Lys Leu Ile Glu Arg Val Arg His                 |     |     |
|                                                                 | 165 | 170 |

(2) INFORMATION FOR SEQ ID NO:1560:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1724 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1724

(D) OTHER INFORMATION: / Ceres Seq. ID 1570376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1560:

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| aatttttagt  | ctccctccgc  | gtagaagcgt | ctccgagact  | tgtctctgct  | tgtattgaag  | 60   |
| aagacgcttg  | atcgaaaaatt | cccttagatt | tcgtaaatag  | gggttttacg  | aaggtgagat  | 120  |
| tacacagaga  | tcggtatttc  | gaaaaaaaaa | aatgggaagt  | ccaaagaaga  | acgagacaac  | 180  |
| aggctctctc  | gccgcacatg  | cttctggcgt | ctccatgttc  | ggtaaccgcc  | gtctcgagatc | 240  |
| cgtttaacggc | gtgcaaggta  | atgaaggagt | tgaggtcata  | aatccagaag  | gtggcaagga  | 300  |
| agatgctgaa  | gaggaaggac  | agaaaaggac | gtggaaggac  | gaggaacgag  | atagttacta  | 360  |
| gaagatgatg  | cagaaatata  | taggttcgga | tattacgtca  | atggtgactc  | ttcctgttgt  | 420  |
| tatatattgag | cctatgacta  | gtgtccagaa | gatggctgag  | ataatggagt  | attctcattt  | 480  |
| gttggtatcaa | gcagatgaat  | gcgaagatcc | atacttgctg  | ttagtatatg  | cttcacatgt  | 540  |
| ggctatatct  | gtttactatg  | ccttccaacg | aacttggaaag | cttttcaatc  | ctattcttgg  | 600  |
| ggagacatat  | gagatgtgtc  | accatgggtg | gattttcttt  | atttctgagc  | aggtttagcca | 660  |
| tcataccacca | atagtgctgt  | gtcatgccga | gaacgacgac  | ttcattttac  | acatcacatc  | 720  |
| aaagtgtgaaa | actRaacttt  | tgggtaactc | tgttgatgtt  | taccctgtgg  | gaagaacggc  | 780  |
| tgtaaccctc  | aagaaaagtg  | gtgtggttct | ggatttgggt  | cgcctctcca  | ctaagattca  | 840  |
| caatctaata  | tttggacgaa  | cctgggttga | ctcacctggg  | gaaatgggtc  | tgacaaatct  | 900  |
| aaccactgga  | gacaaaagtg  | tgtctttatt | ccagccatgt  | ggctgggtcg  | gttctggccc  | 960  |
| ctatgaagtt  | gatggctacg  | tttacagcgc | agctgaagaa  | ccgaaaaatc  | tgatgacagg  | 1020 |
| aaaatggaa   | gagaaaaatg  | gctaccaacc | ttgtgatgcc  | gaagggggaac | cccttccagg  | 1080 |
| aacagagctg  | aaagaggtgt  | ggcatttggc | tgatgtcccc  | aaaaacgcga  | aatttcagta  | 1140 |
| cactcacttt  | gtctcacaga  | taaacagcgt | cgacacagcg  | cctgctaagc  | tccttgcttc  | 1200 |
| agactcacgt  | atccgtcctg  | atagatatcc | ccttgagcag  | ggtagacctt  | ctaaaagctg  | 1260 |
| ttccgagaaa  | cacagccttg  | aggagagaca | aagccgaaaa  | gaggaccaga  | gagacaaga   | 1320 |
| gacaaaaagt  | cactccaaga  | tggttcgtac | taacggatga  | gtcacacct   | actccatggg  | 1380 |
| gagatatatt  | agtataccaa  | tacaacggga | agtacaatga  | acaccgagac  | acggcagaga  | 1440 |
| gctcaagtag  | tgctcccaac  | gaaacggacc | ctaaatcgat  | cgagttttaa  | ccctggcaat  | 1500 |
| atggtaatat  | ctcaaacgaa  | tgaagtaact | cttatagttt  | aatttggatt  | ctctatatac  | 1560 |
| gaatgctgtg  | attcatgttc  | acttggaa   | gagtcacatg  | tgttttttaa  | ctttgtttca  | 1620 |
| gactgaaaaa  | tctgattatg  | tgatttggat | gataaaacat  | aagttttgtg  | ttctctgtct  | 1680 |
| attgtatctt  | tgtccattt   | cgatcaatag | taattatggt  | tgttt       |             |      |

(2) INFORMATION FOR SEQ ID NO:1561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..331

(D) OTHER INFORMATION: / Ceres Seq. ID 1570377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1561:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Gln | Lys | Tyr | Ile | Gly | Ser | Asp | Ile | Thr | Ser | Met | Val | Thr | Leu |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |
| Pro | Val | Val | Ile | Phe | Glu | Pro | Met | Thr | Met | Leu | Gln | Lys | Met | Ala | Glu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ile | Met | Glu | Tyr | Ser | His | Leu | Leu | Asp | Gln | Ala | Asp | Glu | Cys | Glu | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Tyr | Leu | Arg | Leu | Val | Tyr | Ala | Ser | Ser | Trp | Ala | Ile | Ser | Val | Tyr |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Tyr | Ala | Phe | Gln | Arg | Thr | Trp | Lys | Pro | Phe | Asn | Pro | Ile | Leu | Gly | Glu |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     | 80  |     |     |
| Thr | Tyr | Glu | Met | Val | Asn | His | Gly | Gly | Ile | Ser | Phe | Ile | Ser | Glu | Gln |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |     |
| Val | Ser | His | His | Pro | Pro | Met | Ser | Ala | Gly | His | Ala | Glu | Asn | Glu | His |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Phe | Ile | Tyr | Asp | Ile | Thr | Ser | Lys | Leu | Lys | Thr | Xaa | Leu | Leu | Gly | Asn |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Val | Asp | Val | Tyr | Pro | Val | Gly | Arg | Thr | Arg | Val | Thr | Leu | Lys | Lys |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Asp | Gly | Val | Val | Leu | Asp | Leu | Val | Pro | Pro | Leu | Thr | Lys | Ile | His | Asn |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |

Leu Ile Phe Gly Arg Thr Trp Val Asp Ser Pro Gly Glu Met Val Met  
165 170 175  
Thr Asn Leu Thr Thr Gly Asp Lys Val Val Leu Tyr Phe Gln Pro Cys  
180 185 190  
Gly Trp Phe Gly Ser Gly Arg Tyr Glu Val Asp Gly Tyr Val Tyr Ser  
195 200 205  
Ala Ala Glu Glu Pro Lys Ile Met Met Thr Gly Lys Trp Asn Glu Lys  
210 215 220  
Met Ser Tyr Gln Pro Cys Asp Ala Glu Gly Glu Pro Leu Pro Gly Thr  
225 230 235 240  
Glu Leu Lys Glu Val Trp His Leu Ala Asp Val Pro Lys Asn Asp Lys  
245 250 255  
Phe Gln Tyr Thr His Phe Ala His Lys Ile Asn Ser Phe Asp Thr Ala  
260 265 270  
Pro Ala Lys Leu Leu Ala Ser Asp Ser Arg Ile Arg Pro Asp Arg Tyr  
275 280 285  
Ser Leu Glu Gln Gly Asp Leu Ser Lys Ala Gly Ser Glu Lys His Ser  
290 295 300  
Leu Glu Glu Arg Gln Ser Arg Lys Glu Asp Gln Arg Asp Lys Gly Thr  
305 310 315 320  
Lys Val His Ser Lys Met Val Arg Ser Asn Gly  
325 330

(2) INFORMATION FOR SEQ ID NO:1562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..330

(D) OTHER INFORMATION: / Ceres Seq. ID 1570378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1562:

Met Gln Lys Tyr Ile Gly Ser Asp Ile Thr Ser Met Val Thr Leu Pro  
1 5 10 15  
Val Val Ile Phe Glu Pro Met Thr Met Leu Gln Lys Met Ala Glu Ile  
20 25 30  
Met Glu Tyr Ser His Leu Leu Asp Gln Ala Asp Glu Cys Glu Asp Pro  
35 40 45  
Tyr Leu Arg Leu Val Tyr Ala Ser Ser Trp Ala Ile Ser Val Tyr Tyr  
50 55 60  
Ala Phe Gln Arg Thr Trp Lys Pro Phe Asn Pro Ile Leu Gly Glu Thr  
65 70 75 80  
Tyr Glu Met Val Asn His Gly Gly Ile Ser Phe Ile Ser Glu Gln Val  
85 90 95  
Ser His His Pro Pro Met Ser Ala Gly His Ala Glu Asn Glu His Phe  
100 105 110  
Ile Tyr Asp Ile Thr Ser Lys Leu Lys Thr Xaa Leu Leu Gly Asn Ser  
115 120 125  
Val Asp Val Tyr Pro Val Gly Arg Thr Arg Val Thr Leu Lys Lys Asp  
130 135 140  
Gly Val Val Leu Asp Leu Val Pro Pro Leu Thr Lys Ile His Asn Leu  
145 150 155 160  
Ile Phe Gly Arg Thr Trp Val Asp Ser Pro Gly Glu Met Val Met Thr  
165 170 175  
Asn Leu Thr Thr Gly Asp Lys Val Val Leu Tyr Phe Gln Pro Cys Gly  
180 185 190  
Trp Phe Gly Ser Gly Arg Tyr Glu Val Asp Gly Tyr Val Tyr Ser Ala  
195 200 205  
Ala Glu Glu Pro Lys Ile Met Met Thr Gly Lys Trp Asn Glu Lys Met

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 210                                                             | 215 | 220 |
| Ser Tyr Gln Pro Cys Asp Ala Glu Gly Glu Pro Leu Pro Gly Thr Glu |     |     |
| 225                                                             | 230 | 240 |
| Leu Lys Glu Val Trp His Leu Ala Asp Val Pro Lys Asn Asp Lys Phe |     |     |
|                                                                 | 245 | 255 |
| Gln Tyr Thr His Phe Ala His Lys Ile Asn Ser Phe Asp Thr Ala Pro |     |     |
|                                                                 | 260 | 270 |
| Ala Lys Leu Leu Ala Ser Asp Ser Arg Ile Arg Pro Asp Arg Tyr Ser |     |     |
|                                                                 | 275 | 285 |
| Leu Glu Gln Gly Asp Leu Ser Lys Ala Gly Ser Glu Lys His Ser Leu |     |     |
|                                                                 | 290 | 300 |
| Glu Glu Arg Gln Ser Arg Lys Glu Asp Gln Arg Asp Lys Gly Thr Lys |     |     |
| 305                                                             | 310 | 320 |
| Val His Ser Lys Met Val Arg Ser Asn Gly                         |     |     |
|                                                                 | 325 | 330 |

(2) INFORMATION FOR SEQ ID NO:1563:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..319

(D) OTHER INFORMATION: / Ceres Seq. ID 1570379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1563:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Val Thr Leu Pro Val Val Ile Phe Glu Pro Met Thr Met Leu Gln |     |
| 1                                                               | 5   |
| Lys Met Ala Glu Ile Met Glu Tyr Ser His Leu Leu Asp Gln Ala Asp |     |
|                                                                 | 20  |
| Glu Cys Glu Asp Pro Tyr Leu Arg Leu Val Tyr Ala Ser Ser Trp Ala |     |
|                                                                 | 35  |
| Ile Ser Val Tyr Tyr Ala Phe Gln Arg Thr Trp Lys Pro Phe Asn Pro |     |
|                                                                 | 50  |
| Ile Leu Gly Glu Thr Tyr Glu Met Val Asn His Gly Gly Ile Ser Phe |     |
| 65                                                              | 70  |
| Ile Ser Glu Gln Val Ser His His Pro Pro Met Ser Ala Gly His Ala |     |
|                                                                 | 85  |
| Glu Asn Glu His Phe Ile Tyr Asp Ile Thr Ser Lys Leu Lys Thr Xaa |     |
|                                                                 | 100 |
| Leu Leu Gly Asn Ser Val Asp Val Tyr Pro Val Gly Arg Thr Arg Val |     |
|                                                                 | 115 |
| Thr Leu Lys Lys Asp Gly Val Val Leu Asp Leu Val Pro Pro Leu Thr |     |
|                                                                 | 130 |
| Lys Ile His Asn Leu Ile Phe Gly Arg Thr Trp Val Asp Ser Pro Gly |     |
| 145                                                             | 150 |
| Glu Met Val Met Thr Asn Leu Thr Thr Gly Asp Lys Val Val Leu Tyr |     |
|                                                                 | 165 |
| Phe Gln Pro Cys Gly Trp Phe Gly Ser Gly Arg Tyr Glu Val Asp Gly |     |
|                                                                 | 180 |
| Tyr Val Tyr Ser Ala Ala Glu Glu Pro Lys Ile Met Met Thr Gly Lys |     |
|                                                                 | 195 |
| Trp Asn Glu Lys Met Ser Tyr Gln Pro Cys Asp Ala Glu Gly Glu Pro |     |
| 210                                                             | 215 |
| Leu Pro Gly Thr Glu Leu Lys Glu Val Trp His Leu Ala Asp Val Pro |     |
| 225                                                             | 230 |
| Lys Asn Asp Lys Phe Gln Tyr Thr His Phe Ala His Lys Ile Asn Ser |     |
|                                                                 | 245 |
| Phe Asp Thr Ala Pro Ala Lys Leu Leu Ala Ser Asp Ser Arg Ile Arg |     |
|                                                                 | 260 |

Pro Asp Arg Tyr Ser Leu Glu Gln Gly Asp Leu Ser Lys Ala Gly Ser  
275 280 285  
Glu Lys His Ser Leu Glu Glu Arg Gln Ser Arg Lys Glu Asp Gln Arg  
290 295 300  
Asp Lys Gly Thr Lys Val His Ser Lys Met Val Arg Ser Asn Gly  
305 310 315

(2) INFORMATION FOR SEQ ID NO:1564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1195

(D) OTHER INFORMATION: / Ceres Seq. ID 1570380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1564:

|            |            |            |             |             |             |      |
|------------|------------|------------|-------------|-------------|-------------|------|
| ataagatcca | aaaccataaa | actaggtttc | acactttctc  | tctaaacact  | gtctcttttc  | 60   |
| tccgatacat | atccccccgc | ttccccctgt | tttttcttcg  | ccgtccgtcg  | ttctttttcaa | 120  |
| ctccctagct | ggcatattaa | agcttagaca | caatgagagg  | aaggagctac  | acgccatcac  | 180  |
| caccaagggg | ttatggaagg | aggggcccga | gccctagccc  | tcggggccgg  | tttgatggga  | 240  |
| gtcgtgacag | tgatctccca | accagttctt | tggttcgcaa  | ctacgtcat   | gattgcaggc  | 300  |
| aagaagacct | caggaggcca | tttgagcagt | ttggtccgt   | caaggacatc  | taccttctta  | 360  |
| gggattacta | tactggagat | ccaagggggt | ttggtattcat | tcagtttatg  | gatccctgct  | 420  |
| atgctgctga | ggctaaacat | caaatggatg | gttatcttct  | tcttggtcgt  | gagtgactgt  | 480  |
| tcgtatttgc | tgaagaaaaa | cggaagaagc | caactgagat  | gagaacaagg  | gatcgagggt  | 540  |
| gaaggagcaa | cagattccag | gacagaagac | gttctcctcc  | tcggtactct  | cggctccttc  | 600  |
| ctcgccgtgg | tcgtagatca | cgatcacgta | gctgcggcta  | taattctcct  | cccgtaaaaa  | 660  |
| gacatcaatc | taggtctgtc | tcacctcagg | atagacgata  | tgagaaggag  | agggtcatac  | 720  |
| ctcgctcacc | accccataat | ggctcaaggg | ttcgagtggt  | aagtcctggg  | agagtgaaga  | 780  |
| gccacagcag | aagcccaaga | agaagcgtga | gcccaagaaa  | aaacagagac  | tacacgccag  | 840  |
| aacaagcaag | gagccaaagc | cctgtcccta | ggcagagcag  | gagcccgacc  | ccagtccttc  | 900  |
| gtggagcaca | aaatggagac | cgttctccaa | gccagtatt   | tAacaccatg  | tatctctcta  | 960  |
| ctcttcagtt | tttcagttct | gttctgtttg | atcagatatt  | ttgtttgctc  | cagatttgata | 1020 |
| tttccctact | tagacagata | ttgtagtgct | tattggtatt  | ttgctttatg  | tttgatccat  | 1080 |
| ggatgatctt | gagacagtat | ttgaagtag  | catgtgttat  | ttgtcatctt  | atcttttagt  | 1140 |
| atctcatcta | acattgttat | ggtgaaaaag | atggtcctat  | tacggggagct | ttttg       |      |

(2) INFORMATION FOR SEQ ID NO:1565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..261

(D) OTHER INFORMATION: / Ceres Seq. ID 1570381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1565:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Gly | Arg | Ser | Tyr | Thr | Pro | Ser | Pro | Pro | Arg | Gly | Tyr | Gly | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Gly | Arg | Ser | Pro | Ser | Pro | Arg | Gly | Arg | Phe | Gly | Gly | Ser | Arg | Asp |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Ser | Asp | Leu | Pro | Thr | Ser | Leu | Leu | Val | Arg | Asn | Leu | Arg | His | Asp | Cys |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Arg | Gln | Glu | Asp | Leu | Arg | Arg | Pro | Phe | Glu | Gln | Phe | Gly | Pro | Val | Lys |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |
| Asp | Ile | Tyr | Leu | Pro | Arg | Asp | Asp | Tyr | Tyr | Thr | Gly | Asp | Pro | Arg | Gly |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  | 80  |
| Gly | Phe | Ile | Gln | Phe | Met | Asp | Pro | Ala | Asp | Ala | Glu | Ala | Lys | His |     |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 55  |     |     |     |     |     |     |     |     |     | 90  |     |     |     |     |     |     |     |     |     | 95  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Gln | Met | Asp | Gly | Tyr | Leu | Leu | Leu | Gly | Arg | Glu | Leu | Thr | Val | Val | Phe | Gln | Met | Asp | Gly | Tyr | Leu | Leu | Gly | Arg | Glu | Leu | Thr | Val | Val | Phe | Gln | Met | Asp | Gly | Tyr | Leu | Leu | Gly | Arg | Glu | Leu | Thr | Val | Val | Phe |     |     |
| 100 |     |     |     |     |     |     |     |     |     | 105 |     |     |     |     |     |     |     |     |     | 110 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ala | Glu | Glu | Asn | Arg | Lys | Lys | Pro | Thr | Glu | Met | Arg | Thr | Arg | Asp | Arg | Ala | Glu | Glu | Asn | Arg | Lys | Lys | Pro | Thr | Glu | Met | Arg | Thr | Arg | Asp | Arg | Ala | Glu | Glu | Asn | Arg | Lys | Lys | Pro | Thr | Glu | Met | Arg | Thr | Arg | Asp | Arg |
| 115 |     |     |     |     |     |     |     |     |     | 120 |     |     |     |     |     |     |     |     |     | 125 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Gly | Gly | Gly | Arg | Ser | Asn | Arg | Phe | Gln | Asp | Arg | Arg | Arg | Ser | Pro | Arg | Gly | Gly | Gly | Arg | Ser | Asn | Arg | Phe | Gln | Asp | Arg | Arg | Arg | Ser | Pro | Arg | Gly | Gly | Gly | Arg | Ser | Asn | Arg | Phe | Gln | Asp | Arg | Arg | Arg | Ser | Pro | Arg |
| 130 |     |     |     |     |     |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     | 140 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Tyr | Ser | Arg | Ser | Pro | Pro | Arg | Arg | Gly | Arg | Arg | Ser | Arg | Ser | Arg | Ser | Tyr | Ser | Arg | Ser | Pro | Pro | Arg | Arg | Gly | Arg | Arg | Ser | Arg | Ser | Arg | Ser | Tyr | Ser | Arg | Ser | Pro | Pro | Arg | Arg | Gly | Arg | Arg | Ser | Arg | Ser | Arg | Ser |
| 145 |     |     |     |     |     |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     | 155 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Cys | Gly | Tyr | Asn | Ser | Pro | Pro | Ala | Lys | Arg | His | Gln | Ser | Arg | Ser | Val | Cys | Gly | Tyr | Asn | Ser | Pro | Pro | Ala | Lys | Arg | His | Gln | Ser | Arg | Ser | Val | Cys | Gly | Tyr | Asn | Ser | Pro | Pro | Ala | Lys | Arg | His | Gln | Ser | Arg | Ser | Val |
| 165 |     |     |     |     |     |     |     |     |     | 170 |     |     |     |     |     |     |     |     |     | 175 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ser | Pro | Gln | Asp | Arg | Arg | Tyr | Glu | Lys | Glu | Arg | Ser | Tyr | Ser | Arg | Ser | Ser | Pro | Gln | Asp | Arg | Arg | Tyr | Glu | Lys | Glu | Arg | Ser | Tyr | Ser | Arg | Ser | Ser | Pro | Gln | Asp | Arg | Arg | Tyr | Glu | Lys | Glu | Arg | Ser | Tyr | Ser | Arg | Ser |
| 180 |     |     |     |     |     |     |     |     |     | 185 |     |     |     |     |     |     |     |     |     | 190 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Pro | Pro | His | Gly | Ser | Arg | Val | Arg | Ser | Gly | Ser | Pro | Arg | Arg | Val | Asn | Pro | Pro | His | Gly | Ser | Arg | Val | Arg | Ser | Gly | Ser | Pro | Arg | Arg | Val | Asn | Pro | Pro | His | Gly | Ser | Arg | Val | Arg | Ser | Gly | Ser | Pro | Arg | Arg | Val | Asn |
| 195 |     |     |     |     |     |     |     |     |     | 200 |     |     |     |     |     |     |     |     |     | 205 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Lys | Ser | His | Ser | Arg | Ser | Pro | Arg | Arg | Ser | Val | Ser | Pro | Arg | Val | Asn | Lys | Ser | His | Ser | Arg | Ser | Pro | Arg | Arg | Ser | Val | Ser | Pro | Arg | Val | Asn | Lys | Ser | His | Ser | Arg | Ser | Pro | Arg | Arg | Ser | Val | Ser | Pro | Arg | Val | Asn |
| 210 |     |     |     |     |     |     |     |     |     | 215 |     |     |     |     |     |     |     |     |     | 220 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Arg | Ser | Tyr | Thr | Pro | Glu | Gln | Ala | Arg | Ser | Gln | Ser | Pro | Arg | Val | Asn | Arg | Ser | Tyr | Thr | Pro | Glu | Gln | Ala | Arg | Ser | Gln | Ser | Pro | Arg | Val | Asn | Arg | Ser | Tyr | Thr | Pro | Glu | Gln | Ala | Arg | Ser | Gln | Ser | Pro | Arg | Val | Asn |
| 225 |     |     |     |     |     |     |     |     |     | 230 |     |     |     |     |     |     |     |     |     | 235 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Gln | Ser | Arg | Ser | Pro | Thr | Pro | Val | Pro | Arg | Gly | Ala | Gln | Asn | Gly | Asp | Gln | Ser | Arg | Ser | Pro | Thr | Pro | Val | Pro | Arg | Gly | Ala | Gln | Asn | Gly | Asp | Gln | Ser | Arg | Ser | Pro | Thr | Pro | Val | Pro | Arg | Gly | Ala | Gln | Asn | Gly | Asp |
| 245 |     |     |     |     |     |     |     |     |     | 250 |     |     |     |     |     |     |     |     |     | 255 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Arg | Ser | Pro | Ser | Gln |     |     |     |     |     |     |     |     |     |     |     | Arg | Ser | Pro | Ser | Gln |     |     |     |     |     |     |     |     |     |     |     | Arg | Ser | Pro | Ser | Gln |     |     |     |     |     |     |     |     |     |     |     |
| 260 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..176  
(D) OTHER INFORMATION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1566:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Pro | Ala | Asp | Ala | Ala | Glu | Ala | Lys | His | Gln | Met | Asp | Gly | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Leu | Leu | Gly | Arg | Glu | Leu | Thr | Val | Val | Phe | Ala | Glu | Glu | Asn | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Lys | Pro | Thr | Glu | Met | Arg | Thr | Arg | Asp | Arg | Gly | Gly | Arg | Ser | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Phe | Gln | Asp | Arg | Arg | Arg | Ser | Pro | Pro | Arg | Tyr | Ser | Arg | Ser | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Arg | Arg | Gly | Arg | Arg | Ser | Arg | Ser | Arg | Ser | Cys | Gly | Tyr | Asn | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Pro | Ala | Lys | Arg | His | Gln | Ser | Arg | Ser | Val | Ser | Pro | Gln | Asp | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Tyr | Glu | Lys | Glu | Arg | Ser | Tyr | Ser | Arg | Ser | Pro | Pro | His | Asn | Gly |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Arg | Val | Arg | Ser | Gly | Ser | Pro | Gly | Arg | Val | Lys | Ser | His | Ser | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Pro | Pro | Arg | Arg | Ser | Val | Ser | Pro | Arg | Lys | Asn | Arg | Ser | Tyr | Thr |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Gln | Ala | Arg | Ser | Gln | Ser | Pro | Val | Pro | Arg | Gln | Ser | Arg | Ser | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Pro | Val | Pro | Arg | Gly | Ala | Gln | Asn | Gly | Asp | Arg | Ser | Pro | Ser | Gln |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

(2) INFORMATION FOR SEQ ID NO:1567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..164  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570383  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1567:  
Met Asp Gly Tyr Leu Leu Leu Gly Arg Glu Leu Thr Val Val Phe Ala  
1 5 10 15  
Glu Glu Asn Arg Lys Lys Pro Thr Glu Met Arg Thr Arg Asp Arg Gly  
20 25 30  
Gly Arg Ser Asn Arg Phe Gln Asp Arg Arg Arg Ser Pro Pro Arg Tyr  
35 40 45  
Ser Arg Ser Pro Pro Arg Arg Gly Arg Arg Ser Arg Ser Arg Ser Cys  
50 55 60  
Gly Tyr Asn Ser Pro Pro Ala Lys Arg His Gln Ser Arg Ser Val Ser  
65 70 75 80  
Pro Gln Asp Arg Arg Tyr Glu Lys Glu Arg Ser Tyr Ser Arg Ser Pro  
85 90 95  
Pro His Asn Gly Ser Arg Val Arg Ser Gly Ser Pro Gly Arg Val Lys  
100 105 110  
Ser His Ser Arg Ser Pro Arg Arg Ser Val Ser Pro Arg Lys Asn Arg  
115 120 125  
Ser Tyr Thr Pro Glu Gln Ala Arg Ser Gln Ser Pro Val Pro Arg Gln  
130 135 140  
Ser Arg Ser Pro Thr Pro Val Pro Arg Gly Ala Gln Asn Gly Asp Arg  
145 150 155 160  
Ser Pro Ser Gln

(2) INFORMATION FOR SEQ ID NO:1568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1358 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1358

(D) OTHER INFORMATION: / Ceres Seq. ID 1570384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1568:

aatcgcttcc acgaaaacaa gtagagagag tgattcgagt ttcccaatca taaaatcag 60  
cgaagaagat cttcgttctt gttcattctg tgagggtttca ttgttataaa cgaaacgaat 120  
ctcagggttg agtaatccct gggagagatc cgatttccgt ttccatggcg attcgggtgt 180  
cggagctgtg tatcgtactg ttgcgtcttt cctacgccat vtgcgtcctt gccgggaaga 240  
gttactacga ttgtttgcaa gtccccaag gtgcatctga tgaacagatc aagagagcct 300  
ataggaaact agccttgaag tatcatcccg ataagaatca aggaatgag gaagcgactc 360  
gaaatttcgc tgagatcaac aatgcttatg aagtgttato ggatgaggag aagaggggag 420  
tatataacaa gtatggtgaa gagggaacta aacagttttc tgcaaatgga ggaagaggag 480  
gagKaggagg cggcatgaat atgcaggaca tcttcagctc atttttttgt ggaggttcga 540  
tgagggaaga agagaagggt gtcaaggggg atgacgtaat tgtggaactt gaggcacatc 600  
tagaagattt gtacatggga ggctctatga aggtatggag ggaaaaaatg gtgataaaac 660  
cagctcctgg aaagagaaag tgtaactgca ggaacgaggt ctatcacaga caaatgtgtc 720  
ctggaatggt ccaacagagt acagagcagg tctgtgacaa atgccctaat gtcaaatcac 780  
aacgggaggt atactttgtg acagttgata tcgagaaagg aatgaaagat ggagaagaag 840  
tgtctttcta tgaagacggc gaaAcccCat tcttgacggt gaccctggT gaccttaagt 900  
tcogaatcag aactgcacca catgcccggt Tcagaagggt atggcaacga tctacacatg 960  
aacgtgaaca ttacactggt tgaggcgcta gttgggttttg agaaatcatt caaacacttg 1020

|                                                                   |      |
|-------------------------------------------------------------------|------|
| gatgatcagc aagttgacat cagttccaag ggaattacaa agccgaagga agtaaagaag | 1080 |
| ttcaaaggag aagggatgcc acttcactac agcacaaga aaggcaacot ctttgtcact  | 1140 |
| tttgagggtt tgtttccgtc ttctctcact gacgatcaga agaagaagt taaagaagtc  | 1200 |
| tttgcttagt gctctctctc cgtcttcgct ctctctctct ttagaagttt ggggattaaa | 1260 |
| gagaagaaca tgtgatggtc ctaatgtata acatgattg gttttaatat agaaagaaaa  | 1320 |
| aagatatggg gagacaaagt cggaaggagc ttttgacc                         |      |

(2) INFORMATION FOR SEQ ID NO:1569:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..272

(D) OTHER INFORMATION: / Ceres Seq. ID 1570385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1569:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Ile | Arg | Trp | Ser | Glu | Leu | Cys | Ile | Val | Leu | Phe | Ala | Leu | Ser |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Tyr | Ala | Xaa | Cys | Val | Leu | Ala | Gly | Lys | Ser | Tyr | Tyr | Asp | Val | Leu | Gln |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Pro | Lys | Gly | Ala | Ser | Asp | Glu | Gln | Ile | Lys | Arg | Ala | Tyr | Arg | Lys |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |  |
| Leu | Ala | Leu | Lys | Tyr | His | Pro | Asp | Lys | Asn | Gln | Gly | Asn | Glu | Glu | Ala |  |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |  |
| Thr | Arg | Lys | Phe | Ala | Glu | Ile | Asn | Asn | Ala | Tyr | Glu | Val | Leu | Ser | Asp |  |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |  |
| Glu | Glu | Lys | Arg | Glu | Ile | Tyr | Asn | Lys | Tyr | Gly | Glu | Glu | Gly | Leu | Lys |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Gln | Phe | Ser | Ala | Asn | Gly | Gly | Arg | Gly | Gly | Xaa | Gly | Gly | Gly | Met | Asn |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Met | Gln | Asp | Ile | Phe | Ser | Ser | Phe | Phe | Gly | Gly | Gly | Ser | Met | Glu | Glu |  |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |  |
| Glu | Glu | Lys | Val | Val | Lys | Gly | Asp | Val | Ile | Val | Glu | Leu | Glu | Ala |     |  |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |  |
| Thr | Leu | Glu | Asp | Leu | Tyr | Met | Gly | Gly | Ser | Met | Lys | Val | Trp | Arg | Glu |  |
|     |     |     | 145 |     |     |     |     | 150 |     |     | 155 |     |     |     | 160 |  |
| Lys | Asn | Val | Ile | Lys | Pro | Ala | Pro | Gly | Lys | Arg | Lys | Cys | Asn | Cys | Arg |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |
| Asn | Glu | Val | Tyr | His | Arg | Gln | Ile | Gly | Pro | Gly | Met | Phe | Gln | Gln | Met |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Thr | Glu | Gln | Val | Cys | Asp | Lys | Cys | Pro | Asn | Val | Lys | Tyr | Glu | Arg | Glu |  |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |  |
| Gly | Tyr | Phe | Val | Thr | Val | Asp | Ile | Glu | Lys | Gly | Met | Lys | Asp | Gly | Glu |  |
|     |     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |  |
| Glu | Val | Ser | Phe | Tyr | Glu | Asp | Gly | Glu | Thr | Pro | Phe | Leu | Thr | Val | Thr |  |
|     |     |     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |  |
| Leu | Val | Asp | Leu | Lys | Phe | Arg | Ile | Arg | Thr | Ala | Pro | His | Ala | Arg | Phe |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |  |
| Gln | Lys | Gly | Trp | Gln | Arg | Ser | Thr | His | Glu | Arg | Glu | His | Tyr | Thr | Gly |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1570:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1570386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1570:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Met | Gln | Asp | Ile | Phe | Ser | Ser | Phe | Phe | Gly | Gly | Ser | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Glu | Glu | Glu | Glu | Lys | Val | Val | Lys | Gly | Asp | Asp | Val | Ile | Val | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  | Leu |
| Glu | Ala | Thr | Leu | Glu | Asp | Leu | Tyr | Met | Gly | Gly | Ser | Met | Lys | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     | Trp |
| Arg | Glu | Lys | Asn | Val | Ile | Lys | Pro | Ala | Pro | Gly | Lys | Arg | Lys | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     | Asn |
| Cys | Arg | Asn | Glu | Val | Tyr | His | Arg | Gln | Ile | Gly | Pro | Gly | Met | Phe |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | Gln |
| Gln | Met | Thr | Glu | Gln | Val | Cys | Asp | Lys | Cys | Pro | Asn | Val | Lys | Tyr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  | Glu |
| Arg | Glu | Gly | Tyr | Phe | Val | Thr | Val | Asp | Ile | Glu | Lys | Gly | Met | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 | Asp |
| Gly | Glu | Glu | Val | Ser | Phe | Tyr | Glu | Asp | Gly | Glu | Thr | Pro | Phe | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     | Thr |
| Val | Thr | Leu | Val | Asp | Leu | Lys | Phe | Arg | Ile | Arg | Thr | Ala | Pro | His |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     | Ala |
| Arg | Phe | Gln | Lys | Gly | Trp | Gln | Arg | Ser | Thr | His | Glu | Arg | Glu | His |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | Tyr |
| Thr | Gly |     |     |     |     |     |     |     |     |     |     |     |     | 160 |

(2) INFORMATION FOR SEQ ID NO:1571:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1570387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1571:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Asp | Ile | Phe | Ser | Ser | Phe | Phe | Gly | Gly | Ser | Met | Glu | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     | 15  |     |     |
| Glu | Glu | Lys | Val | Val | Lys | Gly | Asp | Asp | Val | Ile | Val | Glu | Leu | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  | Ala |
| Thr | Leu | Glu | Asp | Leu | Tyr | Met | Gly | Gly | Ser | Met | Lys | Val | Trp | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     | Glu |
| Lys | Asn | Val | Ile | Lys | Pro | Ala | Pro | Gly | Lys | Arg | Lys | Cys | Asn | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     | Arg |
| Asn | Glu | Val | Tyr | His | Arg | Gln | Ile | Gly | Pro | Gly | Met | Phe | Gln | Gln |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | Met |
| Thr | Glu | Gln | Val | Cys | Asp | Lys | Cys | Pro | Asn | Val | Lys | Tyr | Glu | Arg |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  | Glu |
| Gly | Tyr | Phe | Val | Thr | Val | Asp | Ile | Glu | Lys | Gly | Met | Lys | Asp | Gly |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     | Glu |
| Glu | Val | Ser | Phe | Tyr | Glu | Asp | Gly | Glu | Thr | Pro | Phe | Leu | Thr | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     | Thr |
| Leu | Val | Asp | Leu | Lys | Phe | Arg | Ile | Arg | Thr | Ala | Pro | His | Ala | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     | Phe |
| Gln | Lys | Gly | Trp | Gln | Arg | Ser | Thr | His | Glu | Arg | Glu | His | Tyr | Thr |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | Gly |

(2) INFORMATION FOR SEQ ID NO:1572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1879

(D) OTHER INFORMATION: / Ceres Seq. ID 1570388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1572:

```
acagcaaaaa gccactctcc ttctctctc tctctgttc ctctgcatcc atggccacca 60
agctcgacac cagtagetta cttttggccc tcttgtccaa atgtagcctc cttaactcaaa 120
ccaatctctgc tctctctctc ctctgtagcc ccctagcttc tctcgctctt tctctctctt 180
tcttggtctca tcccggagga cccgcatggg gaaagtaact cctccaccgc cgcggtcaaa 240
ccaccgtgat acccgggcca agagggttac cttttgtcgg aagcatgtct ctcatgtcaa 300
acactctggc tcaccgttgc atagccgcaa ccgcagagaa atttagagcc gaacggttaa 360
tgcgcttttag ttgtggagaa actgcgctga tgcgtcaoctg caatcctgat ttagctaaaag 420
agattctaaa cagtcctggg ttgcgtgacc gcccggttaa ggaatcagct tattccotca 480
tggttaacgc tgctatcggt ttcgctcctt acggcggttta ctggcgaacc ttgagaaaaa 540
tcgcgtctaa tcattctttc agcccgaaac agattaaacg ttccgaaacg cagagaaagcg 600
tgatcgcgaa tcaaatcggt aagtgtctca caaaacagag taacacaaaa ggctctctgt 660
tcgcacgtga cttgatcaaa accgcatcgc ttaataacat gatgtgctct gttttcggaa 720
aagaatacga gcttgaggaa gagcatgaag aagtgaagta gctacgtgaa ttggtggaag 780
aaggttatga tttactcggt acactgaatt ggaccgatca tctcccatgc ctctctgaat 840
ttgatctcca aagaatccgg tctagatgct ctaatctcgt cccaaaaagta aacccggttg 900
tgaaacggat tatctctgac caccgtgaac ctacacgagta ctacacgagt gactgctgtg 960
acgtattgct ctctctcgat ggtcctgata aattatccga cctcgatata atcgccgttg 1020
tatgggaaat gatattcaga ggaactgaca cggtgctgtg ttgcatcgag tggattcttg 1080
ctaggatggt cctctcaatca gatattcaat cgacgggttca caatgagttg gatcaaatcg 1140
tgggacgatc aagggctgtc gaagagtcgt acgtgggtgc ttgagcttat ctgaagcgctg 1200
tggtgaaaga agtcttgagg ctccaccgcc caggcccaact actctcatgg gcccgcttag 1260
caatcacaga cagcatcatc gacggtcgtc gtgtcccgcc ggggaacacc gcaatggtga 1320
acatgtgggc tattgcacac gatccacacg tgtggggaga tccgttgtag tttaaaccgc 1380
aacgttttgt agccaaggaa ggtgaggttg agttctcggt tcttggtgct gatttgaggg 1440
ttgcaccggt cgggtccggt cgtcggtgtt gccccgggaa gaatcttggt ttgaccaccg 1500
tgacgttttg gactgcgacg cttttgcata agtttgaaNt Ggctgacgcc gtccgatgag 1560
aagaccgttg acttgtccga gaaactgagg ctctcgtgtg agatggctaa tcctcttgct 1620
gcataattac gccccaggcg cagttttagt gtatgataag ggtaaggcta tacacagata 1680
cagtggtaac taaagcgag gaaaattagt gtgaatttaa agcaaaaagaa taaaataaag 1740
aacaagaaga gtaaaagaaa caaaaaaaaaa gaatcatata aaaaatacta ataagaatgg 1800
taatgaagct tttatatata actaacatct tgatcagtgt tgtatatatg atgaaacat 1860
taatgtcaca aagaaaaagc
```

(2) INFORMATION FOR SEQ ID NO:1573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..518

(D) OTHER INFORMATION: / Ceres Seq. ID 1570389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1573:

```
Ser Lys Lys Pro Leu Ser Phe Leu Ser Leu Ser Cys Ser Ser Ala Ser
1 5 10 15
Met Ala Thr Lys Leu Asp Thr Ser Ser Leu Leu Leu Ala Leu Leu Ser
20 25 30
Lys Cys Ser Leu Leu Thr Gln Thr Asn Leu Ala Leu Ser Leu Leu Val
```

[illegible]

(2) INFORMATION FOR SEQ ID NO:1574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..502

(D) OTHER INFORMATION: / Ceres Seq. ID 1570390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1574:

```
Met Ala Thr Lys Leu Asp Thr Ser Ser Leu Leu Leu Ala Leu Leu Ser
1 5 10
Lys Cys Ser Leu Leu Thr Gln Thr Asn Leu Ala Leu Ser Leu Leu Val
20 25 30
Ala Ser Leu Ala Ser Leu Ala Leu Ser Leu Phe Phe Trp Ser His Pro
35 40 45
Gly Gly Pro Ala Trp Gly Lys Tyr Phe Leu His Arg Arg Arg Gln Thr
50 55 60
Thr Val Ile Pro Gly Pro Arg Gly Leu Pro Phe Val Gly Ser Met Ser
65 70 75 80
Leu Met Ser Asn Thr Leu Ala His Arg Cys Ile Ala Ala Thr Ala Glu
85 90 95
Lys Phe Arg Ala Glu Arg Leu Met Ala Phe Ser Leu Gly Glu Thr Arg
100 105 110
Val Ile Val Thr Cys Asn Pro Asp Val Ala Lys Glu Ile Leu Asn Ser
115 120 125
Pro Val Phe Ala Asp Arg Pro Val Lys Glu Ser Ala Tyr Ser Leu Met
130 135 140
Phe Asn Arg Ala Ile Gly Phe Ala Pro Tyr Gly Val Tyr Trp Arg Thr
145 150 155 160
Leu Arg Lys Ile Ala Ser Asn His Leu Phe Ser Pro Lys Gln Ile Lys
165 170 175
Arg Ser Glu Thr Gln Arg Ser Val Ile Ala Asn Gln Ile Val Lys Cys
180 185 190
Leu Thr Lys Lys Gln Ser Asn Thr Lys Gly Leu Cys Phe Ala Arg Asp Leu
195 200 205
Ile Lys Thr Ala Ser Leu Asn Asn Met Met Cys Ser Val Phe Gly Lys
210 215 220
Glu Tyr Glu Leu Glu Glu Glu His Glu Glu Val Ser Glu Leu Arg Glu
225 230 235 240
Leu Val Glu Glu Gly Tyr Asp Leu Leu Gly Thr Leu Asn Trp Thr Asp
245 250 255
His Leu Pro Trp Leu Ser Glu Phe Asp Pro Gln Arg Ile Arg Ser Arg
260 265 270
Cys Ser Asn Leu Val Pro Lys Val Asn Arg Phe Val Asn Arg Ile Ile
275 280 285
Ser Asp His Arg Glu Gln Thr Arg Asp Ser Pro Ser Asp Phe Val Asp
290 295 300
Val Leu Leu Ser Leu Asp Gly Pro Asp Lys Leu Ser Asp Pro Asp Ile
305 310 315 320
Ile Ala Val Leu Trp Glu Met Ile Phe Arg Gly Thr Asp Thr Val Ala
325 330 335
Val Leu Ile Glu Trp Ile Leu Ala Arg Met Val Leu His Pro Asp Ile
340 345 350
Gln Ser Thr Val His Asn Glu Leu Asp Gln Ile Val Gly Arg Ser Arg
355 360 365
Ala Val Glu Glu Ser Asp Val Val Ser Leu Val Tyr Leu Thr Ala Val
370 375 380
Val Lys Glu Val Leu Arg Leu His Pro Pro Gly Pro Leu Leu Ser Trp
```

|                 |                     |                     |         |
|-----------------|---------------------|---------------------|---------|
| 385             | 390                 | 395                 | 400     |
| Ala Arg Leu Ala | Ile Thr Asp Thr Ile | Ile Asp Gly Arg Arg | Val Pro |
|                 | 405                 | 410                 | 415     |
| Ala Gly Thr Thr | Ala Met Val Asn Met | Trp Ala Ile Ala His | Asp Pro |
|                 | 420                 | 425                 | 430     |
| His Val Trp Glu | Asn Pro Leu Glu Phe | Lys Pro Glu Arg Phe | Val Ala |
|                 | 435                 | 440                 | 445     |
| Lys Glu Gly Glu | Val Glu Phe Ser Val | Leu Gly Ser Asp Leu | Arg Leu |
|                 | 450                 | 455                 | 460     |
| Ala Pro Phe Gly | Ser Gly Arg Arg Val | Cys Pro Gly Lys Asn | Leu Gly |
|                 | 465                 | 470                 | 475     |
| Leu Thr Thr Val | Thr Phe Trp Thr Ala | Thr Leu Leu His Glu | Phe Glu |
|                 | 485                 | 490                 | 495     |
| Xaa Ala Asp Ala | Val Arg             |                     |         |
|                 | 500                 |                     |         |

(2) INFORMATION FOR SEQ ID NO:1575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 424 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..424

(D) OTHER INFORMATION: / Ceres Seq. ID 1570391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1575:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ser Leu Met Ser Asn Thr Leu Ala His Arg Cys Ile Ala Ala Thr |  |
| 1 5 10 15                                                       |  |
| Ala Glu Lys Phe Arg Ala Glu Arg Leu Met Ala Phe Ser Leu Gly Glu |  |
| 20 25 30                                                        |  |
| Thr Arg Val Ile Val Thr Cys Asn Pro Asp Val Ala Lys Glu Ile Leu |  |
| 35 40 45                                                        |  |
| Asn Ser Pro Val Phe Ala Asp Arg Pro Val Lys Glu Ser Ala Tyr Ser |  |
| 50 55 60                                                        |  |
| Leu Met Phe Asn Arg Ala Ile Gly Phe Ala Pro Tyr Gly Val Tyr Trp |  |
| 65 70 75 80                                                     |  |
| Arg Thr Leu Arg Lys Ile Ala Ser Asn His Leu Phe Ser Pro Lys Gln |  |
| 85 90 95                                                        |  |
| Ile Lys Arg Ser Glu Thr Gln Arg Ser Val Ile Ala Asn Gln Ile Val |  |
| 100 105 110                                                     |  |
| Lys Cys Leu Thr Lys Gln Ser Asn Thr Lys Gly Leu Cys Phe Ala Arg |  |
| 115 120 125                                                     |  |
| Asp Leu Ile Lys Thr Ala Ser Leu Asn Asn Met Met Cys Ser Val Phe |  |
| 130 135 140                                                     |  |
| Gly Lys Glu Tyr Glu Leu Glu Glu His Glu Glu Val Ser Glu Leu     |  |
| 145 150 155 160                                                 |  |
| Arg Glu Leu Val Glu Glu Gly Tyr Asp Leu Leu Gly Thr Leu Asn Trp |  |
| 165 170 175                                                     |  |
| Thr Asp His Leu Pro Trp Leu Ser Glu Phe Asp Pro Gln Arg Ile Arg |  |
| 180 185 190                                                     |  |
| Ser Arg Cys Ser Asn Leu Val Pro Lys Val Asn Arg Phe Val Asn Arg |  |
| 195 200 205                                                     |  |
| Ile Ile Ser Asp His Arg Glu Gln Thr Arg Asp Ser Pro Ser Asp Phe |  |
| 210 215 220                                                     |  |
| Val Asp Val Leu Leu Ser Leu Asp Gly Pro Asp Lys Leu Ser Asp Pro |  |
| 225 230 235 240                                                 |  |
| Asp Ile Ile Ala Val Leu Trp Glu Met Ile Phe Arg Gly Thr Asp Thr |  |
| 245 250 255                                                     |  |
| Val Ala Val Leu Ile Glu Trp Ile Leu Ala Arg Met Val Leu His Pro |  |
| 260 265 270                                                     |  |



```

Asp Ile Gln Ser Thr Val His Asn Glu Leu Asp Gln Ile Val Gly Arg
 275 280 285
Ser Arg Ala Val Glu Glu Ser Asp Val Val Ser Leu Val Tyr Leu Thr
 290 295 300
Ala Val Val Lys Glu Val Leu Arg Leu His Pro Pro Gly Pro Leu Leu
 305 310 315 320
Ser Trp Ala Arg Leu Ala Ile Thr Asp Thr Ile Ile Asp Gly Arg Arg
 325 330 335
Val Pro Ala Gly Thr Thr Ala Met Val Asn Met Trp Ala Ile Ala His
 340 345 350
Asp Pro His Val Trp Glu Asn Pro Leu Glu Phe Lys Pro Glu Arg Phe
 355 360 365
Val Ala Lys Glu Gly Glu Val Glu Phe Ser Val Leu Gly Ser Asp Leu
 370 375 380
Arg Leu Ala Pro Phe Gly Ser Gly Arg Arg Val Cys Pro Gly Lys Asn
 385 390 395 400
Leu Gly Leu Thr Thr Val Thr Phe Trp Thr Ala Thr Leu Leu His Glu
 405 410 415
Phe Glu Xaa Ala Asp Ala Val Arg
 420

```

(2) INFORMATION FOR SEQ ID NO:1576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1443
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1576:

```

gtcctaggaa gagcacaagc ctccacaagt ggtgttgccct ctctgttccct aactcccttc 60
tcttatataa aattgtgtat cctccatata tacaacaaga agagaaaact ttgatatggg 120
gttaaagatg tcaagaatcag ccaagcctta ctttgcaatg gtttgtcttc aattcggata 180
cgccggcatg aacctcgtga cgaaggttgt gctagaccgc ggcatgagcc attacgtcct 240
tgtgtgttac cgtaatgcct ttgccacggc tgctatcgca ccttttgctc tactctccga 300
gaggaaagtg aggcgaaga tgacatttcc aatattcatg cagatttttg ttctagctct 360
tctcgggcct ttgatcgatc aaaacttata ttacgcctgt ctcaaaacta ctccaaccaac 420
ttttgcggcg cgactcacaa atactgttcc agctttgacc ttatcatatt ccataatttg 480
caggatggag aaggtggaga tgagaaaagt aagattccaa gcaaaagtgg tggggacatt 540
agtgatagtg gttggagcca tgttgatgat ttattccaaa attcctctaa tccactcttc 600
tccgatctca cctcaaccgc catgtcttgc cgccggcagg tgaggactac ctcaaaagcca 660
ccgtcttccct cctcatcgcc tcattttctt gggcttccct ttctgttctt caggcggcta 720
cgttgaagag atactcatct cacctttcat tatcgacgat ggtgtgttcc atggggcaagt 780
tacagttcac agctctaacg ttgtgatgg agccaaacct ttctgcatgg aacattggct 840
ttgacatgaa cctcttctgc tctgttattg cgggcataat tgctgcgagc atagcgtact 900
acgttcaagg aatgatgacg aagcaaaaga gtgttatctt tgttaactgt tttaactctc 960
ttgtttgcac aatcggatcc atcattggct tcctcatcct caaccaaact ttaaacctgt 1020
gcggggcttc tggaaatggca attttagtgg tgggagtttg cactgttctt tggggaaagg 1080
aaggagatat cgatgaagaa gagaacattg aggagaagtt tgtagaagat gtcgaagtgt 1140
gcaaccgctg cgatatcaag gttctctcga tgaatgcaag aatcgatgag gaagttagacg 1200
ttgaaatgca atccgcaggc acagctaaag tggcgggtggg ttctctcgtaa cctctcgtgt 1260
gtggaaaaag atgttcacga ccttaattag atcttttcaa gtctttttat ttaacaaaaa 1320
ttttgataag aggacaacct ttttcttggc tctatatcat tgcctcaact ttttattttc 1380
tttttagtgt ttgttttata atcttctatta gaagggtaat tattattatt aaataaatgt 1440
tcc

```

(2) INFORMATION FOR SEQ ID NO:1577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..175  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570413  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1577:  
Met Gly Leu Lys Met Ser Glu Ser Ala Lys Pro Tyr Phe Ala Met Val  
1 5 10 15  
Cys Leu Gln Phe Gly Tyr Ala Gly Met Asn Leu Val Thr Lys Val Val  
20 25 30  
Leu Asp Arg Gly Met Ser His Tyr Val Leu Val Ala Tyr Arg Asn Ala  
35 40 45  
Phe Ala Thr Ala Ala Ile Ala Pro Phe Ala Leu Leu Ser Glu Arg Lys  
50 55 60  
Val Arg Pro Lys Met Thr Phe Pro Ile Phe Met Gln Ile Phe Val Leu  
65 70 75 80  
Ala Leu Leu Gly Pro Leu Ile Asp Gln Asn Leu Tyr Tyr Ala Cys Leu  
85 90 95  
Lys Leu Thr Ser Pro Thr Phe Ala Gly Ala Val Thr Asn Ile Val Pro  
100 105 110  
Ala Leu Thr Phe Ile Ile Ser Ile Ile Cys Arg Met Glu Lys Val Glu  
115 120 125  
Met Arg Lys Val Arg Phe Gln Ala Lys Val Val Gly Thr Leu Val Ile  
130 135 140  
Val Val Gly Ala Met Leu Met Ile Leu Phe Lys Ile Pro Leu Met His  
145 150 155 160  
Leu Ser Pro Ile Ser Pro His Arg Pro Cys Phe Val Ala Gly Arg  
165 170 175

(2) INFORMATION FOR SEQ ID NO:1578:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 171 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..171  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1578:

Met Ser Glu Ser Ala Lys Pro Tyr Phe Ala Met Val Cys Leu Gln Phe  
1 5 10 15  
Gly Tyr Ala Gly Met Asn Leu Val Thr Lys Val Val Leu Asp Arg Gly  
20 25 30  
Met Ser His Tyr Val Leu Val Ala Tyr Arg Asn Ala Phe Ala Thr Ala  
35 40 45  
Ala Ile Ala Pro Phe Ala Leu Leu Ser Glu Arg Lys Val Arg Pro Lys  
50 55 60  
Met Thr Phe Pro Ile Phe Met Gln Ile Phe Val Leu Ala Leu Leu Gly  
65 70 75 80  
Pro Leu Ile Asp Gln Asn Leu Tyr Tyr Ala Cys Leu Lys Leu Thr Ser  
85 90 95  
Pro Thr Phe Ala Gly Ala Val Thr Asn Ile Val Pro Ala Leu Thr Phe  
100 105 110  
Ile Ile Ser Ile Ile Cys Arg Met Glu Lys Val Glu Met Arg Lys Val  
115 120 125  
Arg Phe Gln Ala Lys Val Val Gly Thr Leu Val Ile Val Val Gly Ala  
130 135 140  
Met Leu Met Ile Leu Phe Lys Ile Pro Leu Met His Leu Ser Pro Ile

145 150 155 160  
Ser Pro His Arg Pro Cys Phe Val Ala Gly Arg  
165 170

(2) INFORMATION FOR SEQ ID NO:1579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570415

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1579:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Cys | Phe | Met | Gly | Thr | Leu | Gln | Ser | Thr | Ala | Leu | Thr | Phe | Val |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Met | Glu | Pro | Asn | Leu | Ser | Ala | Trp | Asn | Ile | Gly | Phe | Asp | Met | Asn | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ala | Ser | Ala | Tyr | Ala | Gly | Ile | Met | Ser | Ser | Ser | Ile | Ala | Tyr | Tyr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Gln | Gly | Met | Met | Thr | Lys | Gln | Lys | Ser | Val | Ile | Phe | Val | Thr | Ala |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Asn | Pro | Leu | Val | Val | Ile | Ile | Gly | Ser | Ile | Ile | Gly | Phe | Leu | Ile |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     | 80  |     |     |
| Leu | Asn | Gln | Thr | Leu | Asn | Leu | Gly | Gly | Val | Leu | Gly | Met | Ala | Ile | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Val | Val | Gly | Val | Cys | Thr | Val | Leu | Trp | Gly | Lys | Glu | Gly | Asp | Ile | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Glu | Glu | Asn | Ile | Glu | Glu | Lys | Phe | Val | Glu | Ile | Val | Lys | Cys | Cys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Asn | Arg | Cys | Asp | Ile | Lys | Val | Leu | Ser | Met | Met | Pro | Arg | Ile | Asp | Glu |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Glu | Val | Asp | Val | Glu | Met | Gln | Ser | Ala | Gly | Thr | Ala | Lys | Val | Ala | Val |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Phe | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 916 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..916
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1580:

|             |            |             |             |             |             |     |
|-------------|------------|-------------|-------------|-------------|-------------|-----|
| aaagcgaaG   | tttattcggt | tgccttgagct | ccgaagagtg  | gaaacaaaaa  | tggaggaaGa  | 60  |
| agagcacgag  | gtttacgggt | gagaaatccc  | tgaagtcggc  | gatacggatg  | ttcccgatcc  | 120 |
| ggatatcgat  | atgtctgcag | ccgatgagga  | cgccgttacg  | gagcttgcgt  | agatgaagag  | 180 |
| gagattaaag  | gagatggagg | aagaagctcg  | tgcgctacga  | gagatgcaag  | caaaaagtcga | 240 |
| aaaagaaatg  | ggagctactc | aagatcctgc  | tagtatggct  | gcaaatcaag  | aaggaaagga  | 300 |
| ggagggtggat | gctcgatcag | tttatgttgg  | caatgtcgac  | tatgcctgta  | cacctgaaga  | 360 |
| agtgcacaat  | catttccaaa | catgcggaaac | agtcacacgg  | gtaaccattc  | taatggacaa  | 420 |
| gtttggacag  | ccaaagggat | ttgcttatgt  | ggagtttgta  | gaagtggaaG  | ccgtgcaaga  | 480 |
| agctctgcag  | ctgaatgaat | cagagcttca  | tggtcgctcaa | ctgaagggtct | cgcctaagcg  | 540 |
| aaccaatggt  | ctgggaatga | aacagtatca  | ttcctggcgt  | ttcaaccctt  | caatgggata  | 600 |
| ccgcttttcg  | agaccctttg | tgcctccgta  | tttttattcc  | ccatatggat  | acgggaaggc  | 660 |
| tcctagggtc  | agaaggccaa | tgcggtacat  | gccttaccaa  | tagaaacctg  | accggaataa  | 720 |

gaagaactat gacagagatg atgccgaggt cgtccctcca ttctgagctt tatatatgaa 780  
tatgactttg ctgcacchg aacttaattt tgaatctgtc atgtacggat gagattataa 840  
gcttttgttt ctttagatta tgattatatt tggctgatat tactttcagt ttatatcttt 900  
gttagtactt tcttcc

(2) INFORMATION FOR SEQ ID NO:1581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1581:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Arg | Ser | Phe | Ile | Arg | Leu | Leu | Glu | Leu | Arg | Arg | Val | Glu | Thr | Lys |
| 1   |     |     |     | 5   |     |     |     |     |     |     |     | 10  |     |     | 15  |
| Met | Glu | Glu | Glu | Glu | His | Glu | Val | Tyr | Gly | Gly | Glu | Ile | Pro | Glu | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Gly | Asp | Thr | Asp | Val | Pro | Asp | Pro | Asp | Ile | Asp | Met | Ser | Ala | Ala | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Asp | Ala | Val | Thr | Glu | Leu | Ala | Glu | Met | Lys | Arg | Arg | Leu | Lys | Glu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Met | Glu | Glu | Glu | Ala | Ala | Ala | Leu | Arg | Glu | Met | Gln | Ala | Lys | Val | Glu |
|     |     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Glu | Met | Gly | Ala | Thr | Gln | Asp | Pro | Ala | Ser | Met | Ala | Ala | Asn | Gln |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Glu | Gly | Lys | Glu | Glu | Val | Asp | Ala | Arg | Ser | Val | Tyr | Val | Gly | Asn | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Tyr | Ala | Cys | Thr | Pro | Glu | Glu | Val | Gln | Leu | His | Phe | Gln | Thr | Cys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Thr | Val | Asn | Arg | Val | Thr | Ile | Leu | Met | Asp | Lys | Phe | Gly | Gln | Pro |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Lys | Gly | Phe | Ala | Tyr | Val | Glu | Phe | Val | Glu | Val | Glu | Ala | Val | Gln | Glu |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Ala | Leu | Gln | Leu | Asn | Glu | Ser | Glu | Leu | His | Gly | Arg | Gln | Leu | Lys | Val |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ser | Pro | Lys | Arg | Thr | Asn | Val | Pro | Gly | Met | Lys | Gln | Tyr | His | Pro | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Phe | Asn | Pro | Ser | Met | Gly | Tyr | Arg | Phe | Arg | Arg | Pro | Phe | Val | Pro |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Tyr | Phe | Tyr | Ser | Pro | Tyr | Gly | Tyr | Gly | Lys | Ala | Pro | Arg | Phe | Arg |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Arg | Pro | Met | Arg | Tyr | Met | Pro | Tyr | Gln |     |     |     |     |     |     |     |
|     |     |     |     |     | 230 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..217
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1582:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Glu | Glu | Glu | His | Glu | Val | Tyr | Gly | Gly | Glu | Ile | Pro | Glu | Val |
| 1   |     |     |     | 5   |     |     |     |     |     |     |     | 10  |     |     | 15  |
| Gly | Asp | Thr | Asp | Val | Pro | Asp | Pro | Asp | Ile | Asp | Met | Ser | Ala | Ala | Asp |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ala | Ala | Asp | Glu | Asp | Ala | Val | Thr | Glu | Leu | Ala | Glu | Met | Lys |
| 1   | Arg | Arg | Leu | Lys | Glu | Met | Glu | Glu | Glu | Ala | Ala | Ala | Leu | Arg | Glu |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Gln | Ala | Lys | Val | Glu | Lys | Glu | Met | Gly | Ala | Thr | Gln | Asp | Pro | Ala | Ser |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Met | Ala | Ala | Asn | Gln | Glu | Gly | Lys | Glu | Glu | Val | Asp | Ala | Arg | Ser | Val |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Tyr | Val | Gly | Asn | Val | Asp | Tyr | Ala | Cys | Thr | Pro | Glu | Glu | Val | Gln | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| His | Phe | Gln | Thr | Cys | Gly | Thr | Val | Asn | Arg | Val | Thr | Ile | Leu | Met | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Phe | Gly | Gln | Pro | Lys | Gly | Phe | Ala | Tyr | Val | Glu | Phe | Val | Glu | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Ala | Val | Gln | Glu | Ala | Leu | Gln | Leu | Asn | Glu | Ser | Glu | Leu | His | Gly |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Arg | Gln | Leu | Lys | Val | Ser | Pro | Lys | Arg | Thr | Asn | Val | Pro | Gly | Met | Lys |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Gln | Tyr | His | Pro | Gly | Arg | Phe | Asn | Pro | Ser | Met | Gly | Tyr | Arg | Phe | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Arg | Pro | Phe | Val | Pro | Pro | Tyr | Phe | Tyr | Ser | Pro | Tyr | Gly | Tyr | Gly | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Pro | Arg | Phe | Arg | Arg | Pro | Met | Arg | Tyr | Met | Pro | Tyr | Gln |     |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

(2) INFORMATION FOR SEQ ID NO:1584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..617
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1584:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| aatatataac | tttaaaacat | tgaagctaac | ttctcacaag  | tcaccaccat | ttctctctag | 60  |
| aaaaaatctg | aaaaaacaaa | ccatctcaaa | gtttcttgag  | aagaaaaaaa | gggtcaagaa | 120 |
| agatgcctaa | agacaggaat | atcggaatcg | ccatgggattt | ctcagagagc | agcaagaacg | 180 |
| ctctgaaatg | ggcgatcgag | aacttagcag | acaaaggaga  | cacgatttac | atcatccaca | 240 |
| ctctaccact | ctctggcgat | gaatctcgta | actccctctg  | gttcaaatcc | gggtctcctc | 300 |
| tcataccggt | ggcagagttt | agggaaacgg | agattatgga  | gaaatacgg  | gtcaaaacgg | 360 |
| acatcgcatg | tcttgatatg | ctcgacactg | gttcgaggca  | gaaagaggtg | catgtagtga | 420 |
| ccaagtata  | ctggggagat | gcaagagaga | agcttggtga  | tgctgttaaa | gatcttaaac | 480 |
| tcgattctat | tgctatggga | agcagaggac | tcagtgctct  | tcaaaggata | ataatgggaa | 540 |
| gcgtgaGcag | ctttgtgtgc | caacacgcgc | cttgccctgt  | caccgttgtc | aaggataacg | 600 |
| aataaacgat | ttctact    |            |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1585:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Pro | Lys | Asp | Arg | Asn | Ile | Gly | Ile | Ala | Met | Asp | Phe | Ser | Glu | Ser |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Ser | Lys | Asn | Ala | Leu | Lys | Trp | Ala | Ile | Glu | Asn | Leu | Ala | Asp | Lys | Gly |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Asp | Thr | Ile | Tyr | Ile | Ile | His | Thr | Leu | Pro | Leu | Ser | Gly | Asp | Glu | Ser |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Asn | Ser | Leu | Trp | Phe | Lys | Ser | Gly | Ser | Pro | Leu | Ile | Pro | Leu | Ala |  |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Glu | Phe | Arg | Glu | Pro | Glu | Ile | Met | Glu | Lys | Tyr | Gly | Val | Lys | Thr | Asp |  |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     | 80  |     |     |  |
| Ile | Ala | Cys | Leu | Asp | Met | Leu | Asp | Thr | Gly | Ser | Arg | Gln | Lys | Glu | Val |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| His | Val | Val | Thr | Lys | Leu | Tyr | Trp | Gly | Asp | Ala | Arg | Glu | Lys | Leu | Val |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Asp | Ala | Val | Lys | Asp | Leu | Lys | Leu | Asp | Ser | Ile | Val | Met | Gly | Ser | Arg |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Gly | Leu | Ser | Ala | Leu | Gln | Arg | Ile | Ile | Met | Gly | Ser | Val | Ser | Ser | Phe |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Val | Ile | Gln | His | Ala | Pro | Cys | Pro | Val | Thr | Val | Val | Lys | Asp | Asn | Glu |  |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |  |

(2) INFORMATION FOR SEQ ID NO:1586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..150  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570439  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1586:  
Met Asp Phe Ser Glu Ser Ser Lys Asn Ala Leu Lys Trp Ala Ile Glu  
1          5          10          15  
Asn Leu Ala Asp Lys Gly Asp Thr Ile Tyr Ile Ile His Thr Leu Pro  
          20          25          30  
Leu Ser Gly Asp Glu Ser Arg Asn Ser Leu Trp Phe Lys Ser Gly Ser  
          35          40          45  
Pro Leu Ile Pro Leu Ala Glu Phe Arg Glu Pro Glu Ile Met Glu Lys  
          50          55          60  
Tyr Gly Val Lys Thr Asp Ile Ala Cys Leu Asp Met Leu Asp Thr Gly  
65          70          75          80  
Ser Arg Gln Lys Glu Val His Val Val Thr Lys Leu Tyr Trp Gly Asp  
          85          90          95  
Ala Arg Glu Lys Leu Val Asp Ala Val Lys Asp Leu Lys Leu Asp Ser  
          100         105         110  
Ile Val Met Gly Ser Arg Gly Leu Ser Ala Leu Gln Arg Ile Ile Met  
115         120         125  
Gly Ser Val Ser Ser Phe Val Ile Gln His Ala Pro Cys Pro Val Thr  
130         135         140  
Val Val Lys Asp Asn Glu  
145         150

(2) INFORMATION FOR SEQ ID NO:1587:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 89 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..89  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570440  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1587:  
Met Glu Lys Tyr Gly Val Lys Thr Asp Ile Ala Cys Leu Asp Met Leu  
1          5          10          15  
Asp Thr Gly Ser Arg Gln Lys Glu Val His Val Val Thr Lys Leu Tyr  
          20          25          30  
Trp Gly Asp Ala Arg Glu Lys Leu Val Asp Ala Val Lys Asp Leu Lys  
          35          40          45  
Leu Asp Ser Ile Val Met Gly Ser Arg Gly Leu Ser Ala Leu Gln Arg  
50          55          60  
Ile Ile Met Gly Ser Val Ser Ser Phe Val Ile Gln His Ala Pro Cys  
65          70          75          80  
Pro Val Thr Val Val Lys Asp Asn Glu  
          85

(2) INFORMATION FOR SEQ ID NO:1588:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 641 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -

(B) LOCATION: 1..641

(D) OTHER INFORMATION: / Ceres Seq. ID 1570446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1588:

|             |             |            |            |             |             |     |
|-------------|-------------|------------|------------|-------------|-------------|-----|
| aatattatttg | tgttttggtcc | tatttattac | tctctgctct | cttcctgaag  | cttcttcac   | 60  |
| tttttgtttg  | acaagaagag  | gtagagaaga | agatgtctca | atcaatctcc  | tccagcacaa  | 120 |
| aggcagaaga  | agttgttagt  | gtagatgtga | gccaagccaa | gactctctcc  | cagttctgggc | 180 |
| atcaatatct  | tgacgttagg  | actcaggacg | agtttaggag | aggccattgt  | gaggcagcta  | 240 |
| agatcgctcaa | cattccctac  | atgctcaaca | cacctcaagg | tagagtgaag  | aatcgagagt  | 300 |
| tcttgtagca  | agtatcttct  | cttctaaacc | cagctgatga | tatccttggt  | ggttgtcaga  | 360 |
| gtggagccag  | atccttaaaa  | gccacaactg | aacttggtgc | tgccaggttac | aagaaagtga  | 420 |
| gaaacgtggg  | aggtggctac  | ttggcttggg | tagatcacag | cttcccctac  | aacaaggagg  | 480 |
| aggagggacc  | actctgcta   | taataatctt | aagattctct | ctttttstta  | atcaaatMat  | 540 |
| ataactgcct  | gtgtgatgta  | gtaatcattt | tcaatttaaa | attccagttt  | cttgtaataca | 600 |
| aaactctcgt  | gtaccaaat   | caataaaagc | tgtgtttctc | t           |             |     |

(2) INFORMATION FOR SEQ ID NO:1589:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1570447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1589:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Gln | Ser | Ile | Ser | Ser | Ser | Thr | Lys | Ala | Glu | Glu | Val | Val | Ser |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Val | Asp | Val | Ser | Gln | Ala | Lys | Thr | Leu | Leu | Gln | Ser | Gly | His | Gln | Tyr |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Asp | Val | Arg | Thr | Gln | Asp | Glu | Phe | Arg | Arg | Gly | His | Cys | Glu | Ala |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     |     |     |  |
| Ala | Lys | Ile | Val | Asn | Ile | Pro | Tyr | Met | Leu | Asn | Thr | Pro | Gln | Gly | Arg |  |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |  |
| Val | Lys | Asn | Arg | Glu | Phe | Leu | Glu | Gln | Val | Ser | Ser | Leu | Leu | Asn | Pro |  |
|     |     |     | 65  |     |     |     |     | 70  |     |     | 75  |     |     | 80  |     |  |
| Ala | Asp | Asp | Ile | Leu | Val | Gly | Cys | Gln | Ser | Gly | Ala | Arg | Ser | Leu | Lys |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Ala | Thr | Thr | Glu | Leu | Val | Ala | Ala | Gly | Tyr | Lys | Lys | Val | Arg | Asn | Val |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Gly | Gly | Gly | Tyr | Leu | Ala | Trp | Val | Asp | His | Ser | Phe | Pro | Ile | Asn | Lys |  |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |  |
| Glu | Glu | Glu | Glu | Pro | Ser | Ala | Asn |     |     |     |     |     |     |     |     |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1590:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1570448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1590:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Leu | Asn | Thr | Pro | Gln | Gly | Arg | Val | Lys | Asn | Arg | Glu | Phe | Leu | Glu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Gln | Val | Ser | Ser | Leu | Leu | Asn | Pro | Ala | Asp | Asp | Ile | Leu | Val | Gly | Cys |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gln | Ser | Gly | Ala | Arg | Ser | Leu | Lys | Ala | Thr | Thr | Glu | Leu | Val | Ala | Ala |  |



(2) INFORMATION FOR SEQ ID NO:1591:

(A) LENGTH: 702 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (a

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..702

(D) OTHER INFORMATION: / Ceres Seq. ID 1570449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1591:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| aacaaacaat | cgaaacacac  | atgagggtta | tctcaaaact | gttcgatctc | gacagaagac | 60  |
| gaatacacga | atcgccgaag  | cattttgatt | cgcggcgaag | cgccacatct | ctctctctac | 120 |
| tcagcagcga | aaccacacgc  | ctaacgacgt | tctatagcag | tctctctctc | caaacgctct | 180 |
| ctctcagttc | ctctctctac  | aaataacatt | ccaccacgtt | cacgcgtctc | ctctacccgt | 240 |
| acctctctgt | ttaaaactcg  | tgaacgagct | ctctctgtaa | cttgtctctc | cgtaacgctt | 300 |
| ggcatatctt | tcgcgcgttc  | tggacacgaa | Gtaagtatct | acgatcgcga | catgtgttgt | 360 |
| catctcgcac | cattcaacgc  | ccaagatctc | tcttcagcaa | cgtggaactc | ctgcggtctc | 420 |
| tcgcggtgag | aaattcttcac | ggcgcatcaa | gacggtaaaa | tcggagtttg | gaaactaacg | 480 |
| gttaaaacgc | gttataaaac  | ggttaacagc | cttccaactt | taaaacacgc | tttaacagct | 540 |
| tttgctctct | ctataaaacta | cttcaacgat | cgcgcgtata | gaaacgcttc | ctggatcgaa | 600 |
| catgCtagct | ccgtttactgc | tcttcgcggt | aatgacggat | ctatttaact | gtttctctgg | 660 |
| gagaagactg | ttaagaatatg | gaagacctcc | gacttctggt | gc         |            |     |

(2) INFORMATION FOR SEQ ID NO:1592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1570450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1592:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1593:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1570451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1593:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Arg | Val | Ile | Ser | Lys | Leu | Phe | Asp | Ser | Asp | Arg | Arg | Arg | Ile | Pro |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys | Ser | Pro | Lys | His | Leu | Asp | Ser | Gly | Glu | Ser | Ala | Thr | Ser | Ser | Ser |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Leu | Ser | Asp | Val | Thr | Thr | Gly | Ser | Ser | Ser | Leu | His | Ser | Ser | Leu |  |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |  |
| Ser | Leu | Gln | Thr | Leu | Pro | Ser | Val | Pro | Ser | Leu | Gln | Lys | Ile | Pro | Ser |  |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |  |
| Thr | Thr | Val | Thr | Val | Xaa | Ser | Leu | Arg | Tyr | Leu | Leu | Val |     |     |     |  |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1594:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1570452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1594:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Cys | Ala | His | Leu | Asp | Thr | Phe | Asn | Gly | Gln | Asp | Pro | Phe | Ser | Gly |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Thr | Val | Lys | Ser | Val | Gly | Phe | Ser | Gly | Glu | Lys | Ile | Phe | Thr | Ala | His |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gln | Asp | Gly | Lys | Ile | Gly | Val | Trp | Lys | Leu | Thr | Ala | Lys | Ser | Gly | Tyr |  |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |  |
| Lys | Gln | Leu | Thr | Thr | Leu | Pro | Thr | Leu | Asn | Asp | Arg | Leu | Arg | Arg | Phe |  |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |  |
| Ala | Leu | Pro | Lys | Asn | Tyr | Val | Gln | Val | Arg | Arg | His | Lys | Lys | Arg | Leu |  |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |  |
| Trp | Ile | Glu | His | Ala | Asp | Ala | Val | Thr | Ala | Leu | Ala | Val | Asn | Asp | Gly |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     | 95  |     |     |     |  |
| Phe | Ile | Tyr | Ser | Val | Ser | Trp | Asp | Lys | Thr | Leu | Lys | Ile | Trp | Arg | Ala |  |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ser | Asp | Leu | Arg | Cys |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1595:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 751 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..751

(D) OTHER INFORMATION: / Ceres Seq. ID 1570474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1595:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atccaccaca | tatttatgtt | tgatccaaaa | gccaacacaa | gcaaagaaat | taaaagtgtt | 60  |
| cttgttgctg | tagaacacaa | acagaacaaa | caaaaaatca | attgaagagt | ctctcagtcg | 120 |
| ttaggggaag | caaatagaga | aatggctagc | tttactgcct | ccgcttccac | cgctctccgc | 180 |
| gctcgctcgg | ctctcctctc | caagcctacc | gtcgccatct | ctgctcctgt | tcttggtttg | 240 |
| cttccaatgg | gtaagaagaa | gggaggagtg | agatgttcaa | tggagacaaa | gcaaggaaac | 300 |

|                                    |             |             |            |             |             |     |
|------------------------------------|-------------|-------------|------------|-------------|-------------|-----|
| gtctcagtc                          | atggggctg   | agtttcagct  | gcagcaacag | ctgtctttgac | ggcgggtgatg | 360 |
| agcaatcccg                         | cgatggcttt  | ggttgatgag  | aggatgtcaa | cagaaggaa   | aggattaccc  | 420 |
| tttggtctaa                         | gcaacaacct  | cttgggttgg  | attctgtttg | gagtccttgg  | tttgatctgg  | 480 |
| actttctct                          | tgcgtctacac | ttcatctctc  | gaggaggatg | aagaatctgg  | tccttctactc | 540 |
| tgaaggaaga                         | atcaatcttt  | cgtctttctca | tttccatttt | catgtgagaa  | catgaatcaa  | 600 |
| gtgttcaccc                         | ttctagtttc  | ttgtaattgt  | taagtaaaga | ctaaaaacta  | ttttcatgtg  | 660 |
| gttttacttt                         | cccccatctt  | ctttatcttg  | tcataacatt | gataaggagg  | agattatSgt  | 720 |
| gattattaaa tatcatgcat gacatgttca t |             |             |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1596:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 133 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1570475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1596:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Phe | Thr | Ala | Ser | Ala | Ser | Thr | Val | Ser | Ala | Ala | Arg | Pro |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Ala | Leu | Leu | Leu | Lys | Pro | Thr | Val | Ala | Ile | Ser | Ala | Pro | Val | Leu | Gly |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Pro | Pro | Met | Gly | Lys | Lys | Lys | Gly | Gly | Val | Arg | Cys | Ser | Met | Glu |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Thr | Lys | Gln | Gly | Asn | Val | Ser | Val | Met | Gly | Ala | Gly | Val | Ser | Ala | Ala |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ala | Thr | Ala | Ala | Leu | Thr | Ala | Val | Met | Ser | Asn | Pro | Ala | Met | Ala | Leu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Asp | Glu | Arg | Met | Ser | Thr | Glu | Gly | Thr | Gly | Leu | Pro | Phe | Gly | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Asn | Asn | Leu | Leu | Gly | Trp | Ile | Leu | Phe | Gly | Val | Phe | Gly | Leu | Ile |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Trp | Thr | Phe | Phe | Phe | Val | Tyr | Thr | Ser | Ser | Leu | Glu | Glu | Asp | Glu | Glu |
|     |     |     |     | 115 |     |     | 120 |     |     |     |     |     |     | 125 |     |
| Ser | Gly | Leu | Ser | Leu |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 130 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1597:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 98 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1570476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1597:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Lys | Lys | Lys | Gly | Gly | Val | Arg | Cys | Ser | Met | Glu | Thr | Lys | Gln |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Gly | Asn | Val | Ser | Val | Met | Gly | Ala | Gly | Val | Ser | Ala | Ala | Ala | Thr | Ala |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ala | Leu | Thr | Ala | Val | Met | Ser | Asn | Pro | Ala | Met | Ala | Leu | Val | Asp | Glu |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Arg | Met | Ser | Thr | Glu | Gly | Thr | Gly | Leu | Pro | Phe | Gly | Leu | Ser | Asn | Asn |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Leu | Leu | Gly | Trp | Ile | Leu | Phe | Gly | Val | Phe | Gly | Leu | Ile | Trp | Thr | Phe |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Phe | Phe | Val | Tyr | Thr | Ser | Ser | Leu | Glu | Glu | Asp | Glu | Glu | Ser | Gly | Leu |

85

90

95

Ser Leu

(2) INFORMATION FOR SEQ ID NO:1598:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1570477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1598:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Thr | Lys | Gln | Gly | Asn | Val | Ser | Val | Met | Gly | Ala | Gly | Val | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Ala | Ala | Thr | Ala | Ala | Leu | Thr | Ala | Val | Met | Ser | Asn | Pro | Ala | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Val | Asp | Glu | Arg | Met | Ser | Thr | Glu | Gly | Thr | Gly | Leu | Pro | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Leu | Ser | Asn | Asn | Leu | Leu | Gly | Trp | Ile | Leu | Phe | Gly | Val | Phe | Gly |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ile | Trp | Thr | Phe | Phe | Phe | Val | Tyr | Thr | Ser | Ser | Leu | Glu | Glu | Asp |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| Glu | Glu | Ser | Gly | Leu | Ser | Leu |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1599:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 782 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..782

(D) OTHER INFORMATION: / Ceres Seq. ID 1570478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1599:

|            |             |            |            |             |             |     |
|------------|-------------|------------|------------|-------------|-------------|-----|
| taaaggaggc | tactctagtc  | acattgttgt | tcatgaaagg | tactgtctaca | agataccctgt | 60  |
| ggactatccc | ttggaatcag  | ctgcaccatt | actctgtgct | ggaatcacgg  | tttatgcacc  | 120 |
| tatgatcgct | cacaatatga  | atcaacctgg | taaatctctt | ggggtgatcg  | ggctaggtgg  | 180 |
| tcttgagcac | atggcgcgtta | agttgtggca | ggcttttggg | cttagtgtta  | cggtttttag  | 240 |
| caccagcatt | tccaagaaga  | aagaagcttt | gaatctgcta | ggagctgaga  | atttcggtat  | 300 |
| ctcatctgac | catgaccaga  | tgaaggcact | agagaaatct | ctagactttc  | tagttgacac  | 360 |
| agcatctggg | gatcacgcgt  | tgtatcctta | catgtctctc | ttgaagattg  | ctggaactta  | 420 |
| tgtattgggt | ggtttcccaa  | gtgaaattaa | aatcagtcct | gccaatctca  | atcttgggtat | 480 |
| gagaatgcct | gctggaagcg  | taaccggggg | gaccaaaata | acacagcaaa  | tggttagattt | 540 |
| ctgtgcagct | cataagattt  | atccaaacat | agaggtgatt | cccatctcaa  | agataaacga  | 600 |
| agctctcgaa | agagttagta  | agaaggacat | caagtaccgt | ttcgtgattg  | acatcaagaa  | 660 |
| ctccctcaaa | tagatgttgc  | tcaaaggaga | gaataatgga | gtctgtataa  | agagaataat  | 720 |
| actcactgct | acaaatttta  | ttacgtattt | tctcgTtttt | bcattagtaa  | agcaataata  | 780 |
| tt         |             |            |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1600:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 223 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..223  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1600:

Lys Gly Gly Tyr Ser Ser His Ile Val Val His Glu Arg Tyr Cys Tyr  
1 5 10 15  
Lys Ile Pro Val Asp Tyr Pro Leu Glu Ser Ala Ala Pro Leu Leu Cys  
20 25 30  
Ala Gly Ile Thr Val Tyr Ala Pro Met Met Arg His Asn Met Asn Gln  
35 40 45  
Pro Gly Lys Ser Leu Gly Val Ile Gly Leu Gly Glu Gly His Met  
50 55 60  
Ala Val Lys Phe Gly Lys Ala Phe Gly Leu Ser Val Thr Val Phe Ser  
65 70 75 80  
Thr Ser Ile Ser Lys Lys Glu Glu Ala Leu Asn Leu Leu Gly Ala Glu  
85 90 95  
Asn Phe Val Ile Ser Ser Asp His Asp Gln Met Lys Ala Leu Glu Lys  
100 105 110  
Ser Leu Asp Phe Leu Val Asp Thr Ala Ser Gly Asp His Ala Phe Asp  
115 120 125  
Pro Tyr Met Ser Leu Leu Lys Ile Ala Gly Thr Tyr Val Leu Val Gly  
130 135 140  
Phe Pro Ser Glu Ile Lys Ile Ser Pro Ala Asn Leu Asn Leu Gly Met  
145 150 155 160  
Arg Met Leu Ala Gly Ser Val Thr Gly Gly Thr Lys Ile Thr Gln Gln  
165 170 175  
Met Leu Asp Phe Cys Ala Ala His Lys Ile Tyr Pro Asn Ile Glu Val  
180 185 190  
Ile Pro Ile Gln Lys Ile Asn Glu Ala Leu Glu Arg Val Val Lys Lys  
195 200 205  
Asp Ile Lys Tyr Arg Phe Val Ile Asp Ile Lys Asn Ser Leu Lys  
210 215 220

(2) INFORMATION FOR SEQ ID NO:1601:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..183  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1601:

Met Met Arg His Asn Met Asn Gln Pro Gly Lys Ser Leu Gly Val Ile  
1 5 10 15  
Gly Leu Gly Gly Leu Gly His Met Ala Val Lys Phe Gly Lys Ala Phe  
20 25 30  
Gly Leu Ser Val Thr Val Phe Ser Thr Ser Ile Ser Lys Lys Glu Glu  
35 40 45  
Ala Leu Asn Leu Leu Gly Ala Glu Asn Phe Val Ile Ser Ser Asp His  
50 55 60  
Asp Gln Met Lys Ala Leu Glu Lys Ser Leu Asp Phe Leu Val Asp Thr  
65 70 75 80  
Ala Ser Gly Asp His Ala Phe Asp Pro Tyr Met Ser Leu Leu Lys Ile  
85 90 95  
Ala Gly Thr Tyr Val Leu Val Gly Phe Pro Ser Glu Ile Lys Ile Ser  
100 105 110  
Pro Ala Asn Leu Asn Leu Gly Met Arg Met Leu Ala Gly Ser Val Thr  
115 120 125  
Gly Gly Thr Lys Lys Ile Thr Gln Gln Met Leu Asp Phe Cys Ala Ala His

(2) INFORMATION FOR SEO ID NO:1602:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 1570481

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1602:
```

(2) INFORMATION FOR SEQ ID NO:1603:

(A) LENGTH: 990 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..990

(D) OTHER INFORMATION: / Ceres Seq. ID 1570485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1603:

|             |             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| agagctcttta | accgcgcgaaa | gaaaccaccc  | tctgactgtt  | aagaaaattc  | tcattcggcgt | 60  |
| tcagatcaga  | aactctggaaa | ctcgagaagc  | tcaactgaaa  | caatcgattat | gagacgtgtc  | 120 |
| tgtatgtcta  | tgatgtttaat | tctgctcttc  | tctgctcttc  | tctcggtgtt  | tgcccaattg  | 180 |
| gtgatctgca  | gtgaagaaaa  | aggaacgtac  | aacgacaacg  | tCgtaaagat  | gaagcttggt  | 240 |
| ggatttagctg | atttccaaaga | cgaattgaaac | ggtggaaaag  | atgatcgatga | tattgcaact  | 300 |
| ttcgcgtgtc  | aadagacacaa | acagacagaa  | aatgcctgttc | tgcagcttgc  | taagaatttg  | 360 |

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| aaggcaacag | agcagggtgt  | tgctggcaag | ctataccgct  | ttactcttga | agttattgaa | 420 |
| gctggtgaga | aaaagattta  | tgaagctaaa | gtttgggtga  | agCcatggat | gaactttaag | 480 |
| cagcttcaag | agttcaagaa  | tattatcccc | tccttcaact  | tctctgacct | tggtttcaaa | 540 |
| ccagatggca | atggatttga  | ctggagatca | gtatcaacaa  | ataaccctga | agccaagaa  | 600 |
| gcagcgaagc | acggcatgaa  | atcacttcaa | cagaaatcaa  | actcactgtt | ccctataaaa | 660 |
| ctcatagata | taattcctagc | caggggcaag | gtggttgaag  | agcgtgtgaa | attcgaactg | 720 |
| ctgctgaagc | tagagagggg  | caacaaactg | gagaagtcca  | tggtagaagt | gatgaagagt | 780 |
| caaacccgca | agtatgagta  | gaagttgcag | atagcttttg  | gggtgtgtgc | catgtgtgaa | 840 |
| tggatccctt | atagtatata  | gtataactaa | tactgtctatg | tagtgaaaaa | aaacatgggt | 900 |
| attgtttggc | tttaaacaag  | gtttcttgta | aataaatata  | tgacttcaca | tatgtaaaaa | 960 |
| ttacaaatat | gatatgatta  | tgctgtgttg |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..232

(D) OTHER INFORMATION: / Ceres Seq. ID 1570486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1604:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Met | Arg | Arg | Ala | Ser | Met | Cys | Met | Met | Leu | Ile | Cys | Val | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Val | Leu | Leu | Ser | Gly | Phe | Gly | Gln | Phe | Val | Ile | Cys | Ser | Glu | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Lys | Gly | Thr | Tyr | Asn | Asp | Asn | Val | Val | Lys | Met | Lys | Leu | Gly | Gly | Phe |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Asp | Ser | Ser | Lys | Asn | Asp | Trp | Asn | Gly | Gly | Lys | Glu | Ile | Asp | Asp |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Ala | Leu | Phe | Ala | Val | Gln | Glu | His | Asn | Arg | Arg | Glu | Asn | Ala | Val | Leu |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Glu | Leu | Ala | Arg | Val | Leu | Lys | Ala | Thr | Glu | Gln | Val | Val | Ala | Gly | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Tyr | Arg | Leu | Thr | Leu | Glu | Val | Ile | Glu | Ala | Gly | Glu | Lys | Lys | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Glu | Ala | Lys | Val | Trp | Val | Lys | Pro | Trp | Met | Asn | Phe | Lys | Gln | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Glu | Phe | Lys | Asn | Ile | Ile | Pro | Ser | Phe | Thr | Ile | Ser | Asp | Leu | Gly |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Phe | Lys | Pro | Asp | Gly | Asn | Gly | Phe | Asp | Trp | Arg | Ser | Val | Ser | Thr | Asn |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     | 160 |     |
| Asn | Pro | Glu | Val | Gln | Glu | Ala | Ala | Lys | His | Ala | Met | Lys | Ser | Leu | Gln |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Gln | Lys | Ser | Asn | Ser | Leu | Phe | Pro | Tyr | Lys | Leu | Ile | Asp | Ile | Ile | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Arg | Ala | Lys | Val | Val | Glu | Glu | Arg | Val | Lys | Phe | Glu | Leu | Leu | Leu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Leu | Glu | Arg | Gly | Asn | Lys | Leu | Glu | Lys | Phe | Met | Val | Glu | Val | Met |
|     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Lys | Asp | Gln | Thr | Gly | Lys | Tyr | Glu |     |     |     |     |     |     |     |     |
|     |     |     | 225 |     |     |     | 230 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..230

(D) OTHER INFORMATION: / Ceres Seq. ID 1570487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1605:

```
Met Arg Arg Ala Ser Met Cys Met Met Leu Ile Cys Val Ser Leu Val
1 5 10 15
Leu Leu Ser Gly Phe Gly Gln Phe Val Ile Cys Ser Glu Glu Lys Gly
20 25 30
Thr Tyr Asn Asp Asn Val Val Lys Met Lys Leu Gly Gly Phe Ser Asp
35 40 45
Ser Lys Asn Asp Trp Asn Gly Gly Lys Glu Ile Asp Asp Ile Ala Leu
50 55 60
Phe Ala Val Gln Glu His Asn Arg Arg Glu Asn Ala Val Leu Glu Leu
65 70 75 80
Ala Arg Val Leu Lys Ala Thr Glu Gln Val Val Ala Gly Lys Leu Tyr
85 90 95
Arg Leu Thr Leu Glu Val Ile Glu Ala Gly Glu Lys Lys Ile Tyr Glu
100 105 110 115
Ala Lys Val Trp Val Lys Pro Trp Met Asn Phe Lys Gln Leu Gln Glu
120 125
Phe Lys Asn Ile Ile Pro Ser Phe Thr Ile Ser Asp Leu Gly Phe Lys
130 135 140
Pro Asp Gly Asn Gly Phe Asp Trp Arg Ser Val Ser Thr Asn Asn Pro
145 150 155 160
Glu Val Gln Glu Ala Ala Lys His Ala Met Lys Ser Leu Gln Gln Lys
165 170 175
Ser Asn Ser Leu Phe Pro Tyr Lys Leu Ile Asp Ile Ile Leu Ala Arg
180 185 190
Ala Lys Val Val Glu Glu Arg Val Lys Phe Glu Leu Leu Lys Leu
195 200 205
Glu Arg Gly Asn Lys Leu Glu Lys Phe Met Val Glu Val Met Lys Asp
210 215 220
Gln Thr Gly Lys Tyr Glu
225 230
```

(2) INFORMATION FOR SEQ ID NO:1606:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..225

(D) OTHER INFORMATION: / Ceres Seq. ID 1570488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1606:

```
Met Cys Met Met Leu Ile Cys Val Ser Leu Val Leu Leu Ser Gly Phe
1 5 10 15
Gly Gln Phe Val Ile Cys Ser Glu Glu Lys Gly Thr Tyr Asn Asp Asn
20 25 30
Val Val Lys Met Lys Leu Gly Gly Phe Ser Asp Ser Lys Asn Asp Trp
35 40 45
Asn Gly Gly Lys Glu Ile Asp Asp Ile Ala Leu Phe Ala Val Gln Glu
50 55 60
His Asn Arg Arg Glu Asn Ala Val Leu Glu Leu Ala Arg Val Leu Lys
65 70 75 80
Ala Thr Glu Gln Val Val Ala Gly Lys Leu Tyr Arg Leu Thr Leu Glu
85 90 95
Val Ile Glu Ala Gly Glu Lys Lys Ile Tyr Glu Ala Lys Val Trp Val
100 105 110
Lys Pro Trp Met Asn Phe Lys Gln Leu Gln Glu Phe Lys Asn Ile Ile
```



|                                             |                     |     |
|---------------------------------------------|---------------------|-----|
| 115                                         | 120                 | 125 |
| Pro Ser Phe Thr Ile Ser Asp Leu Gly Phe Lys | Pro Asp Gly Asn Gly |     |
| 130                                         | 135                 | 140 |
| Phe Asp Trp Arg Ser Val Ser Thr Asn Asn Pro | Glu Val Gln Glu Ala |     |
| 145                                         | 150                 | 155 |
| Ala Lys His Ala Met Lys Ser Leu Gln Gln Lys | Ser Asn Ser Leu Phe |     |
| 165                                         | 170                 | 175 |
| Pro Tyr Lys Leu Ile Asp Ile Ile Leu Ala Arg | Ala Lys Val Val Glu |     |
| 180                                         | 185                 | 190 |
| Glu Arg Val Lys Phe Glu Leu Leu Leu Lys Leu | Glu Arg Gly Asn Lys |     |
| 195                                         | 200                 | 205 |
| Leu Glu Lys Phe Met Val Glu Val Met Lys Asp | Gln Thr Gly Lys Tyr |     |
| 210                                         | 215                 | 220 |

Glu  
225

(2) INFORMATION FOR SEQ ID NO:1607:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 799 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..799
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1607:

|             |            |            |             |             |            |     |
|-------------|------------|------------|-------------|-------------|------------|-----|
| aagcatcaact | atgctcgaaa | atctctcttt | gttcgctttg  | tggggaacga  | actatggccg | 60  |
| agagatggag  | gaacacggct | ctactcgta  | tcgacatgca  | gaacgatttc  | atagaggaa  | 120 |
| gtgctgtgac  | gcaagtga   | ggaggaaa   | ctatagtctc  | taatgttacc  | agagtcgtcg | 180 |
| aactcgcgag  | gcagcgtggt | attctcgtaa | tttggtgtgt  | tcgagaacat  | gatcgtaag  | 240 |
| gaagagatgt  | tgaattattc | aggcgccata | actacagttc  | tgagaaaagtc | gggcagatta | 300 |
| ttaaaggcac  | cgtagGagca | gaattggttg | atggattgat  | gatcaacgaa  | gaagatgat  | 360 |
| ataagattgt  | gaaaactcgt | ttcagtgctt | tctttagtac  | taattctcat  | tccttcttgc | 420 |
| aaacttcagg  | ggttaccaag | ttagtgattg | ctgggtgtgca | aaacgcgaac  | tgtatccggc | 480 |
| aaacggtggt  | tgtatgcagt | gcgctggatt | atccCaatgt  | gactgttatt  | acagatgcc  | 540 |
| cagctgtctg  | aacaccagag | atccatactg | cgaatattct  | tgacatgaag  | aattatggag | 600 |
| tcaaaactcc  | tacattacac | gagtggtccg | aagaacttgc  | ttgacaaa    | ccatcctaaa | 660 |
| gcccttcgtt  | tatctttttt | cttggttgta | catgtaataa  | agaaaatggt  | aattctgtgt | 720 |
| ttgtaagtta  | caaaatctcc | accatttggt | gtatactttt  | cttgtaattcc | cgtccaaaaa | 780 |
| aataaaatgt  | attacgttt  |            |             |             |            |     |

(2) INFORMATION FOR SEQ ID NO:1608:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 213 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1608:

|                                                                 |          |
|-----------------------------------------------------------------|----------|
| Ala Ser Leu Cys Ser Lys Ile Ser Leu Cys Ser Leu Cys Gly Glu Arg |          |
| 1                                                               | 5 10 15  |
| Thr Met Ala Glu Arg Trp Arg Asn Thr Ala Leu Leu Val Ile Asp Met |          |
|                                                                 | 20 25 30 |
| Gln Asn Asp Phe Ile Glu Glu Gly Ala Val Thr Gln Val Lys Gly Gly |          |
|                                                                 | 35 40 45 |
| Lys Ser Ile Val Pro Asn Val Ile Arg Val Val Glu Leu Ala Arg Gln |          |
|                                                                 | 50 55 60 |

Arg Gly Ile Leu Val Ile Trp Val Val Arg Glu His Asp Arg Gln Gly  
65 70 75 80  
Arg Asp Val Glu Leu Phe Arg Arg His Asn Tyr Ser Ser Glu Lys Val  
85 90 95  
Gly Pro Val Ile Lys Gly Thr Val Gly Ala Glu Leu Val Asp Gly Leu  
100 105 110  
Met Ile Asn Glu Glu Asp Asp Tyr Lys Ile Val Lys Thr Arg Phe Ser  
115 120 125  
Ala Phe Phe Ser Thr Asn Leu His Ser Phe Leu Gln Thr Ser Gly Val  
130 135 140  
Thr Lys Leu Val Ile Ala Gly Val Gln Thr Pro Asn Cys Ile Arg Gln  
145 150 155 160  
Thr Val Phe Asp Ala Val Ala Leu Asp Tyr Pro Asn Val Thr Val Ile  
165 170 175  
Thr Asp Ala Thr Ala Ala Ala Thr Pro Glu Ile His Thr Ala Asn Ile  
180 185 190  
Leu Asp Met Lys Asn Ile Gly Val Lys Thr Pro Thr Leu His Glu Trp  
195 200 205  
Ser Glu Glu Leu Ala  
210

(2) INFORMATION FOR SEQ ID NO:1609:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..196

(D) OTHER INFORMATION: / Ceres Seq. ID 1570491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1609:

Met Ala Glu Arg Trp Arg Asn Thr Ala Leu Leu Val Ile Asp Met Gln  
1 5 10  
Asn Asp Phe Ile Glu Glu Gly Ala Val Thr Gln Val Lys Gly Gly Lys  
20 25 30  
Ser Ile Val Pro Asn Val Ile Arg Val Val Glu Leu Ala Arg Gln Arg  
35 40 45  
Gly Ile Leu Val Ile Trp Val Val Arg Glu His Asp Arg Gln Gly Arg  
50 55 60  
Asp Val Glu Leu Phe Arg Arg His Asn Tyr Ser Ser Glu Lys Val Gly  
65 70 75 80  
Pro Val Ile Lys Gly Thr Val Gly Ala Glu Leu Val Asp Gly Leu Met  
85 90 95  
Ile Asn Glu Glu Asp Asp Tyr Lys Ile Val Lys Thr Arg Phe Ser Ala  
100 105 110  
Phe Phe Ser Thr Asn Leu His Ser Phe Leu Gln Thr Ser Gly Val Thr  
115 120 125  
Lys Leu Val Ile Ala Gly Val Gln Thr Pro Asn Cys Ile Arg Gln Thr  
130 135 140  
Val Phe Asp Ala Val Ala Leu Asp Tyr Pro Asn Val Thr Val Ile Thr  
145 150 155 160  
Asp Ala Thr Ala Ala Ala Thr Pro Glu Ile His Thr Ala Asn Ile Leu  
165 170 175  
Asp Met Lys Asn Ile Gly Val Lys Thr Pro Thr Leu His Glu Trp Ser  
180 185 190  
Glu Glu Leu Ala  
195

(2) INFORMATION FOR SEQ ID NO:1610:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..182  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570492  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1610:  
Met Gln Asn Asp Phe Ile Glu Glu Gly Ala Val Thr Gln Val Lys Gly  
1                  5                  10                  15  
Gly Lys Ser Ile Val Pro Asn Val Ile Arg Val Val Glu Leu Ala Arg  
                  20                  25                  30  
Gln Arg Gly Ile Leu Val Ile Trp Val Val Arg Glu His Asp Arg Gln  
                  35                  40                  45  
Gly Arg Asp Val Glu Leu Phe Arg Arg His Asn Tyr Ser Ser Glu Lys  
                  50                  55                  60  
Val Gly Pro Val Ile Lys Gly Thr Val Gly Ala Glu Leu Val Asp Gly  
65                  70                  75                  80  
Leu Met Ile Asn Glu Glu Asp Asp Tyr Lys Ile Val Lys Thr Arg Phe  
                  85                  90                  95  
Ser Ala Phe Phe Ser Thr Asn Leu His Ser Phe Leu Gln Thr Ser Gly  
                  100                  105                  110  
Val Thr Lys Leu Val Ile Ala Gly Val Gln Thr Pro Asn Cys Ile Arg  
                  115                  120                  125  
Gln Thr Val Phe Asp Ala Val Ala Leu Asp Tyr Pro Asn Val Thr Val  
                  130                  135                  140  
Ile Thr Asp Ala Thr Ala Ala Ala Thr Pro Glu Ile His Thr Ala Asn  
145                  150                  155                  160  
Ile Leu Asp Met Lys Asn Ile Gly Val Lys Thr Pro Thr Leu His Glu  
                  165                  170                  175  
Trp Ser Glu Glu Leu Ala  
                  180

(2) INFORMATION FOR SEQ ID NO:1611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..642  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1611:

atcattcaaca atggcatatg caactattct catgatcttc tcgggtggtgg cactaatgtc 60  
cggcgagaga gctcatgcag cagtggactg ctcatggtg atactaaaca tggcgtgatt 120  
tttgtctttt gtgactagtg gtagtacagt tgtcaaagcg gaaggaaacat gttgttcagg 180  
gcttaagact gtggttagga caggaccaga atgtctatgt gaggctttca agaacagtgg 240  
ttctcttggt ttaactcttg atctttctaa agctgottct ctccctttctg ttgtgaaagt 300  
tgctgtctct cctctgtctc gtttgtgccc ttctgtctct ggagatcttc ctgctactgc 360  
ccctggttta tctcCtaagg ccggagcagg agcaaccgag ttgtccagtg gtgcaaatgc 420  
ggcaactcca gtttctgtcc cgaggagttc cgatgcgtcc ttgctctctg tatcttttgc 480  
atttgtctac ttcattggcac ctattctctc ttctattga gtcttaaaat ttaattgtctw 540  
cttggtgagt tatttttggt tgetatgtag ctgaagagtt tgggtgttact gatcatattt 600  
acctttcatg tgtaaatatt aatgagaaat ctcttttag tt

(2) INFORMATION FOR SEQ ID NO:1612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..172  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570494  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1612:  
Ser Phe Thr Met Ala Tyr Ala Thr Ile Leu Met Ile Phe Ser Val Val  
1                  5                  10                  15  
Ala Leu Met Ser Gly Glu Arg Ala His Ala Ala Val Asp Cys Ser Ser  
                  20                  25                  30  
Leu Ile Leu Asn Met Ala Asp Cys Leu Ser Phe Val Thr Ser Gly Ser  
                  35                  40                  45  
Thr Val Val Lys Pro Glu Gly Thr Cys Cys Ser Gly Leu Lys Thr Val  
                  50                  55                  60  
Val Arg Thr Gly Pro Glu Cys Leu Cys Glu Ala Phe Lys Asn Ser Gly  
65                  70                  75                  80  
Ser Leu Gly Leu Thr Leu Asp Leu Ser Lys Ala Ala Ser Leu Pro Ser  
                  85                  90                  95  
Val Cys Lys Val Ala Ala Pro Pro Ser Ala Arg Cys Gly Leu Ser Val  
                  100                 105                 110  
Ser Gly Asp Pro Pro Ala Thr Ala Pro Gly Leu Ser Pro Thr Ala Gly  
                  115                 120                 125  
Ala Gly Ala Pro Ala Leu Ser Ser Gly Ala Asn Ala Ala Thr Pro Val  
                  130                 135                 140  
Ser Ser Pro Arg Ser Ser Asp Ala Ser Leu Leu Ser Val Ser Phe Ala  
145                 150                 155                 160  
Phe Val Ile Phe Met Ala Leu Ile Ser Ser Phe Tyr  
                  165                 170  
(2) INFORMATION FOR SEQ ID NO:1613:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 169 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..169  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570495  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1613:  
Met Ala Tyr Ala Thr Ile Leu Met Ile Phe Ser Val Val Ala Leu Met  
1                  5                  10                  15  
Ser Gly Glu Arg Ala His Ala Ala Val Asp Cys Ser Ser Leu Ile Leu  
                  20                  25                  30  
Asn Met Ala Asp Cys Leu Ser Phe Val Thr Ser Gly Ser Thr Val Val  
                  35                  40                  45  
Lys Pro Glu Gly Thr Cys Cys Ser Gly Leu Lys Thr Val Val Arg Thr  
50                  55                  60  
Gly Pro Glu Cys Leu Cys Glu Ala Phe Lys Asn Ser Gly Ser Leu Gly  
65                  70                  75                  80  
Leu Thr Leu Asp Leu Ser Lys Ala Ala Ser Leu Pro Ser Val Cys Lys  
                  85                  90                  95  
Val Ala Ala Pro Pro Ser Ala Arg Cys Gly Leu Ser Val Ser Gly Asp  
                  100                 105                 110  
Pro Pro Ala Thr Ala Pro Gly Leu Ser Pro Thr Ala Gly Ala Gly Ala  
                  115                 120                 125  
Pro Ala Leu Ser Ser Gly Ala Asn Ala Ala Thr Pro Val Ser Ser Pro  
130                 135                 140  
Arg Ser Ser Asp Ala Ser Leu Leu Ser Val Ser Phe Ala Phe Val Ile  
145                 150                 155                 160

Phe Met Ala Leu Ile Ser Ser Phe Tyr  
165

(2) INFORMATION FOR SEQ ID NO:1614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1614:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Phe | Ser | Val | Val | Ala | Leu | Met | Ser | Gly | Glu | Arg | Ala | His | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     | 15  |     |     |     |     |
| Ala | Val | Asp | Cys | Ser | Ser | Leu | Ile | Leu | Asn | Met | Ala | Asp | Cys | Leu | Ser |
|     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Phe | Val | Thr | Ser | Gly | Ser | Thr | Val | Val | Lys | Pro | Glu | Gly | Thr | Cys | Cys |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ser | Gly | Leu | Lys | Thr | Val | Val | Arg | Thr | Gly | Pro | Glu | Cys | Leu | Cys | Glu |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Ala | Phe | Lys | Asn | Ser | Gly | Ser | Leu | Gly | Leu | Thr | Leu | Asp | Leu | Ser | Lys |
|     | 65  |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Ala | Ala | Ser | Leu | Pro | Ser | Val | Cys | Lys | Val | Ala | Ala | Pro | Pro | Ser | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | Cys | Gly | Leu | Ser | Val | Ser | Gly | Asp | Pro | Pro | Ala | Thr | Ala | Pro | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Leu | Ser | Pro | Thr | Ala | Gly | Ala | Gly | Ala | Pro | Ala | Leu | Ser | Ser | Gly | Ala |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     | 125 |     |
| Asn | Ala | Ala | Thr | Pro | Val | Ser | Ser | Pro | Arg | Ser | Ser | Asp | Ala | Ser | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Leu | Ser | Val | Ser | Phe | Ala | Phe | Val | Ile | Phe | Met | Ala | Leu | Ile | Ser | Ser |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Phe | Tyr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 863 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..863
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1615:

|             |             |            |            |             |             |     |
|-------------|-------------|------------|------------|-------------|-------------|-----|
| ttttggctgc  | acgatctcag  | tttttcagat | caatgtttta | caatactcta  | gcagagaaca  | 60  |
| acagcgacgt  | aGgatcagc   | gatttggaa  | ctaaggtttt | caaggccttg  | ttacacttca  | 120 |
| tgtataaaga  | ttccctccca  | ggagatgtg  | aaccattaac | ggctcatcca  | tttgacctat  | 180 |
| taaggccgtc  | cgaaatagat  | gataactga  | ttgtaaagct | tctggcagct  | gcggaatgt   | 240 |
| acaactctgag | taggtctcaga | ttattgtgtg | aatctcacat | ctgcaaaaggc | atatctatca  | 300 |
| gctccgtgtc  | caagatctta  | gctttatccg | acaaatataa | tgcatccgaa  | ctaaaaaggcg | 360 |
| tttccctaaa  | attcactgca  | gaaaacctag | cagctgttct | gcagacaaaa  | gcataatgaag | 420 |
| attctgaagga | tgactgtcca  | aacctccagt | ctgagctact | aaaggcggtc  | gcgtgttatg  | 480 |
| acgacacaag  | tagcagcgga  | ggaggaaagt | ctcagagtgt | ttgggtctcaa | ctctctaacg  | 540 |
| gtgggtgagac | cagtagccga  | agggtcaggc | agcgaaccac | ttagaagagc  | ttcttccact  | 600 |
| gtgtttaaaca | aactactttt  | gcttaccact | cgtaaacaga | ttaacgggtt  | tatctagtat  | 660 |
| gtaccgaatg  | aaagggaagc  | ggagccagaa | attctgtacc | acaagagaag  | agctatgcgg  | 720 |
| ctgtgcacta  | gtgattaacc  | ggtgcttcac | ctttcagttc | cttcacgtct  | ctgtggatttt | 780 |

ttgttgttga gtctttttttt caaattctttt tcccagcttc aaattactag aaacttatga 840

tgatataata gaaagagtta act

(2) INFORMATION FOR SEQ ID NO:1616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..193
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1616:

```
Leu Ala Ala Arg Ser Gln Phe Phe Arg Ser Met Phe Tyr Asn Thr Leu
1 5 10 15
Ala Glu Asn Asn Ser Asp Val Val Ile Ser Asp Leu Glu Pro Lys Val
20 25 30
Phe Lys Ala Leu Leu His Phe Met Tyr Lys Asp Ser Leu Pro Gly Asp
35 40 45
Val Glu Pro Leu Thr Ala His Ser Phe Asp Leu Leu Arg Pro Ser Glu
50 55 60
Ile Asp Asp Thr Leu Ile Val Lys Leu Ala Ala Glu Met Tyr
65 70 75 80
Asn Leu Ser Arg Leu Arg Leu Leu Cys Glu Ser His Ile Cys Lys Gly
85 90 95
Ile Ser Ile Ser Ser Val Ser Lys Ile Leu Ala Leu Ser Asp Lys Tyr
100 105 110
Asn Ala Ser Glu Leu Lys Ser Val Ser Leu Lys Phe Thr Ala Glu Asn
115 120 125
Leu Ala Ala Val Leu Gln Thr Lys Ala Tyr Glu Asp Leu Lys Asp Asp
130 135 140
Cys Pro Asn Leu Gln Ser Glu Leu Leu Lys Ala Val Ala Gly Tyr Asp
145 150 155 160
Asp Thr Ser Ser Ser Gly Gly Gly Lys Ser Gln Ser Val Trp Ala Gln
165 170 175
Leu Ser Asn Gly Gly Glu Thr Ser Ser Arg Arg Val Arg Gln Arg Thr
180 185 190
Thr
```

(2) INFORMATION FOR SEQ ID NO:1617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1617:

```
Met Phe Tyr Asn Thr Leu Ala Glu Asn Asn Ser Asp Val Val Ile Ser
1 5 10 15
Asp Leu Glu Pro Lys Val Phe Lys Ala Leu Leu His Phe Met Tyr Lys
20 25 30
Asp Ser Leu Pro Gly Asp Val Glu Pro Leu Thr Ala His Ser Phe Asp
35 40 45
Leu Leu Arg Pro Ser Glu Ile Asp Asp Thr Leu Ile Val Lys Leu Leu
50 55 60
Ala Ala Ala Glu Met Tyr Asn Leu Ser Arg Leu Arg Leu Leu Cys Glu
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |
| Ser | His | Ile | Cys | Lys | Gly | Ile | Ser | Ile | Ser | Val | Ser | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     | 95  |
| Ala | Leu | Ser | Asp | Lys | Tyr | Asn | Ala | Ser | Glu | Leu | Lys | Ser |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     | 110 |
| Lys | Phe | Thr | Ala | Glu | Asn | Leu | Ala | Val | Leu | Gln | Thr | Lys |
|     |     |     |     | 115 |     |     | 120 |     |     |     | 125 | Ala |
| Glu | Asp | Leu | Lys | Asp | Asp | Cys | Pro | Asn | Leu | Gln | Ser | Glu |
|     |     |     |     | 130 |     | 135 |     |     |     | 140 |     | Leu |
| Ala | Val | Ala | Gly | Tyr | Asp | Asp | Thr | Ser | Ser | Ser | Gly | Gly |
|     |     |     |     | 145 |     | 150 |     |     |     | 155 |     | Lys |
| Gln | Ser | Val | Trp | Ala | Gln | Leu | Ser | Asn | Gly | Gly | Glu | Thr |
|     |     |     |     | 165 |     |     | 170 |     |     |     |     | Ser |
| Arg | Val | Arg | Gln | Arg | Thr | Thr |     |     |     |     |     | 175 |
|     |     |     |     | 180 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1570500

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1618:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Lys | Asp | Ser | Leu | Pro | Gly | Asp | Val | Glu | Pro | Leu | Thr | Ala | His |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Phe | Asp | Leu | Leu | Arg | Pro | Ser | Glu | Ile | Asp | Asp | Thr | Leu | Ile | Val |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Lys | Leu | Leu | Ala | Ala | Ala | Glu | Met | Tyr | Asn | Leu | Ser | Arg | Leu | Arg | Leu |
|     |     |     |     | 35  |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Leu | Cys | Glu | Ser | His | Ile | Cys | Lys | Gly | Ile | Ser | Ile | Ser | Ser | Val | Ser |
|     |     |     |     | 50  |     | 55  |     |     | 60  |     |     |     |     |     |     |
| Lys | Ile | Leu | Ala | Leu | Ser | Asp | Lys | Tyr | Asn | Ala | Ser | Glu | Leu | Lys | Ser |
|     |     |     |     | 65  |     | 70  |     |     | 75  |     |     |     |     | 80  |     |
| Val | Ser | Leu | Lys | Phe | Thr | Ala | Glu | Asn | Leu | Ala | Ala | Val | Leu | Gln | Thr |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Ala | Tyr | Glu | Asp | Leu | Lys | Asp | Asp | Cys | Pro | Asn | Leu | Gln | Ser | Glu |
|     |     |     |     | 100 |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Leu | Leu | Lys | Ala | Val | Ala | Gly | Tyr | Asp | Asp | Thr | Ser | Ser | Ser | Gly | Gly |
|     |     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Lys | Ser | Gln | Ser | Val | Trp | Ala | Gln | Leu | Ser | Asn | Gly | Gly | Glu | Thr |
|     |     |     |     | 130 |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Ser | Ser | Arg | Arg | Val | Arg | Gln | Arg | Thr | Thr |     |     |     |     |     |     |
|     |     |     |     | 145 |     | 150 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1002 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1002
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1619:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| attcaatttt | tgttggtctt | ttcaaaagt  | gaaatacaac | aaaacaatgt | cgggacttag | 60  |
| aagattggat | ggcaagatcg | caattataac | aggcggagct | agtgggattg | gagctgaagc | 120 |

(2) INFORMATION FOR SEQ ID NO:1620:

(A) LENGTH: 276 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..276

(D) OTHER INFORMATION: / Ceres Seq. ID 1570502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1620:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   | Asn | Phe | Trp | Trp | Ser | Phe | Gln | Lys | Trp | Lys | Tyr | Asn | Lys | Thr | Met |
| Ser | Gly | Leu | Arg | Arg | Leu | Asp | Gly | Lys | Ile | Ala | Ile | Ile | Thr | Gly | Gly |
| Ala | Ser | Gly | Ile | Gly | Ala | Glu | Ala | Val | Arg | Leu | Phe | Thr | Asp | His | Gly |
| Ala | Lys | Val | Val | Ile | Val | Asp | Ile | Gln | Glu | Glu | Leu | Gly | Gln | Asn | Leu |
| Ala | Val | Ser | Ile | Gly | Leu | Asp | Lys | Ala | Ser | Phe | Tyr | Arg | Cys | Asn | Val |
| 65  | Thr | Asp | Glu | Thr | Asp | Val | Glu | Asn | Ala | Val | Lys | Phe | Thr | Val | Glu |
| His | Gly | Lys | Leu | Asp | Val | Leu | Phe | Ser | Asn | Ala | Gly | Val | Leu | Glu | Ala |
| Phe | Gly | Ser | Val | Leu | Asp | Leu | Asp | Leu | Glu | Ala | Phe | Asp | Arg | Thr | Met |
| Ala | Val | Asn | Val | Arg | Gly | Ala | Ala | Phe | Ile | Lys | His | Ala | Ala | Arg |     |
| 130 | Ser | Met | Val | Ala | Ser | Gly | Thr | Arg | Gly | Ser | Ile | Val | Cys | Thr | Ser |
| 145 | Ile | Ala | Ala | Glu | Ile | Gly | Gly | Pro | Gly | Pro | His | Ser | Tyr | Thr | Ser |
| Lys | His | Ala | Leu | Leu | Gly | Leu | Ile | Arg | Ser | Ala | Cys | Ala | Gly | Leu | Gly |
| Gln | Tyr | Gly | Ile | Arg | Val | Asn | Gly | Val | Ala | Pro | Tyr | Gly | Val | Ala | Thr |
| Gly | Met | Thr | Ser | Ala | Tyr | Asn | Glu | Glu | Ala | Val | Lys | Met | Leu | Glu | Glu |
| 210 | Tyr | Gly | Glu | Ala | Leu | Gly | Asn | Leu | Lys | Gly | Val | Val | Leu | Lys | Ala |
| 225 | His | Ile | Ala | Glu | Ala | Ala | Leu | Phe | Leu | Ala | Ser | Asp | Asp | Ser | Val |
| Ile | Ser | Gly | Gln | Asn | Leu | Val | Val | Asp | Gly | Gly | Phe | Ser | Val | Val | Lys |



Leu Met Ser Thr  
275

(2) INFORMATION FOR SEQ ID NO:1621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..261
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1621:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gly | Leu | Arg | Arg | Leu | Asp | Gly | Lys | Ile | Ala | Ile | Ile | Thr | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ala | Ser | Gly | Ile | Gly | Ala | Glu | Ala | Val | Arg | Leu | Phe | Thr | Asp | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ala | Lys | Val | Val | Ile | Val | Asp | Ile | Gln | Glu | Glu | Leu | Gly | Gln | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Ala | Val | Ser | Ile | Gly | Leu | Asp | Lys | Ala | Ser | Phe | Tyr | Arg | Cys | Asn |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Thr | Asp | Glu | Thr | Asp | Val | Glu | Asn | Ala | Val | Lys | Phe | Thr | Val | Glu |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | His | Gly | Lys | Leu | Asp | Val | Leu | Phe | Ser | Asn | Ala | Gly | Val | Leu | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ala | Phe | Gly | Ser | Val | Leu | Asp | Leu | Asp | Leu | Glu | Ala | Phe | Asp | Arg | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Met | Ala | Val | Asn | Val | Arg | Gly | Ala | Ala | Ala | Phe | Ile | Lys | His | Ala | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Ser | Met | Val | Ala | Ser | Gly | Thr | Arg | Gly | Ser | Ile | Val | Cys | Thr | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Ser | Ile | Ala | Ala | Glu | Ile | Gly | Gly | Pro | Gly | Pro | His | Ser | Tyr | Thr | Ala |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Lys | His | Ala | Leu | Leu | Gly | Leu | Ile | Arg | Ser | Ala | Cys | Ala | Gly | Leu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Gly | Gln | Tyr | Gly | Ile | Arg | Val | Asn | Gly | Val | Ala | Pro | Tyr | Gly | Val | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Gly | Met | Thr | Ser | Ala | Tyr | Asn | Glu | Glu | Ala | Val | Lys | Met | Leu | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Tyr | Gly | Glu | Ala | Leu | Gly | Asn | Leu | Lys | Gly | Val | Val | Leu | Lys | Ala |
|     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Arg | His | Ile | Ala | Glu | Ala | Ala | Leu | Phe | Leu | Ala | Ser | Asp | Asp | Ser | Val |
|     | 225 |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Tyr | Ile | Ser | Gly | Gln | Asn | Leu | Val | Val | Asp | Gly | Gly | Phe | Ser | Val | Val |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Lys | Leu | Met | Ser | Thr |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 260 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1622:

Met Ala Val Asn Val Arg Gly Ala Ala Ala Phe Ile Lys His Ala Ala

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Arg Ser Met Val Ala Ser Gly Thr Arg Gly Ser Ile Val Cys Thr Thr |     |     |     |
|                                                                 | 20  | 25  | 30  |
| Ser Ile Ala Ala Glu Ile Gly Gly Pro Gly Pro His Ser Tyr Thr Ala |     |     |     |
|                                                                 | 35  | 40  | 45  |
| Ser Lys His Ala Leu Leu Gly Leu Ile Arg Ser Ala Cys Ala Gly Leu |     |     |     |
|                                                                 | 50  | 55  | 60  |
| Gly Gln Tyr Gly Ile Arg Val Asn Gly Val Ala Pro Tyr Gly Val Ala |     |     |     |
|                                                                 | 65  | 70  | 75  |
| Thr Gly Met Thr Ser Ala Tyr Asn Glu Glu Ala Val Lys Met Leu Glu |     |     |     |
|                                                                 | 85  | 90  | 95  |
| Glu Tyr Gly Glu Ala Leu Gly Asn Leu Lys Gly Val Val Leu Lys Ala |     |     |     |
|                                                                 | 100 | 105 | 110 |
| Arg His Ile Ala Glu Ala Ala Leu Phe Leu Ala Ser Asp Asp Ser Val |     |     |     |
|                                                                 | 115 | 120 | 125 |
| Tyr Ile Ser Gly Gln Asn Leu Val Val Asp Gly Gly Phe Ser Val Val |     |     |     |
|                                                                 | 130 | 135 | 140 |
| Lys Leu Met Ser Thr                                             |     |     |     |
| 145                                                             |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..812

(D) OTHER INFORMATION: / Ceres Seq. ID 1570505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1623:

|             |             |             |             |            |            |     |
|-------------|-------------|-------------|-------------|------------|------------|-----|
| aacaaaaaag  | cctaaaacgg  | agagagggcg  | agaggagaag  | gaagacggcg | tgaagcaatg | 60  |
| gtgtgcgtga  | agctccagaa  | gcggctcgcc  | gcacccgtaa  | tgaatgcggg | gaaaggaaaa | 120 |
| gtttggctcg  | accccaatga  | atcggggcgat | atctctatgg  | ccaattccag | gcagaacatt | 180 |
| aggaagcttg  | tgaaggatgg  | tttcattatc  | aggaagcccta | ctaagatcca | ctcacgttct | 240 |
| cgggctaggg  | ctttgaaagg  | ccaagcgaaa  | gggtcgctcac | tctggatacg | gtaagagaaa | 300 |
| gggtacaaga  | gaggcaaggc  | taccaaccaa  | gattctttgg  | atgaggagaa | tgagggtggt | 360 |
| gaggcgtttc  | ttgagcaagt  | accgtgagtc  | aaagaagatt  | gataggcaca | tgtaccatga | 420 |
| catgtacatg  | aaagtgaagg  | gtaatgtttt  | caagaacaag  | cgtgtgctta | tggagagcat | 480 |
| ccacaagaat  | aaggctgaga  | aggctagaga  | gaagaccctc  | gctgaccagt | ttgaggccaa | 540 |
| gcgtattaag  | aacaaggcta  | gcaggggagag | aaagtttgcc  | agaagagagg | agagattagc | 600 |
| tcagggaacct | ggagggtggag | agacaacgac  | tcctgCtgcc  | gcacctcaac | aaccagaggt | 660 |
| aaccagaaga  | aagtcgaaga  | agtgtatttg  | tgttgaactt  | ttttgcaatt | gaatctttga | 720 |
| gtttacctgt  | agaagaagcg  | tttttttttt  | atcttttata  | tgattttgtc | ggagattctt | 780 |
| ttcttcaaaa  | atattttcta  | tgttatggat  | cc          |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1570506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1624:

|                                                                 |    |    |    |
|-----------------------------------------------------------------|----|----|----|
| Asn Lys Lys Ala Leu Asn Gly Glu Arg Arg Arg Gly Glu Gly Arg Arg |    |    |    |
| 1                                                               | 5  | 10 | 15 |
| Arg Glu Ala Met Val Ser Leu Lys Leu Gln Lys Arg Leu Ala Ala Ser |    |    |    |
|                                                                 | 20 | 25 | 30 |

Val Met Lys Cys Gly Lys Gly Lys Val Trp Leu Asp Pro Asn Glu Ser  
35 40 45  
Gly Asp Ile Ser Met Ala Asn Ser Arg Gln Asn Ile Arg Lys Leu Val  
50 55 60  
Lys Asp Gly Phe Ile Ile Arg Lys Pro Thr Lys Ile His Ser Arg Ser  
65 70 75 80  
Arg Ala Arg Ala Leu Lys Gly Gln Ala Lys Gly Ser Ser Leu Trp Ile  
85 90 95  
Arg

(2) INFORMATION FOR SEQ ID NO:1625:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1570507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1625:

Met Arg Arg Met Arg Val Leu Arg Arg Phe Leu Ser Lys Tyr Arg Glu  
1 5 10 15  
Ser Lys Lys Ile Asp Arg His Met Tyr His Asp Met Tyr Met Lys Val  
20 25 30  
Lys Gly Asn Val Phe Lys Asn Lys Arg Val Leu Met Glu Ser Ile His  
35 40 45  
Lys Met Lys Ala Glu Lys Ala Arg Glu Lys Thr Leu Ala Asp Gln Phe  
50 55 60  
Glu Ala Lys Arg Ile Lys Asn Lys Ala Ser Arg Glu Arg Lys Phe Ala  
65 70 75 80  
Arg Arg Glu Glu Arg Leu Ala Gln Gly Pro Gly Gly Gly Glu Thr Thr  
85 90 95  
Thr Pro Ala Gly Ala Pro Gln Gln Pro Glu Val Thr Lys Lys Lys Ser  
100 105 110  
Lys Lys

(2) INFORMATION FOR SEQ ID NO:1626:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1570508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1626:

Met Arg Val Leu Arg Arg Phe Leu Ser Lys Tyr Arg Glu Ser Lys Lys  
1 5 10 15  
Ile Asp Arg His Met Tyr His Asp Met Tyr Met Lys Val Lys Gly Asn  
20 25 30  
Val Phe Lys Asn Lys Arg Val Leu Met Glu Ser Ile His Lys Met Lys  
35 40 45  
Ala Glu Lys Ala Arg Glu Lys Thr Leu Ala Asp Gln Phe Glu Ala Lys  
50 55 60  
Arg Ile Lys Asn Lys Ala Ser Arg Glu Arg Lys Phe Ala Arg Arg Glu  
65 70 75 80  
Glu Arg Leu Ala Gln Gly Pro Gly Gly Glu Thr Thr Thr Pro Ala

85 90 95  
Gly Ala Pro Gln Gln Pro Glu Val Thr Lys Lys Lys Ser Lys Lys  
100 105 110

(2) INFORMATION FOR SEQ ID NO:1627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..875

(D) OTHER INFORMATION: / Ceres Seq. ID 1570515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1627:

```
aaaatgatgc ctgcgacagc gagtgtgtga cgttaaaccc taaatctggt gtctttgtgc 60
aatcgcaaga ttcatctcact cgacactaaa gatcgaaact tttgaattgc agaaattgcg 120
acacttttag ttccaagctc tccaaaggac gttcattgct tggagggtct tgcaattgct 180
tctctggttt gatgaattcc tcctccaatg gaatgatgaa tgggaagcatc ctctctcagc 240
aacaacatag gacattcatt caaatgggga cgattctcaa atgcgtggat aactcgtgtg 300
ctaaaggagt gatgtgcatt caatccctga gaggtaagaa aggagcaaga cttggcgata 360
tcattgttgg ttacgtgaaa gaagctaacc caattgttca aaaaaaagta aagaaagacg 420
ctgtcccaaa aggtaaaagt aagaaaaggga tggtcgtgta cggtgtggtt gtgcgtgctg 480
cgatgcctaa aggacgtgct gatggaagcc aagtcaagtt tgatgacaat gccattgtag 540
ttgttggcat taaggaagaa aaagggcaga ataattcaca tggttccaag aggaaaattg 600
agtaacaaca accgactggt acccgagtggt ttggtcctgt tggcgcagag atgcccctca 660
ggaaacagct caagatcctt tctttggctc agcacattgt ttgagacaat acaccacact 720
aaaaacatag ttatgatctc ctttatgtga ctctctttga tccattcatc acttgggttt 780
ctgttgatcc ttaaacatct caactcatta tttttgttaa ttctaatgaa ttatgaaacc 840
```

(2) INFORMATION FOR SEQ ID NO:1628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1570516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1628:

```
Met Asn Ser Ser Ser Asn Gly Met Met Asn Gly Ser Ile Leu Ser Gln
1 5 10 15
Gln Gln His Arg Thr Phe Ile Gln Met Gly Thr Ile Leu Lys Cys Val
20 25 30
Asp Asn Ser Cys Ala Lys Glu Val Met Cys Ile Gln Ser Leu Arg Gly
35 40 45
Lys Lys Gly Ala Arg Leu Gly Asp Ile Ile Val Gly Ser Val Lys Glu
50 55 60
Ala Asn Pro Ile Val Gln Lys Lys Val Lys Lys Asp Ala Val Pro Lys
65 70 75 80
Gly Lys Val Lys Lys Gly Met Val Val Tyr Gly Val Val Val Arg Ala
85 90 95
Ala Met Pro Lys Gly Arg Ala Asp Gly Ser Gln Val Lys Phe Asp Asp
100 105 110
Asn Ala Ile Val Val Val Gly Ile Lys Glu Lys Lys Gly Gln Asn Asn
115 120 125
Ser His Gly Ser Lys Arg Lys Met Glu Tyr Asn Gln Pro Thr Gly Thr
130 135 140
Arg Val Phe Gly Pro Val Pro His Glu Met Arg Leu Arg Lys Gln Leu
```

(2) INFORMATION FOR SEQ ID NO:1629:

## (1) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1629:

(2) INFORMATION FOR SEQ ID NO:1630:

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1630:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Gly | Ser | Ile | Leu | Ser | Gln | Gln | Gln | His | Arg | Thr | Phe | Ile | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Gly | Thr | Ile | Leu | Lys | Cys | Val | Asp | Asn | Ser | Cys | Ala | Lys | Glu | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Cys | Ile | Gln | Ser | Leu | Arg | Gly | Lys | Lys | Gly | Ala | Arg | Leu | Gly | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ile | Val | Gly | Ser | Val | Lys | Glu | Ala | Asn | Pro | Ile | Val | Gln | Lys | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Lys | Lys | Asp | Ala | Val | Pro | Lys | Gly | Lys | Val | Lys | Lys | Gly | Met | Val |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Tyr | Gly | Val | Val | Val | Arg | Ala | Ala | Met | Pro | Lys | Gly | Arg | Ala | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

Gly Ser Gln Val Lys Phe Asp Asp Asn Ala Ile Val Val Val Gly Ile  
100 105 110  
Lys Glu Lys Lys Gly Gln Asn Asn Ser His Gly Ser Lys Arg Lys Met  
115 120 125  
Glu Tyr Asn Gln Pro Thr Gly Thr Arg Val Phe Gly Pro Val Pro His  
130 135 140  
Glu Met Arg Leu Arg Lys Gln Leu Lys Ile Leu Ser Leu Ala Gln His  
145 150 155 160  
Ile Val

(2) INFORMATION FOR SEQ ID NO:1631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1027

(D) OTHER INFORMATION: / Ceres Seq. ID 1570534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1631:

|             |            |            |            |            |             |      |
|-------------|------------|------------|------------|------------|-------------|------|
| attcgctcttc | tccaattttc | tcgcgaagaa | aacttttcta | ctttgtttca | atccaaacga  | 60   |
| gtcaaaatgc  | tatatcaagc | tgtttcttca | tcttcttctt | cagctctctc | gctgggtgaat | 120  |
| ttccatggcg  | tgaagaagga | tgtgtctctc | ttgttacott | ccatttcate | gaactctcga  | 180  |
| gtttctctcg  | gaaaatctgg | aaaattaact | ttctctgttc | gcgcacataa | aagctcaacc  | 240  |
| accgacgcgc  | taagcggcgt | tgtcttcgag | ccgttttaag | aagtaaaaaa | ggagctcgat  | 300  |
| ctcgctcccta | ccagctctca | ttctctcact | gctcgacaaa | agtactcaga | cgagtgcgaa  | 360  |
| gccgccatta  | acgacgagat | caatgtggva | tacaatgtct | cgtatgtgta | tcacgctatg  | 420  |
| tatgcttact  | ttgatcgga  | taacatcgcg | ctcaaaggct | ttgcgaagtt | ctttaaggaa  | 480  |
| tcaagtctgg  | aagaagaaga | gcattgctag | aagttaattg | agtatcagaa | caaacctggt  | 540  |
| gggagggtta  | agttacagtc | cattgtaatg | ctcttttcag | agtttgaaca | tggtgacaaa  | 600  |
| ggagatgctc  | tttatggcat | ggagcttgct | ctgtcaactg | agaaactagt | taatgagaag  | 660  |
| ctcttaaac   | ttcacagtgt | tgtcttcagg | aacaatgatg | tccacttggc | agatttttatt | 720  |
| gagagcgagt  | ttctgacaga | gcaggtggaa | gcaatcaagt | tgatctcaga | atatgtggct  | 780  |
| caactgcgac  | gagttggcaa | aggacacgga | acatggcatt | tcaatcagat | gcttctggaa  | 840  |
| gggtaagcag  | cttcgaggga | ctcttgtgtc | tactgtgttt | ctatatgaag | ctctcttagt  | 900  |
| gatattgatg  | gaactacttt | atgtttatgt | ctttagcttt | taagattttg | tgaggtagta  | 960  |
| gaactctttt  | tcgtgaagac | acaaaagaca | tgatcacata | actttatatt | ctgtgtataag | 1020 |
| gttcacc     |            |            |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:1632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..281

(D) OTHER INFORMATION: / Ceres Seq. ID 1570535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1632:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Arg | Leu | Leu | Gln | Phe | Ser | Arg | Glu | Glu | Asn | Phe | Pro | Thr | Leu | Phe |
| 1   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gln | Ser | Lys | Arg | Val | Lys | Met | Leu | Ile | Lys | Thr | Val | Ser | Ser | Ser | Ser |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ser | Ser | Ala | Leu | Ser | Leu | Val | Asn | Phe | His | Gly | Val | Lys | Lys | Asp | Val |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Pro | Leu | Leu | Pro | Ser | Ile | Ser | Ser | Asn | Leu | Arg | Val | Ser | Ser | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Lys | Ser | Gly | Lys | Leu | Thr | Phe | Ser | Val | Arg | Ala | Ser | Lys | Ser | Ser | Thr |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ile | Lys | Thr | Val | Ser | Ser | Ser | Ser | Ser | Ser | Ala | Leu | Ser | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Val | Asn | Phe | His | Gly | Val | Lys | Lys | Asp | Val | Ser | Pro | Leu | Leu | Pro | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Ile | Ser | Ser | Asn | Leu | Arg | Val | Ser | Ser | Gly | Lys | Ser | Gly | Lys | Leu | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Ser | Val | Arg | Ala | Ser | Lys | Ser | Ser | Thr | Thr | Asp | Ala | Leu | Ser | Gly |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Val | Phe | Glu | Pro | Phe | Lys | Glu | Val | Lys | Lys | Glu | Leu | Asp | Leu | Val |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Thr | Ser | Ser | His | Leu | Ser | Leu | Ala | Arg | Gln | Lys | Tyr | Ser | Asp | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys | Glu | Ala | Ala | Ile | Asn | Glu | Gln | Ile | Asn | Val | Xaa | Tyr | Asn | Val | Ser |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Val | Tyr | His | Ala | Met | Tyr | Ala | Tyr | Phe | Asp | Arg | Asp | Asn | Ile | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Lys | Gly | Leu | Ala | Lys | Phe | Phe | Lys | Glu | Ser | Ser | Leu | Glu | Glu | Arg |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Glu | His | Ala | Glu | Lys | Leu | Met | Glu | Tyr | Gln | Asn | Lys | Arg | Gly | Gly | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Lys | Leu | Gln | Ser | Ile | Val | Met | Pro | Leu | Ser | Glu | Phe | Glu | His | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |     |     |

Asp Lys Gly Asp Ala Leu Tyr Gly Met Glu Leu Ala Leu Ser Leu Glu  
180 185 190  
Lys Leu Val Asn Glu Lys Leu Leu Asn Leu His Ser Val Ala Ser Arg  
195 200 205  
Asn Asn Asp Val His Leu Ala Asp Phe Ile Glu Ser Glu Phe Leu Thr  
210 215 220  
Glu Gln Val Glu Ala Ile Lys Leu Ile Ser Glu Tyr Val Ala Gln Leu  
225 230 235 240  
Arg Arg Val Gly Lys Gly His Gly Thr Trp His Phe Asn Gln Met Leu  
245 250 255  
Leu Glu Gly

(2) INFORMATION FOR SEQ ID NO:1634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1634:

Met Tyr Ala Tyr Phe Asp Arg Asp Asn Ile Ala Leu Lys Gly Leu Ala  
1 5 10 15  
Lys Phe Phe Lys Glu Ser Ser Leu Glu Glu Arg Glu His Ala Glu Lys  
20 25 30  
Leu Met Glu Tyr Gln Asn Lys Arg Gly Gly Arg Val Lys Leu Gln Ser  
35 40 45  
Ile Val Met Pro Leu Ser Glu Phe Glu His Val Asp Lys Gly Asp Ala  
50 55 60  
Leu Tyr Gly Met Glu Leu Ala Leu Ser Leu Glu Lys Leu Val Asn Glu  
65 70 75 80  
Lys Leu Leu Asn Leu His Ser Val Ala Ser Arg Asn Asn Asp Val His  
85 90 95  
Leu Ala Asp Phe Ile Glu Ser Glu Phe Leu Thr Glu Gln Val Glu Ala  
100 105 110  
Ile Lys Leu Ile Ser Glu Tyr Val Ala Gln Leu Arg Arg Val Gly Lys  
115 120 125  
Gly His Gly Thr Trp His Phe Asn Gln Met Leu Leu Glu Gly  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..976
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1635:

|             |            |             |             |             |            |     |
|-------------|------------|-------------|-------------|-------------|------------|-----|
| agatttcaaaa | tctttgttta | caatctcttc  | tctggctatc  | ttagagggat  | ttttgattga | 60  |
| gattttaaaa  | ttttctTgag | ttggattagt  | tggttggttaa | agagatggat  | ccggataccg | 120 |
| tgaagtcgac  | cctctcgaat | ctggcattcg  | ggaatgtatt  | ggcggcagct  | gctagagatt | 180 |
| ataaaaaagg  | agttcttgca | aatgaaaaagg | cacaaggatc  | aagacctgtGt | caacgaggaa | 240 |
| gttgatcttg  | acgaattgat | gagatgatcca | gagctagaaa  | agttgcacgc  | agataggatt | 300 |
| gcagcactca  | ggagagaagt | ggaaaaagaga | gaagcattca  | aaagacaagg  | acatggtgaa | 360 |
| taccgagaag  | ttagcgaagg | cgacttcttg  | ggagaagtca  | caaggagtga  | aaaagtata  | 420 |



|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tgctacttct | accacaagga | gttctatcgc | tgcaagataa | tggacaagca | tttgaagacc | 480 |
| cttgcctcca | gacatgtgga | cacaaagtcc | attaagatgg | acgctgagaa | cgctcccttc | 540 |
| ttcgtcacca | agcttgcaat | caagactttg | ccgtgtgtta | tcctttttag | caagggaatc | 600 |
| gcgatggata | ggcttgtcgg | gtttcaagat | ctaggtgcc  | aggacgattt | ctccacgacg | 660 |
| aagctggaga | atcttctcgt | caagaaagga | atgcttagtg | aaaagagaaa | agaggaagat | 720 |
| gaggaagatt | acgagtatca | agaaagcata | cgctcggtcc | ttaggtcttc | agcgaatgtc | 780 |
| gactctgatt | cagattgata | tcgaagcttt | tctcatagta | gacctccgag | cctttttgtg | 840 |
| ttttgttttc | accgctgctc | tggttgaatt | gtttgtgtca | tgaattctat | gcttctataa | 900 |
| gtctttatag | tgggaaatct | cggtccacaa | tggttttgtt | tatttgaaaa | ctgcaaaata | 960 |
| tggtgtctaa | ccatat     |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1636:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1570539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1636:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Trp | Arg | Gln | Leu | Leu | Glu | Ile | Lys | Arg | Lys | Phe | Leu | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Lys | Arg | His | Lys | Asp | Gln | Asp | Leu | Val | Asn | Glu | Glu | Val | Asp |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  | Leu |
| Asp | Glu | Leu | Met | Asp | Asp | Pro | Glu | Leu | Glu | Lys | Leu | His | Ala | Asp |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  | Arg |
| Ile | Ala | Ala | Leu | Arg | Arg | Glu | Val | Glu | Lys | Arg | Glu | Ala | Phe | Lys |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  | Arg |
| Gln | Gly | His | Gly | Glu | Tyr | Arg | Glu | Val | Ser | Glu | Gly | Asp | Phe | Leu |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     | 80  | Gly |
| Glu | Val | Thr | Arg | Ser | Glu | Lys | Val | Ile | Cys | His | Phe | Tyr | His | Lys |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  | Glu |
| Phe | Tyr | Arg | Cys | Lys | Ile | Met | Asp | Lys | His | Leu | Lys | Thr | Leu | Ala |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 | Pro |
| Arg | His | Val | Asp | Thr | Lys | Phe | Ile | Lys | Met | Asp | Ala | Glu | Asn | Ala |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 | Pro |
| Phe | Phe | Val | Thr | Lys | Leu | Ala | Ile | Lys | Thr | Leu | Pro | Cys | Val | Ile |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 | Leu |
| Phe | Ser | Lys | Gly | Ile | Ala | Met | Asp | Arg | Leu | Val | Gly | Phe | Gln | Asp |
|     |     |     |     | 145 |     |     |     | 150 |     |     |     |     | 155 | Leu |
| Gly | Ala | Lys | Asp | Asp | Phe | Ser | Thr | Thr | Lys | Leu | Glu | Asn | Leu | Val |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     | 175 | Val |
| Lys | Lys | Gly | Met | Leu | Ser | Glu | Lys | Arg | Lys | Glu | Glu | Asp | Glu | Asp |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |
| Tyr | Glu | Tyr | Gln | Glu | Ser | Ile | Arg | Arg | Ser | Val | Arg | Ser | Ser | Ala |
|     |     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 | Asn |
| Val | Asp | Ser | Asp | Ser | Asp |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 210 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1637:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..198

(D) OTHER INFORMATION: / Ceres Seq. ID 1570540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1637:

Met Lys Arg His Lys Asp Gln Asp Leu Val Asn Glu Glu Val Asp Leu  
1 5 10 15  
Asp Glu Leu Met Asp Asp Pro Glu Leu Glu Lys Leu His Ala Asp Arg  
20 25 30  
Ile Ala Ala Leu Arg Arg Glu Val Glu Lys Arg Glu Ala Phe Lys Arg  
35 40 45  
Gln Gly His Gly Glu Tyr Arg Glu Val Ser Glu Gly Asp Phe Leu Gly  
50 55 60  
Glu Val Thr Arg Ser Glu Lys Val Ile Cys His Phe Tyr His Lys Glu  
65 70 75 80  
Phe Tyr Arg Cys Lys Ile Met Asp Lys His Leu Lys Thr Leu Ala Pro  
85 90 95  
Arg His Val Asp Thr Lys Phe Ile Lys Met Asp Ala Glu Asn Ala Pro  
100 105 110  
Phe Phe Val Thr Lys Leu Ala Ile Lys Thr Leu Pro Cys Val Ile Leu  
115 120 125  
Phe Ser Lys Gly Ile Ala Met Asp Arg Leu Val Gly Phe Gln Asp Leu  
130 135 140  
Gly Ala Lys Asp Asp Phe Ser Thr Thr Lys Leu Glu Asn Leu Leu Val  
145 150 155 160  
Lys Lys Gly Met Leu Ser Glu Lys Arg Lys Glu Glu Asp Glu Glu Asp  
165 170 175  
Tyr Glu Tyr Gln Glu Ser Ile Arg Arg Ser Val Arg Ser Ser Ala Asn  
180 185 190  
Val Asp Ser Asp Ser Asp  
195

(2) INFORMATION FOR SEQ ID NO:1638:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1570541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1638:

Met Asp Asp Pro Glu Leu Glu Lys Leu His Ala Asp Arg Ile Ala Ala  
1 5 10 15  
Leu Arg Arg Glu Val Glu Lys Arg Glu Ala Phe Lys Arg Gln Gly His  
20 25 30  
Gly Glu Tyr Arg Glu Val Ser Glu Gly Asp Phe Leu Gly Glu Val Thr  
35 40 45  
Arg Ser Glu Lys Val Ile Cys His Phe Tyr His Lys Glu Phe Tyr Arg  
50 55 60  
Cys Lys Ile Met Asp Lys His Leu Lys Thr Leu Ala Pro Arg His Val  
65 70 75 80  
Asp Thr Lys Phe Ile Lys Met Asp Ala Glu Asn Ala Pro Phe Phe Val  
85 90 95  
Thr Lys Leu Ala Ile Lys Thr Leu Pro Cys Val Ile Leu Phe Ser Lys  
100 105 110  
Gly Ile Ala Met Asp Arg Leu Val Gly Phe Gln Asp Leu Gly Ala Lys  
115 120 125  
Asp Asp Phe Ser Thr Thr Lys Leu Glu Asn Leu Leu Val Lys Lys Gly  
130 135 140  
Met Leu Ser Glu Lys Arg Lys Glu Glu Asp Glu Glu Asp Tyr Glu Tyr  
145 150 155 160  
Gln Glu Ser Ile Arg Arg Ser Val Arg Ser Ser Ala Asn Val Asp Ser  
165 170 175

Asp Ser Asp

(2) INFORMATION FOR SEQ ID NO:1639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1089 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1089
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1639:

|            |             |             |            |            |             |      |
|------------|-------------|-------------|------------|------------|-------------|------|
| acagagacaa | caaactaaag  | ttggtggtga  | tagagtgaga | gagaaacatg | gaaggcaaa   | 60   |
| aagaagacgt | caatgttgga  | gccacaagt   | tcccagagag | acagccgac  | ggtacggcg   | 120  |
| ctcagacgga | gagcaaggac  | tataaggaa   | caccaccggc | gccgtttttc | gaaccggcg   | 180  |
| agctcaaatc | ttggtctttc  | tacagagcag  | ggatagctga | gttcatagcc | actttccttt  | 240  |
| tcctctacgt | caccgttttg  | acagtcacgg  | gtgttaagag | agctcccaat | atgtgtgcct  | 300  |
| ctgttggaat | ccaaggcatc  | gcttgggctt  | ttggtggcat | gatcttttgt | ctgtgttaact | 360  |
| gtactgtcgg | aatctcagga  | ggacatatata | atccggcggt | gaacttttgt | ttgttcttgg  | 420  |
| cgaggaagct | atctttaacc  | agagctctgt  | tctacatagt | aatgcagtc  | cttggagcta  | 480  |
| tatgttggtg | tggtgtgggt  | aaagggtttc  | aaccagggct | gtaccagacg | aatgcgggtg  | 540  |
| gagctaagt  | ggtggctcat  | ggttacacaa  | agggttcagg | tcttggtgca | gagattgttg  | 600  |
| gaacttttgt | tctggtttac  | actgttttct  | cagctactga | tgctaagaga | aglgccagag  | 660  |
| actctcaagt | cgtatcttgt  | gctccgcttc  | caattggggt | tgctgtcttc | ttggtgcaact | 720  |
| tggtaccatc | cccaattact  | ggaactggca  | ttaaccggcg | caggagcttc | ggagctgcc   | 780  |
| tcatctacaa | caaggaatcat | gcttgggatg  | accattggat | ctctgggttc | gggtcattca  | 840  |
| ttggtGctgc | gcttgctgct  | ctgtaccatc  | agatagtcac | cagagctatt | cttttcaagt  | 900  |
| ccaagacata | aagtttctca  | catattctct  | gatcatcatc | aagctaagaa | tatatcaatc  | 960  |
| tttaattcta | tatgctttct  | tctgtttctc  | tatgtcatgt | gtgatgatct | ctatatgtac  | 1020 |
| cactagagct | ttgatcttgt  | aacagtgtaa  | atgtgttaac | tattatgtat | caatggcatt  | 1080 |
| gtatcttgt  |             |             |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:1640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..287
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1640:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gly | Lys | Glu | Glu | Asp | Val | Asn | Val | Gly | Ala | Asn | Lys | Phe | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Arg | Gln | Pro | Ile | Gly | Thr | Ala | Ala | Gln | Thr | Glu | Ser | Lys | Asp | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Glu | Pro | Pro | Pro | Ala | Pro | Phe | Phe | Glu | Pro | Gly | Glu | Leu | Lys | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Trp | Ser | Phe | Tyr | Arg | Ala | Gly | Ile | Ala | Glu | Phe | Ile | Ala | Thr | Phe | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Phe | Leu | Tyr | Val | Thr | Val | Leu | Thr | Val | Met | Gly | Val | Lys | Arg | Ala | Pro |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Asn | Met | Cys | Ala | Ser | Val | Gly | Ile | Gln | Gly | Ile | Ala | Trp | Ala | Phe | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Met | Ile | Phe | Ala | Leu | Val | Tyr | Cys | Thr | Ala | Gly | Ile | Ser | Gly | Gly |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |
| His | Ile | Asp | Pro | Ala | Val | Thr | Phe | Gly | Leu | Phe | Leu | Ala | Arg | Lys | Leu |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |

Ser Leu Thr Arg Ala Leu Phe Tyr Ile Val Met Gln Ser Leu Gly Ala  
130 135 140  
Ile Cys Gly Ala Gly Val Val Lys Gly Phe Gln Pro Gly Leu Tyr Gln  
145 150 155 160  
Thr Asn Gly Gly Gly Ala Asn Val Val Ala His Gly Tyr Thr Lys Gly  
165 170 175  
Ser Gly Leu Gly Ala Glu Ile Val Gly Thr Phe Val Leu Val Tyr Thr  
180 185 190  
Val Phe Ser Ala Thr Asp Ala Lys Arg Ser Ala Arg Asp Ser His Val  
195 200 205  
Arg Ile Leu Ala Pro Leu Pro Ile Gly Phe Ala Val Phe Leu Val His  
210 215 220  
Leu Ala Thr Ile Pro Ile Thr Gly Thr Gly Ile Asn Pro Ala Arg Ser  
225 230 235 240  
Leu Gly Ala Ala Ile Ile Tyr Asn Lys Asp His Ala Trp Asp Asp His  
245 250 255  
Trp Ile Phe Trp Val Gly Pro Phe Ile Gly Ala Ala Leu Ala Ala Leu  
260 265 270  
Tyr His Gln Ile Val Ile Arg Ala Ile Pro Phe Lys Ser Lys Thr  
275 280 285

(2) INFORMATION FOR SEQ ID NO:1641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1570563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1641:

Met Gly Val Lys Arg Ala Pro Asn Met Cys Ala Ser Val Gly Ile Gln  
1 5 10 15  
Gly Ile Ala Trp Ala Phe Gly Gly Met Ile Phe Ala Leu Val Tyr Cys  
20 25 30  
Thr Ala Gly Ile Ser Gly Gly His Ile Asn Pro Ala Val Thr Phe Gly  
35 40 45  
Leu Phe Leu Ala Arg Lys Leu Ser Leu Thr Arg Ala Leu Phe Tyr Ile  
50 55 60  
Val Met Gln Ser Leu Gly Ala Ile Cys Gly Ala Gly Val Val Lys Gly  
65 70 75 80  
Phe Gln Pro Gly Leu Tyr Gln Thr Asn Gly Gly Ala Asn Val Val  
85 90 95  
Ala His Gly Tyr Thr Lys Gly Ser Gly Leu Gly Ala Glu Ile Val Gly  
100 105 110  
Thr Phe Val Leu Val Tyr Thr Val Phe Ser Ala Thr Asp Ala Lys Arg  
115 120 125  
Ser Ala Arg Asp Ser His Val Arg Ile Leu Ala Pro Leu Pro Ile Gly  
130 135 140  
Phe Ala Val Phe Leu Val His Leu Ala Thr Ile Pro Ile Thr Gly Thr  
145 150 155 160  
Gly Ile Asn Pro Ala Arg Ser Leu Gly Ala Ala Ile Ile Tyr Asn Lys  
165 170 175  
Asp His Ala Trp Asp Asp His Trp Ile Phe Trp Val Gly Pro Phe Ile  
180 185 190  
Gly Ala Ala Leu Ala Ala Leu Tyr His Gln Ile Val Ile Arg Ala Ile  
195 200 205  
Pro Phe Lys Ser Lys Thr  
210

(2) INFORMATION FOR SEQ ID NO:1642:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 206 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..206  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570564  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1642:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Ala | Ser | Val | Gly | Ile | Gln | Gly | Ile | Ala | Trp | Ala | Phe | Gly | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Met | Ile | Phe | Ala | Leu | Val | Tyr | Cys | Thr | Ala | Gly | Ile | Ser | Gly | Gly | His |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ile | Asn | Pro | Ala | Val | Thr | Phe | Gly | Leu | Phe | Leu | Ala | Arg | Lys | Leu | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Thr | Arg | Ala | Leu | Phe | Tyr | Ile | Val | Met | Gln | Ser | Leu | Gly | Ala | Ile |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Cys | Gly | Ala | Gly | Val | Val | Lys | Gly | Phe | Gln | Pro | Gly | Leu | Tyr | Gln | Thr |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Asn | Gly | Gly | Gly | Ala | Asn | Val | Val | Ala | His | Gly | Tyr | Thr | Lys | Gly | Ser |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Leu | Gly | Ala | Glu | Ile | Val | Gly | Thr | Phe | Val | Leu | Val | Tyr | Thr | Val |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Phe | Ser | Ala | Thr | Asp | Ala | Lys | Arg | Ser | Ala | Arg | Asp | Ser | His | Val | Arg |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Leu | Ala | Pro | Leu | Pro | Ile | Gly | Phe | Ala | Val | Phe | Leu | Val | His | Leu |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Thr | Ile | Pro | Ile | Thr | Gly | Thr | Gly | Ile | Asn | Pro | Ala | Arg | Ser | Leu |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |     |
| Gly | Ala | Ala | Ile | Ile | Tyr | Asn | Lys | Asp | His | Ala | Trp | Asp | Asp | His | Trp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ile | Phe | Trp | Val | Gly | Pro | Phe | Ile | Gly | Ala | Ala | Leu | Ala | Ala | Leu | Tyr |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     |     | 190 |     |
| His | Gln | Ile | Val | Ile | Arg | Ala | Ile | Pro | Phe | Lys | Ser | Lys | Thr |     |     |
|     |     |     | 195 |     |     | 200 |     |     |     |     |     | 205 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1122 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1122

(D) OTHER INFORMATION: / Ceres Seq. ID 1570565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1643:

|             |             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| aaaaatcctg  | atttAytgag  | ctttaaaaCcc | haRacccttc  | tcttctctct  | tctccacgcc  | 60  |
| atttccagaa  | ttttcaggtg  | ttcgtgaaaa  | gatgaatttt  | aagaatgtca  | aagttcccaa  | 120 |
| aggtcctggt  | gggtgtgtta  | tagctgcggt  | ggttattggg  | gggtcagtc   | tttacgggtgc | 180 |
| taagcaact   | ctctacaatg  | tcatgagagg  | tcactcgacc  | attgtcttta  | accgcttgt   | 240 |
| tggtatcaaa  | gacaaggctc  | accctgaggg  | taactcaact  | atgattccat  | gggtcgaaa   | 300 |
| gccaatcatc  | tatgacgttc  | gtgcaaaagg  | ttatctagtt  | gagagcacat  | ctgggagccg  | 360 |
| tgatctccag  | atgggttaaga | tggggcttcg  | gggtctccac  | cgctcctatgg | ctgaccaatt  | 420 |
| accagagcta  | taccgggtccc | ttggtgagaa  | taccgcggag  | agagtctctg  | ctctctatcat | 480 |
| ccacagagacc | tgtgaaagctg | tgggtgtctca | gtacaaacgca | agccaaactta | ttactcagag  | 540 |
| agagtcgggt  | agttagagaaa | tcaggaaaaat | cctaactcta  | agagccgca   | acttccacat  | 600 |
| tgactcggtg  | gatgtgtcca  | tcacaggcct  | gacattcgga  | aaggagtcca  | cggcagccat  | 660 |
| agaaggaaa   | caggctgctg  | ctcaagaggc  | cgaacgggct  | aagttcattg  | tcgagaaaagc | 720 |

|             |            |            |            |            |             |      |
|-------------|------------|------------|------------|------------|-------------|------|
| tgaacaggac  | aagagaagt  | ctgttatccg | cgccgagggg | gaagccaaga | gtgctcagct  | 780  |
| cattgggtcaa | gcaatcgcaa | acaaccaagc | gttcttaaca | ctgaggaaga | tcgaagcagc  | 840  |
| tagagagatc  | gcacagacca | tctctaggtc | ggcgaacaag | gtttacttga | gctctaacga  | 900  |
| tctgttgctt  | aactacacag | ctatggacat | tgaatggaag | cogaagaagt | agagaatgat  | 960  |
| atgattaaac  | cacaccagag | ctctctttcc | ataatcgtat | tttcaattca | cggattcttta | 1020 |
| gaccaaagc   | tatgagttct | atcttgtgaa | tttcagacac | tatcgtgcgt | ttgtagtctt  | 1080 |
| tcttttgtga  | gatcaagaag | aaaagaaaag | atttatgttt | tt         |             |      |

(2) INFORMATION FOR SEQ ID NO:1644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..286

(D) OTHER INFORMATION: / Ceres Seq. ID 1570566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1644:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Phe | Lys | Asn | Val | Lys | Val | Pro | Lys | Gly | Pro | Gly | Gly | Gly | Val |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Ala | Ala | Val | Val | Ile | Gly | Gly | Leu | Ser | Leu | Tyr | Gly | Ala | Thr | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Leu | Tyr | Asn | Val | Asp | Gly | Gly | His | Arg | Ala | Ile | Val | Phe | Asn | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Val | Gly | Ile | Lys | Asp | Lys | Val | Tyr | Pro | Glu | Gly | Thr | His | Leu | Met |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Pro | Trp | Phe | Glu | Arg | Pro | Ile | Ile | Tyr | Asp | Val | Arg | Ala | Lys | Pro |
|     |     |     | 65  |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Tyr | Leu | Val | Glu | Ser | Thr | Ser | Gly | Ser | Arg | Asp | Leu | Gln | Met | Val | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |     |
| Ile | Gly | Leu | Arg | Val | Leu | Thr | Arg | Pro | Met | Ala | Asp | Gln | Leu | Pro | Glu |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Val | Tyr | Arg | Ser | Leu | Gly | Glu | Asn | Tyr | Arg | Glu | Arg | Val | Leu | Pro | Ser |
|     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Ile | Ile | His | Glu | Thr | Leu | Lys | Ala | Val | Val | Ala | Gln | Tyr | Asn | Ala | Ser |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Leu | Ile | Thr | Gln | Arg | Glu | Ser | Val | Ser | Arg | Glu | Ile | Arg | Lys | Ile |
|     |     |     | 145 |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Thr | Leu | Arg | Ala | Ala | Asn | Phe | His | Ile | Ala | Leu | Asp | Asp | Val | Ser |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Ile | Thr | Gly | Leu | Thr | Phe | Gly | Lys | Glu | Phe | Thr | Ala | Ala | Ile | Glu | Gly |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Lys | Gln | Val | Ala | Ala | Gln | Glu | Ala | Glu | Arg | Ala | Lys | Phe | Ile | Val | Glu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Ala | Glu | Gln | Asp | Lys | Arg | Ser | Ala | Val | Ile | Arg | Ala | Glu | Gly | Glu |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Lys | Ser | Ala | Gln | Leu | Ile | Gly | Gln | Ala | Ile | Ala | Asn | Asn | Gln | Ala |
|     |     |     | 225 |     |     | 230 |     |     | 235 |     |     |     |     | 240 |     |
| Phe | Leu | Thr | Leu | Arg | Lys | Ile | Glu | Ala | Ala | Arg | Glu | Ile | Ala | Gln | Thr |
|     |     |     | 245 |     |     |     | 250 |     |     |     |     | 255 |     |     |     |
| Ile | Ser | Arg | Ser | Ala | Asn | Lys | Val | Tyr | Leu | Ser | Ser | Asn | Asp | Leu | Leu |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Leu | Asn | Leu | Gln | Ala | Met | Asp | Leu | Asp | Val | Lys | Pro | Lys | Lys |     |     |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1645:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1570567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1645:

```
Met Ile Pro Trp Phe Glu Arg Pro Ile Ile Tyr Asp Val Arg Ala Lys
1 5 10 15
Pro Tyr Leu Val Glu Ser Thr Ser Gly Ser Arg Asp Leu Gln Met Val
 20 25 30
Lys Ile Gly Leu Arg Val Leu Thr Arg Pro Met Ala Asp Gln Leu Pro
 35 40 45
Glu Val Tyr Arg Ser Leu Gly Glu Asn Tyr Arg Glu Arg Val Leu Pro
 50 55 60
Ser Ile Ile His Glu Thr Leu Lys Ala Val Val Ala Gln Tyr Asn Ala
 65 70 75 80
Ser Gln Leu Ile Thr Gln Arg Glu Ser Val Ser Arg Glu Ile Arg Lys
 85 90 95
Ile Leu Thr Leu Arg Ala Ala Asn Phe His Ile Ala Leu Asp Asp Val
 100 105 110
Ser Ile Thr Gly Leu Thr Phe Gly Lys Glu Phe Thr Ala Ala Ile Glu
 115 120 125
Gly Lys Gln Val Ala Ala Gln Glu Ala Glu Arg Ala Lys Phe Ile Val
 130 135 140
Glu Lys Ala Glu Gln Asp Lys Arg Ser Ala Val Ile Arg Ala Glu Gly
 145 150 155 160
Glu Ala Lys Ser Ala Gln Leu Ile Gly Gln Ala Ile Ala Asn Asn Gln
 165 170 175
Ala Phe Leu Thr Leu Arg Lys Ile Glu Ala Ala Arg Glu Ile Ala Gln
 180 185 190
Thr Ile Ser Arg Ser Ala Asn Lys Val Tyr Leu Ser Ser Asn Asp Leu
 195 200 205
Leu Leu Asn Leu Gln Ala Met Asp Leu Asp Val Lys Pro Lys Lys
 210 215 220
```

(2) INFORMATION FOR SEQ ID NO:1646:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1570568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1646:

```
Met Val Lys Ile Gly Leu Arg Val Leu Thr Arg Pro Met Ala Asp Gln
1 5 10 15
Leu Pro Glu Val Tyr Arg Ser Leu Gly Glu Asn Tyr Arg Glu Arg Val
 20 25 30
Leu Pro Ser Ile Ile His Glu Thr Leu Lys Ala Val Val Ala Gln Tyr
 35 40 45
Asn Ala Ser Gln Leu Ile Thr Gln Arg Glu Ser Val Ser Arg Glu Ile
 50 55 60
Arg Lys Ile Leu Thr Leu Arg Ala Ala Asn Phe His Ile Ala Leu Asp
 65 70 75 80
Asp Val Ser Ile Thr Gly Leu Thr Phe Gly Lys Glu Phe Thr Ala Ala
 85 90 95
Ile Glu Gly Lys Gln Val Ala Ala Gln Glu Ala Glu Arg Ala Lys Phe
 100 105 110
Ile Val Glu Lys Ala Glu Gln Asp Lys Arg Ser Ala Val Ile Arg Ala
```

115 120 125  
Glu Gly Glu Ala Lys Ser Ala Gln Leu Ile Gly Gln Ala Ile Ala Asn  
130 135 140  
Asn Gln Ala Phe Leu Thr Leu Arg Lys Ile Gly Ala Ala Arg Glu Ile  
145 150 155 160  
Ala Gln Thr Ile Ser Arg Ser Ala Asn Lys Val Tyr Leu Ser Ser Asn  
165 170 175  
Asp Leu Leu Leu Asn Leu Gln Ala Met Asp Leu Asp Val Lys Pro Lys  
180 185 190  
Lys

(2) INFORMATION FOR SEQ ID NO:1647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 903 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..903
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1647:

|             |             |            |             |             |             |     |
|-------------|-------------|------------|-------------|-------------|-------------|-----|
| ctctcaactc  | cgcgcacGcta | aactttattg | gagaaacccct | aatcgggcgac | aatggggtatt | 60  |
| tctctgtact  | ctatccacaa  | gaggcgtgcc | actggaggcca | agcagaagca  | atgggaggaa  | 120 |
| aagcgaaagt  | atgagatggg  | aaggcagcca | gccaacacca  | agctctcaag  | caacaagacg  | 180 |
| gtcagaagaa  | taagagtctg  | tggtggaaat | gttaagtggc  | gtcggttgag  | gctcgatact  | 240 |
| ggtaactact  | cgtgggggaag | tgaagcaact | accgcgaaga  | ccagagtctc  | tgatgtggtc  | 300 |
| tacaatgcct  | ccaacaatga  | gcttgtacct | actaagacac  | ttgtcaagag  | tgctattgtt  | 360 |
| cagggttgatg | ctgtctcttt  | caagcagtgg | tacctctcgc  | actatgggtg  | tgagcttggg  | 420 |
| cgcaagaaga  | agagtgcctc  | ttccaccaag | aaggacggga  | aggaaggtga  | agaggcagct  | 480 |
| gttgccagctc | ctgaggaggt  | caagaagagc | aaccacctcc  | tgagaagaat  | tgcaaacccgt | 540 |
| caagaggggc  | gcagtcctga  | ttcacacatt | gaggaccaat  | ttgcaagtgg  | acgtttgttg  | 600 |
| gcttgtatct  | cttcaaggcc  | tgggcagctg | gggcgtgctg  | atggatacat  | cttggaaagg  | 660 |
| aaagagttgg  | agttctacat  | gaagaagatc | cagaagaaga  | agggcaaggg  | tgctgcttag  | 720 |
| agtcctctct  | tatctgcctt  | gagcttttgt | cttacaacat  | gttttgagtt  | ttcagttttc  | 780 |
| attgtctgag  | aaactatggt  | tttggattag | cttgtgggtat | ttctttaaaa  | ctcccatcag  | 840 |
| ttattatggt  | acaatgtttt  | tgtcttggat | tttctttata  | attttaatcg  | ataatttcac  | 900 |

tcc

(2) INFORMATION FOR SEQ ID NO:1648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..222
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1648:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Gly Ile Ser Arg Asp Ser Ile His Lys Arg Arg Ala Thr Gly Gly |  |
| 1 5 10 15                                                       |  |
| Lys Gln Lys Gln Trp Arg Lys Lys Arg Lys Tyr Glu Met Gly Arg Gln |  |
| 20 25 30                                                        |  |
| Pro Ala Asn Thr Lys Leu Ser Ser Asn Lys Thr Val Arg Arg Ile Arg |  |
| 35 40 45                                                        |  |
| Val Arg Gly Gly Asn Val Lys Trp Arg Ala Leu Arg Leu Asp Thr Gly |  |
| 50 55 60                                                        |  |
| Asn Tyr Ser Trp Gly Ser Glu Ala Thr Thr Arg Lys Thr Arg Val Leu |  |
| 65 70 75 80                                                     |  |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asp | Val | Val | Tyr | Asn | Ala | Ser | Asn | Asn | Glu | Leu | Val | Arg | Thr | Lys | Thr |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Leu | Val | Lys | Ser | Ala | Ile | Val | Gln | Val | Asp | Ala | Ala | Pro | Phe | Lys | Gln |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Trp | Tyr | Leu | Ser | His | Tyr | Gly | Val | Glu | Leu | Gly | Arg | Lys | Lys | Lys | Ser |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |  |
| Ala | Ser | Ser | Thr | Lys | Lys | Asp | Gly | Glu | Glu | Gly | Glu | Glu | Ala | Ala | Val |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ala | Ala | Pro | Glu | Glu | Val | Lys | Lys | Ser | Asn | His | Leu | Leu | Arg | Lys | Ile |  |
|     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Ala | Ser | Arg | Gln | Glu | Gly | Arg | Ser | Leu | Asp | Ser | His | Ile | Glu | Asp | Gln |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |  |
| Phe | Ala | Ser | Gly | Arg | Leu | Leu | Ala | Cys | Ile | Ser | Ser | Arg | Pro | Gly | Gln |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Cys | Gly | Arg | Ala | Asp | Gly | Tyr | Ile | Leu | Glu | Gly | Lys | Glu | Leu | Glu | Phe |  |
|     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |  |
| Tyr | Met | Lys | Lys | Ile | Gln | Lys | Lys | Lys | Gly | Lys | Gly | Ala | Ala |     |     |  |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1649:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..194

(D) OTHER INFORMATION: / Ceres Seq. ID 1570571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1649:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Arg | Gln | Pro | Ala | Asn | Thr | Lys | Leu | Ser | Ser | Asn | Lys | Thr | Val |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |  |
| Arg | Arg | Ile | Arg | Val | Arg | Gly | Gly | Asn | Val | Lys | Trp | Arg | Ala | Leu | Arg |  |
|     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |     |  |
| Leu | Asp | Thr | Gly | Asn | Tyr | Ser | Trp | Gly | Ser | Glu | Ala | Thr | Thr | Arg | Lys |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Thr | Arg | Val | Leu | Asp | Val | Val | Tyr | Asn | Ala | Ser | Asn | Asn | Glu | Leu | Val |  |
|     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |  |
| Arg | Thr | Lys | Thr | Leu | Val | Lys | Ser | Ala | Ile | Val | Gln | Val | Asp | Ala | Ala |  |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |  |
| Pro | Phe | Lys | Gln | Trp | Tyr | Leu | Ser | His | Tyr | Gly | Val | Glu | Leu | Gly | Arg |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |     |  |
| Lys | Lys | Lys | Ser | Ala | Ser | Ser | Thr | Lys | Lys | Asp | Gly | Glu | Glu | Gly | Glu |  |
|     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |     |  |
| Glu | Ala | Ala | Val | Ala | Ala | Pro | Glu | Glu | Val | Lys | Lys | Ser | Asn | His | Leu |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |  |
| Leu | Arg | Lys | Ile | Ala | Ser | Arg | Gln | Glu | Gly | Arg | Ser | Leu | Asp | Ser | His |  |
|     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |  |
| Ile | Glu | Asp | Gln | Phe | Ala | Ser | Gly | Arg | Leu | Leu | Ala | Cys | Ile | Ser | Ser |  |
|     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |     |  |
| Arg | Pro | Gly | Gln | Cys | Gly | Arg | Ala | Asp | Gly | Tyr | Ile | Leu | Glu | Gly | Lys |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |     |     |     |  |
| Glu | Leu | Glu | Phe | Tyr | Met | Lys | Lys | Ile | Gln | Lys | Lys | Lys | Gly | Lys | Gly |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1650:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 830 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..830  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570576  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1650:  
atttctcttt agtctctcta cggaacctgt cttctgtct tgtccaaaaa cggatttttta 60  
agagtacaag tgaagtttatt ttggggggccg aaatctgtcc tggaggatag agaagcaaga 120  
tgaagtttaat agatcgatag aatgaggtta acggagctgc tcttacgggtg ctcacatcagt 180  
gtcttcgctc tctctcgccgt tattctagtt gtgacagaca ctgagggtcaa gcttatcttc 240  
aatatcaaga agacgggcaa gtacacggac atgaaggcgg ttgtgtcttt ggtggtgctt 300  
aatgggtagat ctgcggtttta ttctttgttg caatcagttc gttgcgtggt gggtagcagt 360  
aaaggaagag ttttgtttas taagcctctt gcttgggctt tttctcbgg gtagcaggcg 420  
atggcgctact tgaatgtggc agccattgca gcaacagcag agtctgggtKT gWRattgtcta 480  
gggaaggaga ggaagatttt caatggatga gagtgtgtac tatgtatgga aagttcttca 540  
accaaatgag tataggagtc tctagcgctt tgttagcctc cattgctatg gttttcgctt 600  
cctgcatttc tgcttttagt ctcttcgcgt gtacaggtgc caccaaaagac cgcagaacca 660  
cgccgtgggt aagtgaatgc ggctttgtct ttagtgtgtg tgaataatgtt Ygtgtgttaa 720  
aaaacatata gtacaaaagac tgtaggctct tgttggttct tcttcttctt cttcttgatg 780  
atgttatatg tgacaaaaca tatgtataaac tagactattg atgttctgtg  
(2) INFORMATION FOR SEQ ID NO:1651:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 122 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..122  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1570577  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1651:  
Met Arg Leu Thr Glu Leu Leu Leu Arg Cys Ser Ile Ser Val Phe Ala  
1 5 10 15  
Leu Leu Ala Leu Ile Leu Val Val Thr Asp Thr Glu Val Lys Leu Ile  
20 25 30  
Phe Thr Ile Lys Lys Thr Ala Lys Tyr Thr Asp Met Lys Ala Val Val  
35 40 45  
Phe Leu Val Val Ala Asn Gly Ile Ala Ala Val Tyr Ser Leu Leu Gln  
50 55 60  
Ser Val Arg Cys Val Val Gly Thr Met Lys Gly Lys Val Leu Phe Xaa  
65 70 75 80  
Lys Pro Leu Ala Trp Ala Phe Phe Xaa Gly Asp Gln Ala Met Ala Tyr  
85 90 95  
Leu Asn Val Ala Ala Ile Ala Ala Thr Ala Glu Ser Gly Xaa Xaa Leu  
100 105 110  
Leu Gly Lys Glu Arg Lys Ile Cys Asn Gly  
115 120  
(2) INFORMATION FOR SEQ ID NO:1652:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 79 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..79  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1570578  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1652:

```

Met Lys Ala Val Val Phe Leu Val Val Ala Asn Gly Ile Ala Ala Val
1 5 10 15
Tyr Ser Leu Leu Gln Ser Val Arg Cys Val Val Gly Thr Met Lys Gly
20 25 30
Lys Val Leu Phe Xaa Lys Pro Leu Ala Trp Ala Phe Phe Xaa Gly Asp
35 40 45
Gln Ala Met Ala Tyr Leu Asn Val Ala Ala Ile Ala Ala Thr Ala Glu
50 55 60
Ser Gly Xaa Xaa Leu Leu Gly Lys Glu Arg Lys Ile Cys Asn Gly
65 70 75

```

(2) INFORMATION FOR SEQ ID NO:1653:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 736 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..736

(D) OTHER INFORMATION: / Ceres Seq. ID 1570583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1653:

```

ctgaaccctt cgattttcga ttctctctcg agccttctct ccttctctcG tttMetctctc 60
aagaggattt tgattgtctc cttactctct ccatgtcaag ttctggtgct ccttcacgca 120
agactctgag taagatgcgc actaatcgtc ttcaagaaga gcttgtggaa tggcagatga 180
atccacctac tgggtttcaaa cacaaagtca ctgataatct ccaaagatgg ataattgaag 240
ttattggagc tccaggaaact ctatatgcc aacatactta tcagcttcaa gttgattttc 300
cagaacatta tccataggaa tcgcacaaag tgatttttct tcctccagct cctctgcatc 360
ctccacattta cagcaatggg catatttgtc tagatatttt gtatgattgg tggctctccag 420
ccatgacggt gacttctatc tgcattagca tctcttccat gctctcaagc tcgactgaaa 480
agcaacgacc aaccgataat gaccgatgtg tgaagaattg taagaacgga agatctccaa 540
aggagaccgg atgggtggttc cagcagcaga aagtataaac ctaaatcaac caaaaaaat 600
gtaaaatagt ccaaaacagt ctttgagggt ttgtgtctat ttttaattta attgggttta 660
agctgtccca aaccctattc caaaatccgt gatgtataaa aacaacacaa taaatttgac 720
taattttgaa tcttcc

```

(2) INFORMATION FOR SEQ ID NO:1654:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1570584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1654:

```

Glu Pro Phe Asp Phe Arg Phe Phe Leu Glu Pro Ser Phe Leu Pro Ser
1 5 10 15
Xaa Leu Leu Gln Glu Asp Phe Asp Cys Leu Leu Thr Leu Ser Met Ser
20 25 30
Ser Ser Gly Ala Pro Ser Arg Lys Thr Leu Ser Lys Ile Ala Thr Asn
35 40 45
Arg Leu Gln Lys Glu Leu Val Glu Trp Gln Met Asn Pro Pro Thr Gly
50 55 60
Phe Lys His Lys Val Thr Asp Asn Leu Gln Arg Trp Ile Ile Glu Val
65 70 75 80
Ile Gly Ala Pro Gly Thr Leu Tyr Ala Asn Asp Thr Tyr Gln Leu Gln
85 90 95
Val Asp Phe Pro Glu His Tyr Pro Met Glu Ser Pro Gln Val Ile Phe
100 105 110

```

Leu His Pro Ala Pro Leu His Pro His Ile Tyr Ser Asn Gly His Ile  
115 120 125  
Cys Leu Asp Ile Leu Tyr Asp Ser Trp Ser Pro Ala Met Thr Val Ser  
130 135 140  
Ser Ile Cys Ile Ser Ile Leu Ser Met Leu Ser Ser Thr Glu Lys  
145 150 155 160  
Gln Arg Pro Thr Asp Asn Asp Arg Tyr Val Lys Asn Cys Lys Asn Gly  
165 170 175  
Arg Ser Pro Lys Glu Thr Arg Trp Trp Phe His Asp Asp Lys Val  
180 185 190

(2) INFORMATION FOR SEQ ID NO:1655:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1570585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1655:

Met Ser Ser Ser Gly Ala Pro Ser Arg Lys Thr Leu Ser Lys Ile Ala  
1 5 10 15  
Thr Asn Arg Leu Gln Lys Glu Leu Val Glu Trp Gln Met Asn Pro Pro  
20 25 30  
Thr Gly Phe Lys His Lys Val Thr Asp Asn Leu Gln Arg Trp Ile Ile  
35 40 45  
Glu Val Ile Gly Ala Pro Gly Thr Leu Tyr Ala Asn Asp Thr Tyr Gln  
50 55 60  
Leu Gln Val Asp Phe Pro Glu His Tyr Pro Met Glu Ser Pro Gln Val  
65 70 75 80  
Ile Phe Leu His Pro Ala Pro Leu His Pro His Ile Tyr Ser Asn Gly  
85 90 95  
His Ile Cys Leu Asp Ile Leu Tyr Asp Ser Trp Ser Pro Ala Met Thr  
100 105 110  
Val Ser Ser Ile Cys Ile Ser Ile Leu Ser Met Leu Ser Ser Ser Thr  
115 120 125  
Glu Lys Gln Arg Pro Thr Asp Asn Asp Arg Tyr Val Lys Asn Cys Lys  
130 135 140  
Asn Gly Arg Ser Pro Lys Glu Thr Arg Trp Trp Phe His Asp Asp Lys  
145 150 155 160  
Val

(2) INFORMATION FOR SEQ ID NO:1656:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1570586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1656:

Met Asn Pro Pro Thr Gly Phe Lys His Lys Val Thr Asp Asn Leu Gln  
1 5 10 15  
Arg Trp Ile Ile Glu Val Ile Gly Ala Pro Gly Thr Leu Tyr Ala Asn  
20 25 30  
Asp Thr Tyr Gln Leu Gln Val Asp Phe Pro Glu His Tyr Pro Met Glu

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
|     | 35  |     | 40  |     | 45  |     |
| Ser | Pro | Gln | Val | Ile | Phe | Leu |
| 50  |     |     |     |     | 55  | His |
| Tyr | Ser | Asn | Gly | His | Ile | Cys |
| 65  |     |     |     |     | 70  | Leu |
| Pro | Ala | Met | Thr | Val | Ser | Ser |
|     |     |     |     |     | 85  | Ile |
| Ser | Ser | Ser | Thr | Glu | Lys | Gln |
|     |     |     |     |     | 100 | Arg |
| Lys | Asn | Cys | Lys | Asn | Gly | Arg |
|     |     |     |     |     | 115 | Ser |
| His | Asp | Asp | Lys | Val |     |     |
|     |     |     |     |     | 130 |     |

(2) INFORMATION FOR SEQ ID NO:1657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..936
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1657:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| ctagacgtcg | aagatgaaGt | tcaacgTbga | gaatccaact | actggatgcc  | agaagaagct | 60  |
| cgagatcgac | gatgaccaga | aactacgtgc | gttttacgac | aagagaatct  | ctcaagaagt | 120 |
| cagtgagat  | gctttgggcg | aggagtcca  | aggatacggt | tccaagatca  | agggtgggtg | 180 |
| cgataagcaa | ggtttcccaa | tgaagcaggg | agttttgact | ccaggccgtg  | ttcgcccttt | 240 |
| gcttcacoga | ggaaactcct | gcttcagagg | acatggaagg | akaactgggtg | agaggagaag | 300 |
| aaagtctgtt | cgtggttgca | ttgtgagccc | tgactctctc | gttctgaacc  | ttgtcattgt | 360 |
| gaagaagggt | gagaacgata | ttcctgggct | taccgatact | gagaagccaa  | gaatgagagg | 420 |
| accaaagaga | gcctccaaga | tcogtaaaat | gtttaacctc | aagaaggaag  | atgatgtcag | 480 |
| gacctatgtc | aacacttacc | gccgcaagtt | cacaaacaag | aagggaagg   | aagttagcaa | 540 |
| agccctcaag | atccagaggg | ttgtgacccc | attgactctt | cagaggaaga  | gagctagaat | 600 |
| tgctgacaag | aagaagaaaa | ttgctaaggc | taattctgat | gctgctgatt  | accagaagct | 660 |
| tctcgctcgt | aggttgaagg | aacagcgtga | caggaggagt | gagagtttgg  | caaagaagag | 720 |
| gtcgagactc | tcttctgctg | ctgccaagcc | ctctgtcaca | gcttaaaaaa  | gcttgagaat | 780 |
| caaatcaaa  | atgtcAcSSc | tttctvtggt | tggtctcttt | tcttctccgg  | ctattaaaaa | 840 |
| gttagttcga | gttcatattc | agctgttttt | gttccaagac | atgggttacac | aatcgctttg | 900 |

(2) INFORMATION FOR SEQ ID NO:1658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..250
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1658:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Phe | Asn | Xaa | Glu | Asn | Pro | Thr | Thr | Gly | Cys | Gln | Lys | Lys | Leu |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Glu | Ile | Asp | Asp | Asp | Gln | Lys | Leu | Arg | Ala | Phe | Tyr | Asp | Lys | Arg | Ile |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Gln | Glu | Val | Ser | Gly | Asp | Ala | Leu | Gly | Glu | Glu | Phe | Lys | Gly | Tyr |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Val | Phe | Lys | Ile | Lys | Gly | Gly | Cys | Asp | Lys | Gln | Gly | Phe | Pro | Met | Lys |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |

```

Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg Gly
65 70 75 80
Thr Pro Cys Phe Arg Gly His Gly Arg Xaa Thr Gly Glu Arg Arg
 85 90 95
Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu Asn
 100 105 110
Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr Asp
 115 120 125
Thr Glu Lys Pro Arg Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg
 130 135 140
Lys Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn
145 150 155 160
Thr Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys
 165 170 175
Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys
 180 185 190
Arg Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser
 195 200 205
Asp Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln
210 215 220
Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Lys Arg Ser Arg Leu Ser
225 230 235 240
Ser Ala Ala Ala Lys Pro Ser Val Thr Ala
 245 250

```

(2) INFORMATION FOR SEQ ID NO:1659:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..188

(D) OTHER INFORMATION: / Ceres Seq. ID 1570605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1659:

```

Met Lys Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His
1 5 10 15
Arg Gly Thr Pro Cys Phe Arg Gly His Gly Arg Xaa Thr Gly Glu Arg
 20 25 30
Arg Arg Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val
 35 40 45
Leu Asn Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu
 50 55 60
Thr Asp Thr Glu Lys Pro Arg Met Arg Gly Pro Lys Arg Ala Ser Lys
65 70 75 80
Ile Arg Lys Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr
 85 90 95
val Asn Thr Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val
 100 105 110
Ser Lys Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln
 115 120 125
Arg Lys Arg Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala
 130 135 140
Asn Ser Ser Asp Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys
145 150 155 160
Glu Gln Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Lys Arg Ser Arg
 165 170 175
Leu Ser Ser Ala Ala Lys Pro Ser Val Thr Ala
 180 185

```

(2) INFORMATION FOR SEQ ID NO:1660:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 833 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..833  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570606  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1660:  
agacgtcgaa gatgaagttc aacgttgccg agttcaaaagg atacgttttc aagatcaagg 60  
gtgggtgcga taagcaagggt ttcccaatga agcagggagt ttgactcca gcccggtgttc 120  
gccttttgct tcaccgagga actcctttgct tcagaggaca tgggaaggaga actggttgaga 180  
ggagaagaaa gtctgttcgt ggttgcaattg tgagccctga tctctctgt ctgaaccttg 240  
tcatttgtaa gaaggggtgag aacgatcttc ctgggcttac cgatactgag aagccaagaa 300  
tgagaggacc aaagagagacc tccaagatcc tgaacctgtt taacctcaag aaggaagatg 360  
atgcaggac ctatgtcaac acttaccgcc gcaagttcac aaacaagaag ggcaagggaag 420  
ttagcaaaag ccctaagatc cagaggcttg tgacccatt gactcttcag aggaagagag 480  
ctagaattgc tgacaagaag aagaaaattg ctaaggctaa ttctgatgct gctgattacc 540  
agaagcttct cgcctcgagg ttgaaggaa acgctgacag gaggagtga agTttggcAa 600  
agaagaggtc gagactctct tctgctgctg ccaagccctc tgtcacagct taaaaaagct 660  
tgagaatcaa atcaaaagatg tcacctttct agtCtttggt ctcttttctt ctccggctat 720  
taaaaaagtta gttcgagttc atattcagct gtttttgttc caagacatgg gtacacaatc 780  
gctttgggct tgtttcatga tttatgcttt tagttgaaga ccattttaaa ctc  
(2) INFORMATION FOR SEQ ID NO:1661:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 216 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..216  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570607  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1661:  
Thr Ser Lys Met Lys Phe Asn Val Ala Glu Phe Lys Gly Tyr Val Phe  
1 5 10 15  
Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met Lys Gln Gly  
20 25 30  
Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg Gly Thr Pro  
35 40 45  
Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg Arg Lys Ser  
50 55 60  
Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu Asn Leu Val  
65 70 75 80  
Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr Asp Thr Glu  
85 90 95  
Lys Pro Arg Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg Lys Leu  
100 105 110  
Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn Thr Tyr  
115 120 125  
Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys Ala Pro  
130 135 140  
Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Lys Gln Arg Lys Arg Ala  
145 150 155 160  
Arg Ile Ala Asp Lys Lys Lys Ile Ala Lys Ala Asn Ser Asp Ala  
165 170 175  
Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln Arg Asp  
180 185 190

Arg Arg Ser Glu Ser Leu Ala Lys Lys Arg Ser Arg Leu Ser Ser Ala  
195 200 205  
Ala Ala Lys Pro Ser Val Thr Ala  
210 215

(2) INFORMATION FOR SEQ ID NO:1662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1662:

Met Lys Phe Asn Val Ala Glu Phe Lys Gly Tyr Val Phe Lys Ile Lys  
1 5 10 15  
Gly Gly Cys Asp Lys Lys Gln Gly Phe Pro Met Lys Gln Gly Val Leu Thr  
20 25 30  
Pro Gly Arg Val Arg Leu Leu Leu His Arg Gly Thr Pro Cys Phe Arg  
35 40 45  
Gly His Gly Arg Arg Thr Gly Glu Arg Arg Arg Lys Ser Val Arg Gly  
50 55 60  
Cys Ile Val Ser Pro Asp Leu Ser Val Leu Asn Leu Val Ile Val Lys  
65 70 75 80  
Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr Asp Thr Glu Lys Pro Arg  
85 90 95  
Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg Lys Leu Phe Asn Leu  
100 105 110  
Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn Thr Tyr Arg Arg Lys  
115 120 125  
Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys Ala Pro Lys Ile Gln  
130 135 140  
Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys Arg Ala Arg Ile Ala  
145 150 155 160  
Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser Asp Ala Ala Asp Tyr  
165 170 175  
Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln Arg Asp Arg Arg Ser  
180 185 190  
Glu Ser Leu Ala Lys Lys Arg Ser Arg Leu Ser Ser Ala Ala Ala Lys  
195 200 205  
Pro Ser Val Thr Ala  
210

(2) INFORMATION FOR SEQ ID NO:1663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..188
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1663:

Met Lys Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His  
1 5 10 15  
Arg Gly Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg  
20 25 30  
Arg Arg Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 35                                                              | 40  | 45  |
| Leu Asn Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu |     |     |
| 50                                                              | 55  | 60  |
| Thr Asp Thr Glu Lys Pro Arg Met Arg Gly Pro Lys Arg Ala Ser Lys |     |     |
| 65                                                              | 70  | 75  |
| Ile Arg Lys Leu Phe Asn Leu Lys Lys Glu Asp Val Arg Thr Tyr     |     |     |
| 85                                                              | 90  | 95  |
| Val Asn Thr Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val |     |     |
| 100                                                             | 105 | 110 |
| Ser Lys Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln |     |     |
| 115                                                             | 120 | 125 |
| Arg Lys Arg Ala Arg Ile Ala Asp Lys Lys Lys Ile Ala Lys Ala     |     |     |
| 130                                                             | 135 | 140 |
| Asn Ser Asp Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys |     |     |
| 145                                                             | 150 | 155 |
| Glu Gln Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Lys Arg Ser Arg |     |     |
| 165                                                             | 170 | 175 |
| Leu Ser Ser Ala Ala Lys Pro Ser Val Thr Ala                     |     |     |
| 180                                                             | 185 |     |

(2) INFORMATION FOR SEQ ID NO:1664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..721
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1664:

|            |            |             |            |             |             |     |
|------------|------------|-------------|------------|-------------|-------------|-----|
| agtttagatt | ctttatccga | ctactttgtt  | catcggtttt | gtttttcttt  | ttgtcttcgcg | 60  |
| gaagcggaat | tacatgtcgg | aagcagcaca  | gctcagaaga | ggctctaaagc | ctaaagggaa  | 120 |
| gacttatggg | ttgaccaatc | agaagagacg  | agagatcaga | ggatctcttg  | atcttttcga  | 180 |
| catagacggg | tcaggtagca | tcgatgctag  | cgagctcaac | gatgtctatga | ggctctcttg  | 240 |
| atttgagatg | aataatcagc | aaataaacga  | attgatggca | gaagtagata  | aaaaccaaag  | 300 |
| tggagccata | gatttcgacg | aatttgtgca  | tatgatgaca | accaaattcg  | gagaacgaga  | 360 |
| ctccatagac | gaattgtcta | agggcgttaa  | gatcattgac | cacgacaata  | gtgggaagat  | 420 |
| ttcacctcgt | gatataaaga | tgatttgctaa | agaattggga | gaaaatttca  | cagataatga  | 480 |
| tatagaagaa | atgatcgaa  | aagcagaccg  | tgacaagaat | ggagaagtta  | acttgaggga  | 540 |
| gttcataaas | gatgatgaag | agaacctctt  | tcggctaagt | ataaatcaat  | tagtaattgg  | 600 |
| tgtgaataat | atttgttaat | caccttgatt  | tataataata | aagaagtgtt  | atttgtggct  | 660 |
| tggtogaata | aaaatgtatt | gttgtataaa  | ataataaatg | taattcacat  | ccattatttt  | 720 |

g

(2) INFORMATION FOR SEQ ID NO:1665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..181
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1665:

|                                                                 |    |
|-----------------------------------------------------------------|----|
| Met Ser Glu Ala Ala Gln Leu Arg Arg Gly Leu Lys Pro Lys Gly Lys |    |
| 1                                                               | 10 |
| Thr Tyr Gly Leu Thr Asn Gln Lys Arg Arg Glu Ile Arg Glu Ile Phe |    |
| 20                                                              | 30 |
| Asp Leu Phe Asp Ile Asp Gly Ser Gly Ser Ile Asp Ala Ser Glu Leu |    |

(2) INFORMATION FOR SEO ID NO:1666:

(A) LENGTH: 130 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..130

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:1666:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1570613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1667:

```

Met Asn Asn Gln Gln Ile Asn Glu Leu Met Ala Glu Val Asp Lys Asn
1 5 10 15
Gln Ser Gly Ala Ile Asp Phe Asp Glu Phe Val His Met Met Thr Thr
 20 25 30
Lys Phe Gly Glu Arg Asp Ser Ile Asp Glu Leu Ser Lys Ala Phe Lys
 35 40 45
Ile Ile Asp His Asp Asn Ser Gly Lys Ile Ser Pro Arg Asp Ile Lys
 50 55 60
Met Ile Ala Lys Glu Leu Gly Glu Asn Phe Thr Asp Asn Asp Ile Glu
65 70 75 80
Glu Met Ile Glu Glu Ala Asp Arg Asp Lys Asp Gly Glu Val Asn Leu
 85 90 95
Glu Glu Phe Met Xaa Asp Asp Glu Glu Asn Leu Phe Arg Leu Ser Ile
 100 105 110
Asn Gln Leu Val Met Val Val Asn Asn Ile Cys
 115 120

```

(2) INFORMATION FOR SEQ ID NO:1668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..922
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1668:

```

actcagagac ttgttgtgaa gttgaaactc tctgaccgta gctttcttat ccttcattca 60
ggttcaactac tatgtacagt ctacacattca aatgaaatgag tacccgggac gtgtgtgtatt 120
gccatctgctt tcaagaagaac agggcagcacc aattttgcact tgtttgaaaa tttttgatat 180
gtctgtgttta aagcttttcag ctttaagtca aattaaagtta atgactgccta taacacaacat 240
agatgatttg aactatccag agaagacaga gacatactat gtgtcacaat tcccgtaacat 300
attctctgctt tggttgaaaa ccataaagcc tctgttgcaa gagagaacaa agaagaagat 360
tcaagttctg aaagggttcg ggaaagatga gttgctaaag ataattggat atgagtctct 420
ccacacatttc tgtagaagag aagggtctgg atctggtagg catatctcaa atggaaacagt 480
agacaattgt ttctctctgg atcactcttt ccaccaagac ctttatgatt atgtcaagca 540
gcaggctctg gttaaaagat caggtgcacc gatcagacat ggttcagtc acgttaagtt 600
ccctgagcca gacaccgaag gcaacaagat cttcgatacc ttagaaaaatg agttccagaa 660
gcttggaaat gaccagaaga tctgagtgat ctacaaccct tataaacaga attgcccata 720
agaaaaccga atttgcctct ggttgatgag cagtatttaa gataagaatc aatcaccttt 780
acttgtatta ctagtgttcg ttgcacacgc tMcgatgcag gttttgtyta aaaagaagat 840
ggaacacaat ttctctcgaa ttgatcttt gatctagtac cattatatat atagaactca 900
ttcttattta tgtccttttg cc

```

(2) INFORMATION FOR SEQ ID NO:1669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1669:

```

Met Asn Glu Tyr Arg Asp Arg Val Val Leu Pro Ser Ala Ser Lys Lys
1 5 10 15
Gln Gly Arg Pro Ile Cys Thr Cys Leu Lys Ile Leu Asp Met Ser Gly
 20 25 30
Leu Lys Leu Ser Ala Leu Ser Gln Ile Lys Leu Met Thr Ala Ile Thr

```

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..154  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570621  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1671:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Ala | Ile | Thr | Thr | Ile | Asp | Asp | Leu | Asn | Tyr | Pro | Glu | Lys | Thr |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Glu | Thr | Tyr | Tyr | Val | Val | Asn | Val | Pro | Tyr | Ile | Phe | Ser | Ala | Cys | Trp |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Lys | Thr | Ile | Lys | Pro | Leu | Leu | Gln | Glu | Arg | Thr | Lys | Lys | Lys | Ile | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Val | Leu | Lys | Gly | Cys | Gly | Lys | Asp | Glu | Leu | Leu | Lys | Ile | Met | Asp | Tyr |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Ser | Leu | Pro | His | Phe | Cys | Arg | Arg | Glu | Gly | Ser | Gly | Ser | Gly | Arg |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| His | Ile | Ser | Asn | Gly | Thr | Val | Asp | Asn | Cys | Phe | Ser | Leu | Asp | His | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Phe | His | Gln | Asp | Leu | Tyr | Asp | Tyr | Val | Lys | Gln | Gln | Ala | Leu | Val | Lys |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Gly | Ser | Gly | Ala | Pro | Ile | Arg | His | Gly | Ser | Val | His | Val | Lys | Phe | Pro |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Glu | Pro | Asp | Thr | Glu | Gly | Asn | Lys | Ile | Phe | Asp | Thr | Leu | Glu | Asn | Glu |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Gln | Lys | Leu | Gly | Asn | Asp | Gln | Lys | Ile |     |     |     |     |     |     |
|     |     | 145 |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1672:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1082 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1082  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570622  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1672:

|            |            |            |             |            |             |      |
|------------|------------|------------|-------------|------------|-------------|------|
| gtttgtccct | ccttctacgc | cgcacactat | cttttctctct | cactcagact | tcctcttccat | 60   |
| ctcaagagaa | atggctgaat | ccaaggtagt | gggtccagag  | tctgtgctaa | agaagatcaa  | 120  |
| gaggcaagag | gaatgggcat | tggccaagaa | agatgaagct  | gtagctgcta | agaagaagag  | 180  |
| gtttgaggcc | cgcaagctta | tottcaagag | agctgagcag  | tatgccaaa  | aatagcgtga  | 240  |
| gaaggataac | gagttgatcc | gattgaagcg | ggaggctaag  | ttgaaaggag | gtttctacgt  | 300  |
| tgacctgag  | gctaagtgtc | tctttatcat | tcgtatccgt  | ggatccaatg | ccattgaccc  | 360  |
| aaaaaccaag | aagattctgc | agctctcg   | tttgagacag  | gtagggttca | cagtttgtta  | 420  |
| ttttcatcca | gctatatatt | octaacatat | gattattgat  | taatatgtgt | tatatgttca  | 480  |
| aactaatatg | tgatagttgc | ctgttcatca | tttttaaaag  | agagtagaag | actatttgcgt | 540  |
| tgtaagaag  | tttacttttc | tatacatatt | tgcatgctct  | caatgggtgt | tttcttaagg  | 600  |
| tgaacaaggc | aacagtaaac | atGctgcg   | gagttgaacc  | atacgtgact | tacggataacc | 660  |
| caaatcttga | gagcgttaag | gaactgatct | acaaaagagg  | ttatggaaag | ctgaaccacc  | 720  |
| agaggatagc | acttactgac | aactccattg | tggatcagcg  | tctcggaaa  | catgggatca  | 780  |
| tctgcgttga | ggatctcatc | cagagatca  | tgactgttgg  | acctcacttc | aaggaagcca  | 840  |
| acaaacttct | gtggccattc | caattgaagg | caccactcgg  | tggccttaag | aagaagagaa  | 900  |
| accactacgt | cgaaggtgtg | gatgctggaa | acaggggaaa  | tttcatcaac | gagcttgctca | 960  |
| ggagaatgaa | ttgatgaag  | cttctctctt | tatctttgca  | aatttcaaag | attttgggac  | 1020 |
| cgagtttttt | tttttttttt | ttcaagttat | cagagacttg  | tgatctttta | tcagagatag  | 1080 |

gc

(2) INFORMATION FOR SEQ ID NO:1673:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 147 amino acids  
    (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..147  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570623  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1673:  
Phe Cys Pro Pro Ser Thr Pro His Thr Ile Phe Ser Ser His Ser Asp  
1          5          10          15  
Phe Leu Phe Ile Ser Arg Glu Met Ala Glu Ser Lys Val Val Val Pro  
          20          25          30  
Glu Ser Val Leu Lys Lys Ile Lys Arg Gln Glu Glu Trp Ala Leu Ala  
35          40          45  
Lys Lys Asp Glu Ala Val Ala Ala Lys Lys Lys Ser Val Glu Ala Arg  
50          55          60  
Lys Leu Ile Phe Lys Arg Ala Glu Gln Tyr Ala Lys Glu Tyr Ala Glu  
65          70          75          80  
Lys Asp Asn Glu Leu Ile Arg Leu Lys Arg Glu Ala Lys Leu Lys Gly  
          85          90          95  
Gly Phe Tyr Val Asp Pro Glu Ala Lys Leu Leu Phe Ile Ile Arg Ile  
          100         105         110  
Arg Gly Ile Asn Ala Ile Asp Pro Lys Thr Lys Lys Ile Leu Gln Leu  
115         120         125  
Leu Arg Leu Arg Gln Val Gly Phe Thr Val Cys Tyr Phe His Pro Ala  
130         135         140  
Ile Leu Ala  
145  
(2) INFORMATION FOR SEQ ID NO:1674:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 124 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..124  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1570624  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1674:  
Met Ala Glu Ser Lys Val Val Val Pro Glu Ser Val Leu Lys Lys Ile  
1          5          10          15  
Lys Arg Gln Glu Trp Ala Leu Ala Lys Lys Asp Glu Ala Val Ala  
20          25          30  
Ala Lys Lys Lys Ser Val Glu Ala Arg Lys Leu Ile Phe Lys Arg Ala  
35          40          45  
Glu Gln Tyr Ala Lys Glu Tyr Ala Glu Lys Asp Asn Glu Leu Ile Arg  
50          55          60  
Leu Lys Arg Glu Ala Lys Leu Lys Gly Gly Phe Tyr Val Asp Pro Glu  
65          70          75          80  
Ala Lys Leu Leu Phe Ile Ile Arg Ile Arg Gly Ile Asn Ala Ile Asp  
          85          90          95  
Pro Lys Thr Lys Lys Ile Leu Gln Leu Leu Arg Leu Arg Gln Val Gly  
100         105         110  
Phe Thr Val Cys Tyr Phe His Pro Ala Ile Leu Ala  
115         120  
(2) INFORMATION FOR SEQ ID NO:1675:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 117 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..117  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570625  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1675:  
Met Leu Arg Arg Val Glu Pro Tyr Val Thr Tyr Gly Tyr Pro Asn Leu  
1                  5                  10                  15  
Lys Ser Val Lys Glu Leu Ile Tyr Lys Arg Gly Tyr Gly Lys Leu Asn  
                  20                  25                  30  
His Gln Arg Ile Ala Leu Thr Asp Asn Ser Ile Val Asp Gln Ala Leu  
                  35                  40                  45  
Gly Lys His Gly Ile Ile Cys Val Glu Asp Leu Ile His Glu Ile Met  
                  50                  55                  60  
Thr Val Gly Pro His Phe Lys Glu Ala Asn Asn Phe Leu Trp Pro Phe  
65                  70                  75                  80  
Gln Leu Lys Ala Pro Leu Gly Gly Leu Lys Lys Arg Asn His Tyr  
                  85                  90                  95  
Val Glu Gly Gly Asp Ala Gly Asn Arg Glu Asn Phe Ile Asn Glu Leu  
                  100                 105                 110  
Val Arg Arg Met Asn  
                  115

(2) INFORMATION FOR SEQ ID NO:1676:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 784 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..784  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570636  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1676:  
aatccaatca aaacacacag agagaagaaa aactcagaag aaaagccaaa gagtgaaca 60  
aaaatggcgt cgacgactct ctcaatcgca acaacaatcc gtctctcatc ttatcctact 120  
ctcgcttcca tcaatcactt ccttcccgca accaccacca tcgaattccc ctctcgcttc 180  
gggtggtggt catcatccac attgaccacac cgtgcaaccc atctccgtcc aatcgccgcc 240  
gtcgaagctc cggagaaaaat cgagaagatc ggatccgaaa tctcatccct aaccctcgaa 300  
gaagctcgta tctctcgctga ctatctccaa gacaaaattcg gtgtctcccc acctctctta 360  
gCccccgcag cagcggcggt tgctgtccca gccagcgggt gcgcggcggc tgtagtggaa 420  
gagcaaacag agttcgatgt ggttatcaat gaagtccca gcagttcccg tattcgagt 480  
ttaaaagctg ttagggtctt aactagcttg gcgttgaagg aagctaagga gctaatacga 540  
ggattaccaa agaagtttaa agaaggtatc actaaagatg aagctgaaga aactaagaag 600  
actcttgaag aagctggtgc taaagtctcc attgcttaag gtttttatta aaaaaaaaaa 660  
agaagtgtgt atcttttctg gaatttgatt ggtcttttgt gttgtttagt atagtttgcg 720  
tctggaattg ttgagaattt gttgtaattt gaatcacatt tggtttccca ttagctgatt 780  
tcgc

(2) INFORMATION FOR SEQ ID NO:1677:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 212 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..212  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570637  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1677:

```

Asn Pro Ile Lys Thr His Arg Glu Lys Lys Asn Ser Glu Glu Lys Pro
1 5 10 15
Lys Ser Glu Thr Lys Met Ala Ser Thr Thr Leu Ser Ile Ala Thr Thr
20 25 30
Ile Arg Ser Ser Ser Tyr Pro Thr Leu Ala Ser Ile Asn His Phe Pro
35 40 45
Ser Arg Thr Thr Thr Ile Glu Phe Pro Ser Arg Phe Gly Gly Gly Ser
50 55 60
Ser Ser Thr Leu Thr His Arg Ala Thr His Leu Arg Pro Ile Ala Ala
65 70 75 80
Val Glu Ala Pro Glu Lys Ile Glu Lys Ile Gly Ser Glu Ile Ser Ser
85 90 95
Leu Thr Leu Glu Glu Ala Arg Ile Leu Val Asp Tyr Leu Gln Asp Lys
100 105 110
Phe Gly Val Ser Pro Leu Ser Leu Ala Pro Ala Ala Ala Val Ala
115 120 125
Ala Pro Ala Asp Gly Gly Ala Ala Ala Val Val Glu Glu Gln Thr Glu
130 135 140
Phe Asp Val Val Ile Asn Glu Val Pro Ser Ser Ser Arg Ile Ala Val
145 150 155 160
Ile Lys Ala Val Arg Ala Leu Thr Ser Leu Ala Leu Lys Glu Ala Lys
165 170 175
Glu Leu Ile Glu Gly Leu Pro Lys Lys Phe Lys Glu Gly Ile Thr Lys
180 185 190
Asp Glu Ala Glu Glu Thr Lys Lys Thr Leu Glu Glu Ala Gly Ala Lys
195 200 205
Val Ser Ile Ala
210

```

(2) INFORMATION FOR SEQ ID NO:1678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1570638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1678:

```

Met Ala Ser Thr Thr Leu Ser Ile Ala Thr Thr Ile Arg Ser Ser Ser
1 5 10 15
Tyr Pro Thr Leu Ala Ser Ile Asn His Phe Pro Ser Arg Thr Thr Thr
20 25 30
Ile Glu Phe Pro Ser Arg Phe Gly Gly Gly Ser Ser Ser Thr Leu Thr
35 40 45
His Arg Ala Thr His Leu Arg Pro Ile Ala Ala Val Glu Ala Pro Glu
50 55 60
Lys Ile Glu Lys Ile Gly Ser Glu Ile Ser Ser Leu Thr Leu Glu Glu
65 70 75 80
Ala Arg Ile Leu Val Asp Tyr Leu Gln Asp Lys Phe Gly Val Ser Pro
85 90 95
Leu Ser Leu Ala Pro Ala Ala Ala Ala Val Ala Ala Pro Ala Asp Gly
100 105 110
Gly Ala Ala Ala Val Val Glu Glu Gln Thr Glu Phe Asp Val Val Ile
115 120 125
Asn Glu Val Pro Ser Ser Ser Arg Ile Ala Val Ile Lys Ala Val Arg
130 135 140
Ala Leu Thr Ser Leu Ala Leu Lys Glu Ala Lys Glu Leu Ile Glu Gly
145 150 155 160
Leu Pro Lys Lys Phe Lys Glu Gly Ile Thr Lys Asp Glu Ala Glu Glu

```



165 170 175  
Thr Lys Lys Thr Leu Glu Glu Ala Gly Ala Lys Val Ser Ile Ala  
180 185 190

(2) INFORMATION FOR SEQ ID NO:1679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1039 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1039

(D) OTHER INFORMATION: / Ceres Seq. ID 1570655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1679:

|            |          |           |        |            |      |            |      |           |        |      |
|------------|----------|-----------|--------|------------|------|------------|------|-----------|--------|------|
| atattacc   | ttgtagaa | aaaga     | aaagaa | agcaaga    | ac   | acttgac    | gtt  | ttctaga   | tag    | 60   |
| agatgga    | agg      | gaaaga    | agag   | gatgttc    | gag  | tgggag     | ctaa | caagtccc  | gagagg | 120  |
| cgatagg    | tac      | atcggtc   | cag    | acggaca    | aaag | actaca     | agga | gccaccac  | ca     | 180  |
| tcgagcca   | g        | cgagctg   | agt    | tcgtgtc    | ctc  | tctacag    | agc  | cggaatcg  | cc     | 240  |
| ccaccttc   | ct       | gtttcata  | c      | ataacgat   | t    | gcacagt    | gat  | gggagtga  | ag     | 300  |
| acatgtgt   | gc       | ctctgttg  | ga     | atccaagg   | ca   | ttgcttgg   | gc   | tttcggtg  | gc     | 360  |
| cccttgct   | c        | ctgtactgc | t      | ggaatctc   | tg   | gtggccac   | at   | aaacccag  | cg     | 420  |
| gtctgttc   | t        | ggctcgt   | aag    | ctgtcaatt  | ga   | cgagagct   | gt   | cttttaca  | tc     | 480  |
| gtctcgg    | g        | acatctgc  | ggc    | gcggag     | gtg  | tcaaagG    | ctt  | ccagccaa  | t      | 540  |
| ctctcgg    | g        | aggagcca  | a      | acagtcgc   | tc   | acggctac   | ac   | taaggggt  | ct     | 600  |
| ctgagata   | at       | cggaacct  | tc     | gtcttgtc   | tc   | acacggtc   | tt   | ctccgccat | cg     | 660  |
| gaagcgct   | gc       | tgactccc  | ac     | gttcogatt  | t    | tggcaccac  | t    | cccaatcg  | gg     | 720  |
| tcttggtt   | ca       | cttgcgca  | gc     | attccaat   | ca   | ccggaacag  | g    | aattaacca | gc     | 780  |
| ttggagct   | gc       | aatcatct  | ac     | aacaaggacc |      | acgcttgg   | ga   | cgaccact  | gt     | 840  |
| tcggaccat  | t        | cattggag  | ca     | gtcttggcg  |      | ctctttacca |      | ccaactgt  | tc     | 900  |
| ttccattcaa |          | gtccagat  | cc     | tgatttgatt |      | tctttcttta |      | taaaactt  | ca     | 960  |
| ttgtttgt   | ta       | attgagct  | gt     | aaaatatgt  | g    | agagatct   | gg   | atcatgtg  | tt     | 1020 |
| aatggact   | tg       | ctcttttc  |        |            |      |            |      |           |        |      |

(2) INFORMATION FOR SEQ ID NO:1680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..286

(D) OTHER INFORMATION: / Ceres Seq. ID 1570656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1680:

|                                                                 |     |     |     |    |
|-----------------------------------------------------------------|-----|-----|-----|----|
| Met Glu Gly Lys Glu Glu Asp Val Arg Val Gly Ala Asn Lys Phe Pro | 1   | 5   | 10  | 15 |
| Glu Arg Gln Pro Ile Gly Thr Ser Ala Glu Thr Asp Lys Asp Tyr Lys | 20  | 25  | 30  |    |
| Glu Pro Pro Pro Ala Pro Phe Phe Glu Pro Gly Glu Leu Ser Ser Trp | 35  | 40  | 45  |    |
| Ser Phe Tyr Arg Ala Gly Ile Ala Glu Phe Ile Ala Thr Phe Leu Phe | 50  | 55  | 60  |    |
| Leu Tyr Ile Thr Val Leu Thr Val Met Gly Val Lys Arg Ala Pro Asn | 65  | 70  | 75  | 80 |
| Met Cys Ala Ser Val Gly Ile Gln Gly Ile Ala Trp Ala Phe Gly Gly | 85  | 90  | 95  |    |
| Met Ile Phe Ala Leu Val Tyr Cys Thr Ala Gly Ile Ser Gly Gly His | 100 | 105 | 110 |    |
| Ile Asn Pro Ala Val Thr Phe Gly Leu Phe Leu Ala Arg Lys Leu Ser | 115 | 120 | 125 |    |

Leu Thr Arg Ala Val Phe Tyr Ile Val Met Gln Cys Leu Gly Ala Ile  
130 135 140  
Cys Gly Ala Gly Val Val Lys Gly Phe Gln Pro Asn Pro Tyr Gln Thr  
145 150 155 160  
Leu Gly Gly Gly Ala Asn Thr Val Ala His Gly Tyr Thr Lys Gly Ser  
165 170 175  
Gly Leu Gly Ala Glu Ile Ile Gly Thr Phe Val Leu Val Tyr Thr Val  
180 185 190  
Phe Ser Ala Thr Asp Ala Lys Arg Ser Ala Arg Asp Ser His Val Pro  
195 200 205  
Ile Leu Ala Pro Leu Pro Ile Gly Phe Ala Val Phe Leu Val His Leu  
210 215 220  
Ala Thr Ile Pro Ile Thr Gly Thr Gly Ile Asn Pro Ala Arg Ser Leu  
225 230 235 240  
Gly Ala Ala Ile Ile Tyr Asn Lys Asp His Ala Trp Asp Asp His Trp  
245 250 255  
Ile Phe Trp Val Gly Pro Phe Ile Gly Ala Ala Leu Ala Ala Leu Tyr  
260 265 270  
His Gln Leu Val Ile Arg Ala Ile Pro Phe Lys Ser Arg Ser  
275 280 285

(2) INFORMATION FOR SEQ ID NO:1681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..214
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1681:

Met Gly Val Lys Arg Ala Pro Asn Met Cys Ala Ser Val Gly Ile Gln  
1 5 10 15  
Gly Ile Ala Trp Ala Phe Gly Gly Met Ile Phe Ala Leu Val Tyr Cys  
20 25 30  
Thr Ala Gly Ile Ser Gly Gly His Ile Asn Pro Ala Val Thr Phe Gly  
35 40 45  
Leu Phe Leu Ala Arg Lys Leu Ser Leu Thr Arg Ala Val Phe Tyr Ile  
50 55 60  
Val Met Gln Cys Leu Gly Ala Ile Cys Gly Ala Gly Val Val Lys Gly  
65 70 75 80  
Phe Gln Pro Asn Pro Tyr Gln Thr Leu Gly Gly Ala Asn Thr Val  
85 90 95  
Ala His Gly Tyr Thr Lys Gly Ser Gly Leu Gly Ala Glu Ile Ile Gly  
100 105 110  
Thr Phe Val Leu Val Tyr Thr Val Phe Ser Ala Thr Asp Ala Lys Arg  
115 120 125  
Ser Ala Arg Asp Ser His Val Pro Ile Leu Ala Pro Leu Pro Ile Gly  
130 135 140  
Phe Ala Val Phe Leu Val His Leu Ala Thr Ile Pro Ile Thr Gly Thr  
145 150 155 160  
Gly Ile Asn Pro Ala Arg Ser Leu Gly Ala Ala Ile Ile Tyr Asn Lys  
165 170 175  
Asp His Ala Trp Asp Asp His Trp Ile Phe Trp Val Gly Pro Phe Ile  
180 185 190  
Gly Ala Ala Leu Ala Ala Leu Tyr His Gln Leu Val Ile Arg Ala Ile  
195 200 205  
Pro Phe Lys Ser Arg Ser  
210

(2) INFORMATION FOR SEQ ID NO:1682:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1142 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..1142

SEQUENCE DESCRIPTION: SEQ ID NO:1683:

|           |             |             |            |            |            |     |
|-----------|-------------|-------------|------------|------------|------------|-----|
| atcttct   | ctctcaaat   | ctctgactctt | tatctcaaca | gttgagaaga | gattcatctg | 120 |
| atcttct   | ctgaagacat  | ggacactctta | actcttctct | taccagaaga | cgaacacgaa | 180 |
| tatttga   | tgaacagacgc | cgtttttctat | gagcctgtg  | ttaaacgcaa | acgtctcaaa | 240 |
| cagcgtt   | ctcacagcgc  | ttcttctgct  | tttctctcac | cgcctcgatc | tgcacccaaa | 300 |
| agaatct   | aagatcttca  | ggagaagaag  | tatctogctc | tttgcctcct | catgctcgct | 360 |
| ctctcaac  | cgtcgcgaac  | gcgatattcat | caacagctgc | aatcgttaac | gcgcgcgcga | 420 |
| caaaaga   | acctctgaac  | caagtgttaac | gtctgtgaaa | aagcgtttct | ttctctacag | 480 |
| cttaggcg  | gtcacaaga   | aagtcacgga  | atcaaacacc | caacgcgtat | ctcacaacct | 540 |
| tattgtatt | caacagctctc | gacctactctc | atcgtctcgc | gagaaaaaac | tcgcattgtc | 600 |
| ctccggaa  | agatcacctga | tgtcttaactc | gtgcataact | gtgttccgac | gggtcaagct | 660 |
| ctccggct  | caaacactga  | tgactacgaa  | ggcctaaagc | cgcctcgagg | acgaacagaa | 720 |

|            |            |            |             |            |             |      |
|------------|------------|------------|-------------|------------|-------------|------|
| agcaaatcaa | tcagtcacag | tggaagcgtg | tcgagcacgg  | tatcggaaga | aaggagccac  | 780  |
| cgtggattca | tcgatctaaa | cctaccggcg | ttacctgaac  | tcagccttca | tcacaatcca  | 840  |
| atcgtcgacg | aagagatctt | gagtcggttg | accggtaaaa  | aaccgctttt | gttgaccgat  | 900  |
| cacgaccaag | tcatacaaga | agaagattta | tctttaaaaa  | tctaatactc | gactattaat  | 960  |
| tcttggtttt | tcattttcat | ttttttagtt | acaaattttt  | aattgttctg | atttgggattg | 1020 |
| aatattggta | tattgttagg | gattgataca | aaaatttgat  | gattgattaa | gtcagaattt  | 1080 |
| cttttaatt  | atgtaacta  | atctcttgat | cagtcaccctc | tgtataaata | ttgcgtggca  | 1140 |
| tt         |            |            |             |            |             |      |

(2) INFORMATION FOR SEQ ID NO:1684:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..273

(D) OTHER INFORMATION: / Ceres Seq. ID 1570670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1684:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Glu | Ala | Met | Asn | Thr | Pro | Thr | Ser | Ser | Phe | Thr | Arg | Ile |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Thr | Lys | Glu | Asp | Leu | Met | Asn | Asp | Ala | Val | Phe | Ile | Glu | Pro | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Lys | Arg | Lys | Arg | Ser | Lys | Arg | Gln | Arg | Ser | His | Ser | Pro | Ser | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ser | Ser | Ser | Pro | Pro | Arg | Ser | Arg | Pro | Lys | Ser | Gln | Asn | Gln | Asp |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Leu | Thr | Glu | Glu | Glu | Tyr | Leu | Ala | Leu | Cys | Leu | Leu | Met | Leu | Ala | Lys |
|     |     |     | 65  |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Gln | Pro | Ser | Gln | Thr | Arg | Phe | His | Gln | Gln | Ser | Gln | Ser | Leu | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Pro | Pro | Glu | Ser | Lys | Asn | Leu | Pro | Tyr | Lys | Cys | Asn | Val | Cys | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Lys | Ala | Phe | Pro | Ser | Tyr | Gln | Ala | Leu | Gly | Gly | His | Lys | Ala | Ser | His |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Ile | Lys | Pro | Pro | Thr | Val | Ile | Ser | Thr | Thr | Ala | Asp | Asp | Ser | Thr |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Pro | Thr | Ile | Ser | Ile | Val | Ala | Gly | Glu | Lys | His | Pro | Ile | Ala | Ala |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Gly | Lys | Ile | His | Glu | Cys | Ser | Ile | Cys | His | Lys | Val | Phe | Pro | Thr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Gly | Gln | Ala | Leu | Gly | Gly | His | Lys | Arg | Cys | His | Tyr | Glu | Gly | Asn | Leu |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Gly | Gly | Gly | Gly | Gly | Gly | Gly | Ser | Lys | Ser | Ile | Ser | His | Ser | Gly | Ser |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Ser | Ser | Thr | Val | Ser | Glu | Glu | Arg | Ser | His | Arg | Gly | Phe | Ile | Asp |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Asn | Leu | Pro | Ala | Leu | Pro | Glu | Leu | Ser | Leu | His | His | Asn | Pro | Ile |
|     |     |     | 225 |     |     | 230 |     |     |     | 235 |     |     |     | 240 |     |
| Val | Asp | Glu | Glu | Ile | Leu | Ser | Pro | Leu | Thr | Gly | Lys | Lys | Pro | Leu | Leu |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Leu | Thr | Asp | His | Asp | Gln | Val | Ile | Lys | Lys | Glu | Asp | Leu | Ser | Leu | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1685:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..268  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1686:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asn | Thr | Pro | Thr | Ser | Ser | Phe | Thr | Arg | Ile | Glu | Thr | Lys | Glu | Asp |  |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |  |
| Leu | Met | Asn | Asp | Ala | Val | Phe | Ile | Glu | Pro | Trp | Leu | Lys | Arg | Lys | Arg |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Lys | Arg | Gln | Arg | Ser | His | Ser | Pro | Ser | Ser | Ser | Ser | Ser | Ser | Pro |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |  |
| Pro | Arg | Ser | Arg | Pro | Lys | Ser | Gln | Asn | Gln | Asp | Leu | Thr | Glu | Glu | Glu |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Tyr | Leu | Ala | Leu | Cys | Leu | Leu | Met | Leu | Ala | Lys | Asp | Gln | Pro | Ser | Gln |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Thr | Arg | Phe | His | Gln | Gln | Ser | Gln | Ser | Leu | Thr | Pro | Pro | Pro | Glu | Ser |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Lys | Asn | Leu | Pro | Tyr | Lys | Cys | Asn | Val | Cys | Glu | Lys | Ala | Phe | Pro | Ser |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Tyr | Gln | Ala | Leu | Gly | Gly | His | Lys | Ala | Ser | His | Arg | Ile | Lys | Pro | Pro |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |
| Thr | Val | Ile | Ser | Thr | Thr | Ala | Asp | Asp | Ser | Thr | Ala | Pro | Thr | Ile | Ser |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ile | Val | Ala | Gly | Glu | Lys | His | Pro | Ile | Ala | Ala | Ser | Gly | Lys | Ile | His |  |
|     |     |     | 145 |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Glu | Cys | Ser | Ile | Cys | His | Lys | Val | Phe | Pro | Thr | Gly | Gln | Ala | Leu | Gly |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |
| Gly | His | Lys | Arg | Cys | His | Tyr | Glu | Gly | Asn | Leu | Gly | Gly | Gly | Gly | Gly |  |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |
| Gly | Gly | Ser | Lys | Ser | Ile | Ser | His | Ser | Gly | Ser | Val | Ser | Ser | Thr | Val |  |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Ser | Glu | Glu | Arg | Ser | His | Arg | Gly | Phe | Ile | Asp | Leu | Asn | Leu | Pro | Ala |  |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Leu | Pro | Glu | Leu | Ser | Leu | His | His | Asn | Pro | Ile | Val | Asp | Glu | Glu | Ile |  |
|     |     |     | 225 |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |  |
| Leu | Ser | Pro | Leu | Thr | Gly | Lys | Lys | Pro | Leu | Leu | Leu | Thr | Asp | His | Asp |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |  |
| Gln | Val | Ile | Lys | Lys | Glu | Asp | Leu | Ser | Leu | Lys | Ile |     |     |     |     |  |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1686:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 251 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..251  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1686:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asn | Asp | Ala | Val | Phe | Ile | Glu | Pro | Trp | Leu | Lys | Arg | Lys | Arg | Ser |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys | Arg | Gln | Arg | Ser | His | Ser | Pro | Ser | Ser | Ser | Ser | Ser | Ser | Pro | Pro |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Arg | Ser | Arg | Pro | Lys | Ser | Gln | Asn | Gln | Asp | Leu | Thr | Glu | Glu | Glu | Tyr |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu | Ala | Leu | Cys | Leu | Leu | Met | Leu | Ala | Lys | Asp | Gln | Pro | Ser | Gln | Thr |  |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |

Arg Phe His Gln Gln Ser Gln Ser Leu Thr Pro Pro Pro Glu Ser Lys  
65 70 75 80  
Asn Leu Pro Tyr Lys Cys Asn Val Cys Glu Lys Ala Phe Pro Ser Tyr  
85 90 95  
Gln Ala Leu Gly Gly His Lys Ala Ser His Arg Ile Lys Pro Thr  
100 105 110  
Val Ile Ser Thr Thr Ala Asp Asp Ser Thr Ala Pro Thr Ile Ser Ile  
115 120 125  
Val Ala Gly Glu Lys His Pro Ile Ala Ala Ser Gly Lys Ile His Glu  
130 135 140  
Cys Ser Ile Cys His Lys Val Phe Pro Thr Gly Gln Ala Leu Gly Gly  
145 150 155 160  
His Lys Arg Cys His Tyr Glu Gly Asn Leu Gly Gly Gly Gly Gly Gly  
165 170 175  
Gly Ser Lys Ser Ile Ser His Ser Gly Ser Val Ser Ser Thr Val Ser  
180 185 190  
Glu Glu Arg Ser His Arg Gly Phe Ile Asp Leu Asn Leu Pro Ala Leu  
195 200 205  
Pro Glu Leu Ser Leu His His Asn Pro Ile Val Asp Glu Glu Ile Leu  
210 215 220  
Ser Pro Leu Thr Gly Lys Lys Pro Leu Leu Leu Thr Asp His Asp Gln  
225 230 235 240  
Val Ile Lys Lys Glu Asp Leu Ser Leu Lys Ile  
245 250

(2) INFORMATION FOR SEQ ID NO:1687:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1083 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1083

(D) OTHER INFORMATION: / Ceres Seq. ID 1570681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1687:

ttttttacga tctgggtctg gataagcctt ttgtctcatt ctcaacttct tctctatcca 60  
aaaaagctcc tccattttcaa tggcgacacGc atcagctctc tcactactct ctctactctc 120  
actccacacc cgaacctctt ctctcatctc ctctctctcc acaaaaatcca tcgtctcttt 180  
ctctctcttc ctcaaccgccc gcttctcatc tctcaactctc gtcaaaagcct catcgaccga 240  
taccgaaacc atcttctctc aagacgaaac accagaaata accgcaaatg tcgtctctga 300  
cccaccaatt gctccccgaag attcgtctct cctccgtatt tcgacgaagg aagcgacgag 360  
acagaggaag agatcgctac cgcttttgaa gagctctatg gacctgcgta tagtggtgag 420  
agtatgcttg ggaaagatat ttatgtgatg gactcaaagc ataagaagag ttcagggtatt 480  
gggtgggaagc caaagaaga gataagtaga gatgggtttg aagagagagt tgtgcaagtt 540  
aggagagtga ctaagggttg taaaggaggg aagcaattga agtttagagc tatcgttgtt 600  
gttggtgata aacaaggaaa tgttggtgtt ggttggtgcta aggtctaaaga agttgttgtc 660  
gctgttcaga aatctgctat tgatgctagg agaaacattg ttcaagttcc tatgactaag 720  
tattctactt tccctcacag atcagagggg gattatggag cagccaagggt gatgcttaga 780  
cctgcttcac caggtactcg tgtgattgct ggaggagcgg ttaggattgt gctagagatg 840  
cgaggagtgc agaatgcatt ggggaaacag cttggaagca acaatgctct caacaatgcg 900  
agagccactc ttgcagcagt acaacagatg agacagttcc gcgatgttgc acaagagcgt 960  
ggaatcccca tggaaagaac ctggaagtga aaactcatc tcgctttaac attttcatcc 1020  
tcttttgttg agatttcttg taatgatgta attcatgaga aaatatgttt attttgaatt 1080  
agc

(2) INFORMATION FOR SEQ ID NO:1688:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1.329

(D) OTHER INFORMATION: / Ceres Seq. ID 1570682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1688:

Phe Phe Thr Ile Trp Cys Trp Ile Ser Leu Leu His Ser His Phe  
1 5 10 15  
Leu Pro His Pro Lys Lys Leu Leu His Phe Asn Gly Asp Ser Ile Ser  
20 25 30  
Ser Leu Ile Thr Leu Phe Thr Leu Thr Pro His Pro Asn Leu Phe Ser  
35 40 45  
His Leu Leu Phe Leu His Lys Ile His Arg Leu Phe Leu Leu Pro  
50 55 60  
Gln Pro Pro Leu Leu Ile Ser His Ser Arg Gln Ser Leu Ile Asp Arg  
65 70 75 80  
Tyr Arg Asn His Leu Leu Arg Arg Arg Asn Thr Arg Asn Asn Arg Lys  
85 90 95  
Cys Arg Leu Arg Pro Thr Asn Cys Ser Arg Arg Phe Val Ser Pro Pro  
100 105 110  
Tyr Phe Asp Glu Gly Ser Asp Glu Thr Glu Glu Ile Ala Thr Ala  
115 120 125  
Phe Glu Glu Leu Tyr Gly Pro Ala Tyr Ser Gly Glu Ser Met Leu Gly  
130 135 140  
Lys Asp Ile Tyr Val Met Asp Ser Lys His Lys Lys Ser Ser Gly Ile  
145 150 155 160  
Gly Gly Lys Pro Lys Lys Asp Lys Ile Arg Asp Gly Phe Glu Glu Arg  
165 170 175  
Val Val Gln Val Arg Arg Val Thr Lys Val Val Lys Gly Gly Lys Gln  
180 185 190  
Leu Lys Phe Arg Ala Ile Val Val Val Gly Asp Lys Gln Gly Asn Val  
195 200 205  
Gly Val Gly Cys Ala Lys Ala Lys Glu Val Val Ala Val Gln Lys  
210 215 220  
Ser Ala Ile Asp Ala Arg Arg Asn Ile Val Gln Val Pro Met Thr Lys  
225 230 235 240  
Tyr Ser Thr Phe Pro His Arg Ser Glu Gly Asp Tyr Gly Ala Ala Lys  
245 250 255  
Val Met Leu Arg Pro Ala Ser Pro Gly Thr Gly Val Ile Ala Gly Gly  
260 265 270  
Ala Val Arg Ile Val Leu Glu Met Ala Gly Val Glu Asn Ala Leu Gly  
275 280 285  
Lys Gln Leu Gly Ser Asn Asn Ala Leu Asn Asn Ala Arg Ala Thr Leu  
290 295 300  
Ala Ala Val Gln Gln Met Arg Gln Phe Arg Asp Val Ala Gln Glu Arg  
305 310 315 320  
Gly Ile Pro Met Glu Glu Leu Trp Lys  
325

(2) INFORMATION FOR SEQ ID NO:1689:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..188

(D) OTHER INFORMATION: / Ceres Seq. ID 1570683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1689:

Met Leu Gly Lys Asp Ile Tyr Val Met Asp Ser Lys His Lys Lys Ser

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Ser Gly Ile Gly Gly Lys Pro Lys Lys Asp Lys Ile Arg Asp Gly Phe | 20  | 25  | 30  |
| Glu Glu Arg Val Val Gln Val Arg Arg Val Thr Lys Val Val Lys Gly | 35  | 40  | 45  |
| Gly Lys Gln Leu Lys Phe Arg Ala Ile Val Val Val Gly Asp Lys Gln | 50  | 55  | 60  |
| Gly Asn Val Gly Val Gly Cys Ala Lys Ala Lys Glu Val Val Ala Ala | 65  | 70  | 75  |
| Val Gln Lys Ser Ala Ile Asp Ala Arg Arg Asn Ile Val Gln Val Pro | 85  | 90  | 95  |
| Met Thr Lys Tyr Ser Thr Phe Pro His Arg Ser Glu Gly Asp Tyr Gly | 100 | 105 | 110 |
| Ala Ala Lys Val Met Leu Arg Pro Ala Ser Pro Gly Thr Gly Val Ile | 115 | 120 | 125 |
| Ala Gly Gly Ala Val Arg Ile Val Leu Glu Met Ala Gly Val Glu Asn | 130 | 135 | 140 |
| Ala Leu Gly Lys Gln Leu Gly Ser Asn Asn Ala Leu Asn Asn Ala Arg | 145 | 150 | 155 |
| Ala Thr Leu Ala Ala Val Gln Gln Met Arg Gln Phe Arg Asp Val Ala | 165 | 170 | 175 |
| Gln Glu Arg Gly Ile Pro Met Glu Glu Leu Trp Lys                 | 180 | 185 |     |

(2) INFORMATION FOR SEQ ID NO:1690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1570684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1690:

|                                                                 |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| Met Asp Ser Lys His Lys Lys Ser Ser Gly Ile Gly Gly Lys Pro Lys | 1   | 5   | 10  | 15  |
| Lys Asp Lys Ile Arg Asp Gly Phe Glu Glu Arg Val Val Gln Val Arg | 20  | 25  | 30  |     |
| Arg Val Thr Lys Val Val Lys Gly Gly Lys Gln Leu Lys Phe Arg Ala | 35  | 40  | 45  |     |
| Ile Val Val Val Gly Asp Lys Gln Gly Asn Val Gly Val Gly Cys Ala | 50  | 55  | 60  |     |
| Lys Ala Lys Glu Val Val Ala Ala Val Gln Lys Ser Ala Ile Asp Ala | 65  | 70  | 75  | 80  |
| Arg Arg Asn Ile Val Gln Val Pro Met Thr Lys Tyr Ser Thr Phe Pro | 85  | 90  | 95  |     |
| His Arg Ser Glu Gly Asp Tyr Gly Ala Ala Lys Val Met Leu Arg Pro | 100 | 105 | 110 |     |
| Ala Ser Pro Gly Thr Gly Val Ile Ala Gly Gly Ala Val Arg Ile Val | 115 | 120 | 125 |     |
| Leu Glu Met Ala Gly Val Glu Asn Ala Leu Gly Lys Gln Leu Gly Ser | 130 | 135 | 140 |     |
| Asn Asn Ala Leu Asn Asn Ala Arg Ala Thr Leu Ala Ala Val Gln Gln | 145 | 150 | 155 | 160 |
| Met Arg Gln Phe Arg Asp Val Ala Gln Glu Arg Gly Ile Pro Met Glu | 165 | 170 | 175 |     |
| Glu Leu Trp Lys                                                 | 180 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1691:

(i) SEQUENCE CHARACTERISTICS:



(A) LENGTH: 1547 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1547

(D) OTHER INFORMATION: / Ceres Seq. ID 1570692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1691:

```
actctctttt ttcttcattg tcttttcgga cagaacaaaa ctccctaata caaatgtcaa 60
ttctcttggt ctactcttga ataactatct ctcttcaaac cctattcaat tttaactatc 120
gatcttcggc taagtcttcca atggcgccgg cggttgccctc tcttcccaca tttagtgtcg 180
tcaatttcctc cagatttccc agaagaagaa tcgggttttc ttgctccaaa aagccctctg 240
aagttcgttg ttcttccggc aatactcggt acactaagca gagaggggca tttaacatct 300
tgaaagaatg tgcgatttca ttacttttat cgggttggtt aatggtttca gtaccttcga 360
ttgcttttgc tcccaatgct caccgaGtGg cgaatccagt gattccagat gtttcagtgt 420
tgatctccgg tctctccgatt aaagatccgg aagctttact aagatatgca ttgctattg 480
acaacaaagc atcaggggaa gtgcagaagc ctcttgagga tatcactgat agcctcaaga 540
ttgctggcgt taaggctcta gattctgttg aacggaatgt gaggcaggca agtagaacat 600
tgacgaaggg gaaaagtata attgtggcag gttttgctga atcgaaagag gatcatggta 660
atgaaatgat tgaaaaattg gaagctggga tgcaagatat gcttaagata gtggaagatc 720
gaaaaagaga cgcagttgct ccaaaacaga aagaaaattct caaataatgtt ggcgggaatg 780
aagaggaatg ggttgatggc ttccatatg aagtgccgga agagtatcgg aacatgcctc 840
tctcaaggcg aagagctagt gtggacatga aggtcaagat caaggacaat cccaacatcg 900
aggactgtgt gttccgcatg ttcttctgat gttataacgc cctgttacc gccggaaact 960
ttgtggactt ggtagagagg catttctacg atggcatgga gatccagaga tctgatgatg 1020
ttgtggtaca aacgggagat ccagagggtc ctgcggaagg attatcgat ccaagcacag 1080
agaaaaacag gacggttctc ctagagatta ttggtactgg agagaaaaac cctttttacg 1140
gctcaactct tgaagaactt ggtctttaca aggctcaggt ttgtagtctt tcaaacgct 1200
ttgggacaat ggcaatggca agagaagagt ttgagaatga ctacagatca agccaagtgt 1260
ttggctgctc aaaaagaggt gagctgacac caagcaattc caacatcttg gatggtcggt 1320
acgctgtctt tggttacggt actgataaac aagattttct agctgatctt aaagtctggt 1380
atgttatcga atccattcaa gttgtctccg gtttagagaa cctcgctaac ccgagttaca 1440
aaatcgccgg ttaactcctc ttatcttttt ccttttctg gtctgtaatt aatactctgt 1500
ttattttaat ttgtgagag tatattaaag gtgcagtgtc ttttccc
```

(2) INFORMATION FOR SEQ ID NO:1692:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..437

(D) OTHER INFORMATION: / Ceres Seq. ID 1570693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1692:

```
Met Ala Ala Ala Phe Ala Ser Leu Pro Thr Phe Ser Val Val Asn Ser
1 5 10 15
Ser Arg Phe Pro Arg Arg Arg Ile Gly Phe Ser Cys Ser Lys Lys Pro
20 25 30
Leu Glu Val Arg Cys Ser Ser Gly Asn Thr Arg Tyr Thr Lys Gln Arg
35 40 45
Gly Ala Phe Thr Ser Leu Lys Glu Cys Ala Ile Ser Leu Ala Leu Ser
50 55 60
Val Gly Leu Met Val Ser Val Pro Ser Ile Ala Leu Pro Pro Asn Ala
65 70 75 80
His Ala Val Ala Asn Pro Val Ile Pro Asp Val Ser Val Leu Ile Ser
85 90 95
Gly Pro Pro Ile Lys Asp Pro Glu Ala Leu Leu Arg Tyr Ala Leu Pro
```

```

100 105 110
Ile Asp Asn Lys Ala Ile Arg Glu Val Gln Lys Pro Leu Glu Asp Ile
115 120 125
Thr Asp Ser Leu Lys Ile Ala Gly Val Lys Ala Leu Asp Ser Val Glu
130 135 140
Arg Asn Val Arg Gln Ala Ser Arg Thr Leu Gln Gln Gly Lys Ser Ile
145 150 155
Ile Val Ala Gly Phe Ala Glu Ser Lys Lys Asp His Gly Asn Glu Met
165 170 175
Ile Glu Lys Leu Glu Ala Gly Met Gln Asp Met Leu Lys Ile Val Glu
180 185 190
Asp Arg Lys Arg Asp Ala Val Ala Pro Lys Gln Lys Glu Ile Leu Lys
195 200 205
Tyr Val Gly Gly Ile Glu Glu Asp Met Val Asp Gly Phe Pro Tyr Glu
210 215 220
Val Pro Glu Glu Tyr Arg Asn Met Pro Leu Leu Lys Gly Arg Ala Ser
225 230 235
Val Asp Met Lys Val Lys Ile Lys Asp Asn Pro Asn Ile Glu Asp Cys
245 250 255
Val Phe Arg Ile Val Leu Asp Gly Tyr Asn Ala Pro Val Thr Ala Gly
260 265 270
Asn Phe Val Asp Leu Val Glu Arg His Phe Tyr Asp Gly Met Glu Ile
275 280 285
Gln Arg Ser Asp Gly Phe Val Val Gln Thr Gly Asp Pro Glu Gly Pro
290 295 300
Ala Glu Gly Phe Ile Asp Pro Ser Thr Glu Lys Thr Arg Thr Val Pro
305 310 315
Leu Glu Ile Met Val Thr Gly Glu Lys Thr Pro Phe Tyr Gly Ser Thr
325 330 335
Leu Glu Glu Leu Gly Leu Tyr Lys Ala Gln Val Val Ile Pro Phe Asn
340 345 350
Ala Phe Gly Thr Met Ala Met Ala Arg Glu Glu Phe Glu Asn Asp Ser
355 360 365
Gly Ser Ser Gln Val Phe Trp Leu Leu Lys Glu Ser Glu Leu Thr Pro
370 375 380
Ser Asn Ser Asn Ile Leu Asp Gly Arg Tyr Ala Val Phe Gly Tyr Val
385 390 395
Thr Asp Asn Glu Asp Phe Leu Ala Asp Leu Lys Val Gly Asp Val Ile
405 410 415
Glu Ser Ile Gln Val Val Ser Gly Leu Glu Asn Leu Ala Asn Pro Ser
420 425 430
Tyr Lys Ile Ala Gly
435

```

(2) INFORMATION FOR SEQ ID NO:1693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..370

(D) OTHER INFORMATION: / Ceres Seq. ID 1570694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1693:

```

Met Val Ser Val Pro Ser Ile Ala Leu Pro Pro Asn Ala His Ala Val
1 5 10 15
Ala Asn Pro Val Ile Pro Asp Val Ser Val Leu Ile Ser Gly Pro Pro
20 25 30
Ile Lys Asp Pro Glu Ala Leu Leu Arg Tyr Ala Leu Pro Ile Asp Asn
35 40 45

```

Lys Ala Ile Arg Glu Val Gln Lys Pro Leu Glu Asp Ile Thr Asp Ser  
50 55 60  
Leu Lys Ile Ala Gly Val Lys Ala Leu Asp Ser Val Glu Arg Asn Val  
65 70 75 80  
Arg Gln Ala Ser Arg Thr Leu Gln Gln Gly Lys Ser Ile Ile Val Ala  
85 90 95  
Gly Phe Ala Glu Ser Lys Lys Asp His Gly Asn Glu Met Ile Glu Lys  
100 105 110  
Leu Glu Ala Gly Met Gln Asp Met Leu Lys Ile Val Glu Asp Arg Lys  
115 120 125  
Arg Asp Ala Val Ala Pro Lys Gln Lys Glu Ile Leu Lys Tyr Val Gly  
130 135 140  
Gly Ile Glu Glu Asp Met Val Asp Gly Phe Pro Tyr Glu Val Pro Glu  
145 150 155 160  
Glu Tyr Arg Asn Met Pro Leu Leu Lys Gly Arg Ala Ser Val Asp Met  
165 170 175  
Lys Val Lys Ile Lys Asp Asn Pro Asn Ile Glu Asp Cys Val Phe Arg  
180 185 190  
Ile Val Leu Asp Gly Tyr Asn Ala Pro Val Thr Ala Gly Asn Phe Val  
195 200 205  
Asp Leu Val Glu Arg His Phe Tyr Asp Gly Met Glu Ile Gln Arg Ser  
210 215 220  
Asp Gly Phe Val Val Gln Thr Gly Asp Pro Glu Gly Pro Ala Glu Gly  
225 230 235 240  
Phe Ile Asp Pro Ser Thr Glu Lys Thr Arg Thr Val Pro Leu Glu Ile  
245 250 255  
Met Val Thr Gly Glu Lys Thr Pro Phe Tyr Gly Ser Thr Leu Glu Glu  
260 265 270  
Leu Gly Leu Tyr Lys Ala Gln Val Val Ile Pro Phe Asn Ala Phe Gly  
275 280 285  
Thr Met Ala Met Ala Arg Glu Glu Phe Glu Asn Asp Ser Gly Ser Ser  
290 295 300  
Gln Val Phe Trp Leu Leu Lys Glu Ser Glu Leu Thr Pro Ser Asn Ser  
305 310 315 320  
Asn Ile Leu Asp Gly Arg Tyr Ala Val Phe Gly Tyr Val Thr Asp Asn  
325 330 335  
Glu Asp Phe Leu Ala Asp Leu Lys Val Gly Asp Val Ile Glu Ser Ile  
340 345 350  
Gln Val Val Ser Gly Leu Glu Asn Leu Ala Asn Pro Ser Tyr Lys Ile  
355 360 365  
Ala Gly  
370

(2) INFORMATION FOR SEQ ID NO:1694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..262
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1694:

Met Ile Glu Lys Leu Glu Ala Gly Met Gln Asp Met Leu Lys Ile Val  
1 5 10 15  
Glu Asp Arg Lys Arg Asp Ala Val Ala Pro Lys Gln Lys Glu Ile Leu  
20 25 30  
Lys Tyr Val Gly Gly Ile Glu Glu Asp Met Val Asp Gly Phe Pro Tyr  
35 40 45  
Glu Val Pro Glu Glu Tyr Arg Asn Met Pro Leu Leu Lys Gly Arg Ala

|                     |                                             |                         |
|---------------------|---------------------------------------------|-------------------------|
| 50                  | 55                                          | 60                      |
| Ser Val Asp Met Lys | Val Lys Ile Lys Asp                         | Asn Pro Asn Ile Glu Asp |
| 65                  | 70                                          | 75                      |
| Cys Val Phe Arg Ile | Val Leu Asp Gly Tyr                         | Asn Ala Pro Val Thr Ala |
| 85                  | 90                                          | 95                      |
| Gly Asn Phe Val Asp | Leu Val Glu Arg His Phe Tyr Asp Gly Met Glu |                         |
| 100                 | 105                                         | 110                     |
| Ile Gln Arg Ser Asp | Gly Phe Val Val Gln Thr Gly Asp Pro Glu Gly |                         |
| 115                 | 120                                         | 125                     |
| Pro Ala Glu Gly Phe | Ile Asp Pro Ser Thr Glu Lys Thr Arg Thr Val |                         |
| 130                 | 135                                         | 140                     |
| Pro Leu Glu Ile Met | Val Thr Gly Glu Lys Thr Pro Phe Tyr Gly Ser |                         |
| 145                 | 150                                         | 155                     |
| Thr Leu Glu Glu Leu | Gly Leu Tyr Lys Ala Gln Val Val Ile Pro Phe |                         |
| 165                 | 170                                         | 175                     |
| Asn Ala Phe Gly Thr | Met Ala Met Ala Arg Glu Glu Phe Glu Asn Asp |                         |
| 180                 | 185                                         | 190                     |
| Ser Gly Ser Ser Gln | Val Phe Trp Leu Leu Lys Glu Ser Glu Leu Thr |                         |
| 195                 | 200                                         | 205                     |
| Pro Ser Asn Ser Asn | Ile Leu Asp Gly Arg Tyr Ala Val Phe Gly Tyr |                         |
| 210                 | 215                                         | 220                     |
| Val Thr Asp Asn Glu | Asp Phe Leu Ala Asp Leu Lys Val Gly Asp Val |                         |
| 225                 | 230                                         | 235                     |
| Ile Glu Ser Ile Gln | Val Val Ser Gly Leu Glu Asn Leu Ala Asn Pro |                         |
| 245                 | 250                                         | 255                     |
| Ser Tyr Lys Ile Ala | Gly                                         |                         |
| 260                 |                                             |                         |

(2) INFORMATION FOR SEQ ID NO:1695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1393
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1695:

|              |             |             |             |             |             |      |
|--------------|-------------|-------------|-------------|-------------|-------------|------|
| atcgattagg   | gtttaggaac  | cttgtcatcg  | gaaatcattt  | cttgtctttg  | tttgtttattc | 60   |
| gaagctttctc  | ctgctttattt | gatacatatt  | ctctctttcca | gttactctac  | atggaacctac | 120  |
| ctggtttgttaa | ggagaaacatc | ctgcatcccg  | cttctctgcc  | gatgaagaag  | cgacggatcg  | 180  |
| atcacactga   | gtcagctgat  | ggttctgcga  | ttaacgcttc  | taactctagt  | agcatcggtg  | 240  |
| gtaacgatac   | ggtgatgaac  | atggcgggagt | ttggtaacga  | caactccaac  | aatcaggagt  | 300  |
| ctcaacaagt   | ttgcactttt  | ttaagaagac  | caacgaaaag  | taaaaaacata | aggaagaagaa | 360  |
| ccattgacgc   | tgatgaagaa  | gacggagatt  | cgaaaagcga  | aaagctctatt | ttacaaaaatc | 420  |
| taaaagaaat   | tgcaaaaccc  | gatagcaact  | tgtacttttc  | ttctggacca  | ctactagaaa  | 480  |
| cgagtggagc   | tccttgagaga | cccgtttttc  | actacgattc  | atccaaaggaa | atccagggttc | 540  |
| gaagacgacg   | tgagcaacaa  | gcgacccttg  | aaactgaaac  | cgacttcaat  | caagacgctc  | 600  |
| gagctatccg   | tgaaaagagt  | cttaaaaaag  | cagaccatgc  | attgaagggg  | aataagaaaaa | 660  |
| agggcttcaga  | tgagaagctg  | tacaaaggaa  | ttcatggata  | tacagatcac  | aaagctgggt  | 720  |
| ttagaagaga   | acaaaacaatc | ctgagcgaga  | aaagctggag  | ctcaacggcg  | cotttaagag  | 780  |
| cttctgctca   | catcagagta  | tcggcttagat | tcgattacca  | gccagacatt  | tgcaaggatt  | 840  |
| acaagaagaa   | cggatactgt  | gatatggag   | attcgtgtaa  | gttcttgcatt | gacgctgggg  | 900  |
| attacaagac   | gggatggcag  | atagagaaga  | agtgggaaga  | ggcagagaaa  | gttaggaaga  | 960  |
| gaataaagac   | tatggggagt  | gaggatgacg  | atgatgaggg  | tgacaaggat  | agcgacgaag  | 1020 |
| acgaaaattgc  | attgcccttt  | gcttgccttca | tttgacaggga | gccttttctt  | gatccagttg  | 1080 |
| tcaccaaatg   | caagcattac  | ttctgtgagc  | attgtgcttt  | aaagcatcac  | acgaagaaca  | 1140 |
| agaaatgctt   | tgtgtgttaac | caaccaacaa  | tgggggattt  | caatgcagca  | catgagatca  | 1200 |
| agaagaggat   | ggctgaagaa  | cggagttaag  | ctgaacaagg  | attgtgaagt  | ccttctttcca | 1260 |
| caggacaaaa   | agggcaaaaac | tatacatttg  | attattttgct | tgaggaaagc  | tttttgtttt  | 1320 |

(2) INFORMATION FOR SEQ ID NO:1696:

(A) LENGTH: 414 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..414

SEQUENCE DESCRIPTION: SEQ ID NO:1696:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 10  |     |     |     |     |     |     |     |     |     | 15  |     |     |     |     |
| Phe | Val | Ile | Arg | Ser | Phe | Ser | Cys | Leu | Phe | Asp | Thr | Tyr | Ser | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  | Phe |
| Gln | Leu | Leu | Tyr | Met | Glu | Pro | Phe | Val | Val | Lys | Glu | Asn | Ile | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     | Ala |
| Ser | Ala | Ser | Ser | Pro | Met | Lys | Lys | Arg | Arg | Ile | Asp | His | Thr | Glu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     | Ser |
| Ala | Asp | Gly | Ser | Ala | Ile | Asn | Ala | Ser | Asn | Ser | Ser | Ser | Ile | Gly |
|     |     |     | 65  |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Asn | Asp | Thr | Val | Met | Asn | Met | Ala | Glu | Phe | Gly | Asn | Asp | Asn | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  | Asn |
| Asn | Gln | Glu | Ser | Gln | Gln | Val | Cys | Thr | Phe | Phe | Lys | Lys | Pro | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 | Lys |
| Ser | Lys | Asn | Ile | Arg | Lys | Arg | Thr | Ile | Asp | Ala | Asp | Glu | Glu | Asp |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     | Gly |
| Asp | Ser | Lys | Ser | Glu | Ser | Ser | Ile | Leu | Gln | Asn | Leu | Lys | Lys | Val |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     | Ala |
| Lys | Pro | Asp | Ser | Asn | Leu | Tyr | Phe | Ser | Ser | Gly | Pro | Ser | Thr | Arg |
|     |     |     | 145 |     | 150 |     |     |     |     | 155 |     |     |     | Thr |
| Ser | Gly | Ala | Pro | Glu | Arg | Pro | Val | Phe | His | Tyr | Asp | Ser | Ser | Lys |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 160 |
| Ile | Gln | Val | Gln | Asn | Asp | Ser | Gly | Ala | Thr | Ala | Thr | Leu | Glu | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 | Glu |
| Thr | Asp | Phe | Asn | Gln | Asp | Ala | Arg | Ala | Ile | Arg | Glu | Arg | Val | Leu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     | Lys |
| Lys | Ala | Asp | His | Ala | Leu | Lys | Gly | Asn | Lys | Lys | Lys | Ala | Ser | Asp |
|     |     |     | 210 |     |     | 215 |     |     |     | 220 |     |     |     | Glu |
| Lys | Leu | Tyr | Lys | Gly | Ile | His | Gly | Tyr | Thr | Asp | His | Lys | Ala | Gly |
|     |     |     | 225 |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Arg | Arg | Glu | Gln | Thr | Ile | Ser | Ser | Glu | Lys | Ala | Gly | Gly | Ser | His |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 | Gly |
| Pro | Leu | Arg | Ala | Ser | Ala | His | Ile | Arg | Val | Ser | Ala | Arg | Phe | Asp |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 | Tyr |
| Gln | Pro | Asp | Ile | Cys | Lys | Asp | Tyr | Lys | Glu | Thr | Gly | Tyr | Cys | Gly |
|     |     |     | 275 |     |     | 280 |     |     |     |     |     | 285 |     | Tyr |
| Gly | Asp | Ser | Cys | Lys | Phe | Leu | His | Asp | Arg | Gly | Asp | Tyr | Lys | Pro |
|     |     |     | 290 |     |     | 295 |     |     |     | 300 |     |     |     | Gly |
| Trp | Gln | Ile | Glu | Lys | Glu | Trp | Glu | Glu | Ala | Glu | Lys | Val | Arg | Lys |
|     |     |     | 305 |     | 310 |     |     |     |     | 315 |     |     |     | 320 |
| Asn | Lys | Ala | Met | Gly | Val | Glu | Asp | Asp | Asp | Asp | Glu | Ala | Asp | Lys |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     | 335 | Asp |
| Ser | Asp | Glu | Asp | Glu | Asn | Ala | Leu | Pro | Phe | Ala | Cys |     |     |     |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 370                                                             | 375 | 380 |
| Cys Asn Gln Pro Thr Met Gly Ile Phe Asn Ala Ala His Glu Ile Lys |     |     |
| 385                                                             | 390 | 395 |
| Lys Arg Met Ala Glu Glu Arg Ser Lys Ala Glu Gln Gly Leu         |     | 400 |
|                                                                 | 405 | 410 |

(2) INFORMATION FOR SEQ ID NO:1697:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..378

(D) OTHER INFORMATION: / Ceres Seq. ID 1570698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1697:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Pro | Phe | Val | Val | Lys | Glu | Asn | Ile | Val | Ala | Ser | Ala | Ser | Ser |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Met | Lys | Lys | Arg | Arg | Ile | Asp | His | Thr | Glu | Ser | Ala | Asp | Gly | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ile | Asn | Ala | Ser | Asn | Ser | Ser | Ser | Ile | Gly | Gly | Asn | Asp | Thr | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Met | Asn | Met | Ala | Glu | Phe | Gly | Asn | Asp | Asn | Ser | Asn | Asn | Gln | Glu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Gln | Val | Cys | Thr | Phe | Phe | Lys | Lys | Pro | Thr | Lys | Ser | Lys | Asn | Ile |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Lys | Arg | Thr | Ile | Asp | Ala | Asp | Glu | Glu | Asp | Gly | Asp | Ser | Lys | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Ser | Ser | Ile | Leu | Gln | Asn | Leu | Lys | Lys | Val | Ala | Lys | Pro | Asp | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Leu | Tyr | Phe | Ser | Ser | Gly | Pro | Ser | Thr | Arg | Thr | Ser | Gly | Ala | Pro |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Arg | Pro | Val | Phe | His | Tyr | Asp | Ser | Ser | Lys | Glu | Ile | Gln | Val | Gln |
|     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Asn | Asp | Ser | Gly | Ala | Thr | Ala | Thr | Leu | Glu | Thr | Glu | Thr | Asp | Phe | Asn |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gln | Asp | Ala | Arg | Ala | Ile | Arg | Glu | Arg | Val | Leu | Lys | Lys | Ala | Asp | His |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Leu | Lys | Gly | Asn | Lys | Lys | Lys | Ala | Ser | Asp | Glu | Lys | Leu | Tyr | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Ile | His | Gly | Tyr | Thr | Asp | His | Lys | Ala | Gly | Phe | Arg | Arg | Glu | Gln |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Ile | Ser | Ser | Glu | Lys | Ala | Gly | Gly | Ser | His | Gly | Pro | Leu | Arg | Ala |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Ala | His | Ile | Arg | Val | Ser | Ala | Arg | Phe | Asp | Tyr | Gln | Pro | Asp | Ile |
|     |     |     | 225 |     |     | 230 |     |     |     | 235 |     |     |     | 240 |     |
| Cys | Lys | Asp | Tyr | Lys | Glu | Thr | Gly | Tyr | Cys | Gly | Tyr | Gly | Asp | Ser | Cys |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Phe | Leu | His | Asp | Arg | Gly | Asp | Tyr | Lys | Pro | Gly | Trp | Gln | Ile | Glu |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Lys | Glu | Trp | Glu | Glu | Ala | Glu | Lys | Val | Arg | Lys | Arg | Asn | Lys | Ala | Met |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Val | Glu | Asp | Asp | Asp | Asp | Glu | Ala | Asp | Lys | Asp | Ser | Asp | Glu | Asp |
|     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Glu | Asn | Ala | Leu | Pro | Phe | Ala | Cys | Phe | Ile | Cys | Arg | Glu | Pro | Phe | Leu |
|     |     |     | 305 |     |     | 310 |     |     |     | 315 |     |     |     | 320 |     |
| Asp | Pro | Val | Val | Thr | Lys | Cys | Lys | His | Tyr | Phe | Cys | Glu | His | Cys | Ala |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Lys | His | His | Thr | Lys | Asn | Lys | Lys | Cys | Phe | Val | Cys | Asn | Gln | Pro |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     |     | 350 |     |     |

Thr Met Gly Ile Phe Asn Ala Ala His Glu Ile Lys Lys Arg Met Ala  
355 360 365  
Glu Glu Arg Ser Lys Ala Glu Gln Gly Leu  
370 375

(2) INFORMATION FOR SEQ ID NO:1698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..361

(D) OTHER INFORMATION: / Ceres Seq. ID 1570699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1698:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Arg | Arg | Ile | Asp | His | Thr | Glu | Ser | Ala | Asp | Gly | Ser | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Ile | Asn | Ala | Ser | Asn | Ser | Ser | Ser | Ile | Gly | Gly | Asn | Asp | Thr | Val | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Met | Ala | Glu | Phe | Gly | Asn | Asp | Asn | Ser | Asn | Asn | Gln | Glu | Ser | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Val | Cys | Thr | Phe | Phe | Lys | Lys | Pro | Thr | Lys | Ser | Lys | Asn | Ile | Arg |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Arg | Thr | Ile | Asp | Ala | Asp | Glu | Glu | Asp | Gly | Asp | Ser | Lys | Ser | Glu |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Ser | Ile | Leu | Gln | Asn | Leu | Lys | Lys | Val | Ala | Lys | Pro | Asp | Ser | Asn |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Tyr | Phe | Ser | Ser | Gly | Pro | Ser | Thr | Arg | Thr | Ser | Gly | Ala | Pro | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Pro | Val | Phe | His | Tyr | Asp | Ser | Ser | Lys | Glu | Ile | Gln | Val | Gln | Asn |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Asp | Ser | Gly | Ala | Thr | Ala | Thr | Leu | Glu | Thr | Glu | Thr | Asp | Phe | Asn | Gln |
|     |     |     | 130 |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Asp | Ala | Arg | Ala | Ile | Arg | Glu | Arg | Val | Leu | Lys | Lys | Ala | Asp | His | Ala |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Lys | Gly | Asn | Lys | Lys | Lys | Ala | Ser | Asp | Glu | Lys | Leu | Tyr | Lys | Gly |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ile | His | Gly | Tyr | Thr | Asp | His | Lys | Ala | Gly | Phe | Arg | Arg | Glu | Gln | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Ser | Ser | Glu | Lys | Ala | Gly | Gly | Ser | His | Gly | Pro | Leu | Arg | Ala | Ser |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Ala | His | Ile | Arg | Val | Ser | Ala | Arg | Phe | Asp | Tyr | Gln | Pro | Asp | Ile | Cys |
|     |     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |
| Lys | Asp | Tyr | Lys | Glu | Thr | Gly | Tyr | Cys | Gly | Tyr | Gly | Asp | Ser | Cys | Lys |
|     |     |     | 225 |     |     | 230 |     |     |     | 235 |     |     |     | 240 |     |
| Phe | Leu | His | Asp | Arg | Gly | Asp | Tyr | Lys | Pro | Gly | Trp | Gln | Ile | Glu | Lys |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Trp | Glu | Glu | Ala | Glu | Lys | Val | Arg | Lys | Arg | Asn | Lys | Ala | Met | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Glu | Asp | Asp | Asp | Asp | Glu | Ala | Asp | Lys | Asp | Ser | Asp | Glu | Asp | Glu |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Asn | Ala | Leu | Pro | Phe | Ala | Cys | Phe | Ile | Cys | Arg | Glu | Pro | Phe | Leu | Asp |
|     |     |     | 290 |     |     | 295 |     |     |     |     |     | 300 |     |     |     |
| Pro | Val | Val | Thr | Lys | Cys | Lys | His | Tyr | Phe | Cys | Glu | His | Cys | Ala | Leu |
|     |     |     | 305 |     |     | 310 |     |     |     | 315 |     |     |     | 320 |     |
| Lys | His | His | Thr | Lys | Asn | Lys | Lys | Cys | Phe | Val | Cys | Asn | Gln | Pro | Thr |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Met | Gly | Ile | Phe | Asn | Ala | Ala | His | Glu | Ile | Lys | Lys | Arg | Met | Ala | Glu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Glu | Arg | Ser | Lys | Ala | Glu | Gln | Gly | Leu |     |     |     |     |     |     |     |

355 360

(2) INFORMATION FOR SEQ ID NO:1699:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 609 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..609

(D) OTHER INFORMATION: / Ceres Seq. ID 1570716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1699:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| gaaaaatggt | gaaaaaagcg  | tattagcaga | Gggacaaaag | cttttaggg  | ttttagattt | 60  |
| cctctgagag | agaattttcg  | aaagcttcag | agagatttcc | aactacgtta | gccatggcga | 120 |
| gcaccaagt  | tcaaaaggatt | atgaccaaac | ctatcaactt | gatttttagg | tttctcaaaa | 180 |
| gtaaaagctg | gatccagatt  | tggctatttg | agcagaaaga | tttgaggatt | gaaggaagaa | 240 |
| tcactggttt | tgacgaatac  | atgaatctag | ttttggatga | ggctgaagaa | gtgagcatca | 300 |
| agaagaacac | caggaaaacca | cttggaaaga | ttttactcaa | aggagacaa  | ataactctga | 360 |
| tgatgaacac | gggaaaagtga | tgtctgtctc | aaacaactct | cttcgatgac | cttcaagctg | 420 |
| atgttaaata | tctgtttgagt | tcttcctcag | cttaattggg | acttgacgat | accctctttt | 480 |
| cttcaatgtc | gtataaatata | ttgcaatgta | gtgagtga   | aaggagcttg | atcgaatcta | 540 |
| gtggattggg | tgggtaaaac  | ttcaaaaaag | agatttgggc | ccttttggtt | aaatctagtg | 600 |
| taattggc   |             |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1700:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1570717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1700:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Ser | Thr | Lys | Val | Gln | Arg | Ile | Met | Thr | Gln | Pro | Ile | Asn | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ile | Phe | Arg | Phe | Leu | Gln | Ser | Lys | Ala | Arg | Ile | Gln | Ile | Trp | Leu | Phe |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | Gln | Lys | Asp | Leu | Arg | Ile | Glu | Gly | Arg | Ile | Thr | Gly | Phe | Asp | Glu |  |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Tyr | Met | Asn | Leu | Val | Leu | Asp | Glu | Ala | Glu | Glu | Val | Ser | Ile | Lys | Lys |  |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |  |
| Asn | Thr | Arg | Lys | Pro | Leu | Gly | Arg | Ile | Leu | Leu | Lys | Gly | Asp | Asn | Ile |  |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     | 75  |     | 80  |  |
| Thr | Leu | Met | Met | Asn | Thr | Gly | Lys |     |     |     |     |     |     |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1701:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1570718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1701:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Thr | Gln | Pro | Ile | Asn | Leu | Ile | Phe | Arg | Phe | Leu | Gln | Ser | Lys | Ala |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|



(2) INFORMATION FOR SEO ID NO:1702:

(A) LENGTH: 533 base pairs

(C) STRANDEDNESS: single

MOLECULE TYPE: DNA (g

(ix) FEATURE:

(B) LOCATION: 1..533

(D) OTHER INFORMATION: / Ceres Seq. ID 1570719

|             |             |             |             |            |             |     |
|-------------|-------------|-------------|-------------|------------|-------------|-----|
| atcacacaaac | tcaacaattac | aaaagactaaa | cagttctctta | aaatcaaatc | aagttttttt  | 60  |
| aggaagagaag | attagaaatt  | gtctaacWaa  | cagtcagagc  | atgagcttca | acgcaggcca  | 120 |
| acgaataaggc | caaaactcagg | agaaggccag  | caactctgatg | cgaaaggcct | ccaattctgc  | 180 |
| ccaattctgct | aaggaattcta | ctcaagaggc  | gtggacagcag | ctgaagcaga | aggccaagaag | 240 |
| tcgcagtgag  | accattaagg  | aaagacccgg  | catcagcagaa | tgagagcgac | gttctaaatg  | 300 |
| taatttttgt  | tttctgtttt  | cgtttttttt  | ctaccagaaa  | taataattag | atagatatgt  | 360 |
| ctctctaaat  | ccaagacatt  | gatttctgat  | cgaaagcaat  | taggcgata  | cttttgcttt  | 420 |
| ttctatgttt  | ttttatatat  | ctataatact  | aagagttttt  | gactcttttc | tattgataat  | 480 |
| ttttagccat  | cgatttattt  | ctataatact  | taataataat  | catctgtwta | atg         |     |

(2) INFORMATION FOR SEQ ID NO:1703:

(A) LENGTH: 93 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1570720

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1703:
```

(2) INFORMATION FOR SEQ ID NO:1704:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..60

(D) OTHER INFORMATION: / Ceres Seq. ID 1570721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1704:

```
Met Ser Phe Asn Ala Gly Gln Ala Lys Gly Gln Thr Gln Glu Lys Ala
1 5 10 15
Ser Asn Leu Met Asp Lys Ala Ser Asn Ala Ala Gln Ser Ala Lys Glu
20 25 30
Ser Ile Gln Glu Gly Gly Gln Gln Leu Lys Gln Lys Ala Gln Gly Ala
35 40 45
Ser Glu Thr Ile Lys Glu Lys Thr Gly Ile Ser Lys
50 55 60
```

(2) INFORMATION FOR SEQ ID NO:1705:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1062 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1062

(D) OTHER INFORMATION: / Ceres Seq. ID 1570735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1705:

```
aatgatctga tctgatctcc caaaaattcc caaatccaaa tctacgaatc tccgtctcct 60
ccgtgcattt ttcgcaggta gagagagaga tcaaacccaa gagacacaga gagagtatcc 120
accgatggaa tccgcagcaa cggctgttgt acctccggca gccgcgcgca ccaccgccac 180
cgccaccgat gataatctcc aatcaagcga ctcatcatct cccgcgcgac cggttaaacg 240
attgatccac gcctttttgc agcgacaaca acatcttctc gacaaaaacgg ttccctcacg 300
tctctatoga tggatogcat gtctctgtgt tgtattgac tacatogttc gtgttttaatt 360
tgttgaaggc ttctacatca tcaactacgc catcggcatc taccttttga atctcatcat 420
tgcttttcta tctctcaag aagatccgca agcttctctc acttcgggtg gttctcttcc 480
tactcggaga tccgatgagt atcgtctctt cgttcccggt ctccctgagt tcaaaattctg 540
gttatcgatc ataagggcct tcatcatcgg atttatgatg acgtttctcg aggtgtttga 600
tgtacctgta ttctggccaa tacttctctt ctactgggtg atgttgtttt tctcttacag 660
gaggaacacg atacagcata tgatcaaata cagatatgtc cctttctctt ttggggaaaaa 720
gcagtatgga aagaaacccg ctccaacaga gacgagtgaa tgatcaatca aaactgttca 780
ggtaacgaat ttacagctct tttagagaga gttagcattg aaaaaggtcgg tcttttgttc 840
tctttttgat gccatatact ttgttaggga tgaagtagag atagacatat ttgtgctctt 900
tatcatctcg actatttttac tggtttcacc tgaactcaat gtacaactctt atttttttac 960
atcctttttt cagtggagaaa ataattgtGt cataactgac ccttttgtaa tcatcatggt 1020
ggaaaactaa agactaatca gtaatcactg tccggttcta tc
```

(2) INFORMATION FOR SEQ ID NO:1706:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1570736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1706:

```
Met Glu Ser Ala Ala Thr Ala Val Val Pro Pro Ala Ala Ala Thr
1 5 10 15
Thr Ala Thr Ala Thr Asp Asp Asn Leu Gln Ser Ser Asp Ser Ser Ser
20 25 30
Pro Ala Asp Ala Val Asn Arg Leu Ile His Ala Phe Ser Gln Arg Gln
35 40 45
```

```

Gln His Leu Leu Asp Lys Thr Val Pro His Val Leu Tyr Arg Trp Ile
 50 55 60
Ala Cys Leu Cys Val Val Leu Ile Tyr Ile Val Arg Val Tyr Phe Val
 65 70 75 80
Glu Gly Phe Tyr Ile Ile Thr Tyr Ala Ile Gly Ile Tyr Leu Leu Asn
 85 90 95
Leu Ile Ile Ala Phe Leu Ser Pro Gln Glu Asp Pro Glu Ala Ser Leu
 100 105 110
Thr Ser Gly Gly Ser Leu Pro Thr Arg Arg Ser Asp Glu Tyr Arg Pro
 115 120 125
Phe Val Arg Arg Leu Pro Glu Phe Lys Phe Trp Leu Ser Ile Ile Arg
 130 135 140
Ala Phe Ile Ile Gly Phe Met Met Thr Phe Phe Glu Val Phe Asp Val
 145 150 155 160
Pro Val Phe Trp Pro Ile Leu Leu Phe Tyr Trp Val Met Leu Phe Phe
 165 170 175
Leu Thr Met Arg Lys Gln Ile Gln His Met Ile Lys Tyr Arg Tyr Val
 180 185 190
Pro Phe Ser Phe Gly Lys Lys Gln Tyr Gly Lys Lys Pro Ala Pro Thr
 195 200 205
Glu Ser Ser Glu
210

```

(2) INFORMATION FOR SEQ ID NO:1707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..562
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1707:

```

atttcatttt cgttttcact ttctccgaac atccaaaagc ttgtagcttg ctctctcaaat 60
cttccttgaaa aatgaaggtt gccgctgctt tctctctcgc cgttttgggc ggaaacgccta 120
atccttcagc cgagaatatt aaagatatca tcggagctgt tgggtcgat gttgatggag 180
agagcattga gcttcattt aaagaagtga gtggttaagg cattgtcgag ctgattgctt 240
ctggtaggga gaaatttagc tctgtgccat ctggtggtgg tgtggctgtt tcagctgcctc 300
catcaagcgg tgggtggtgt gctgctgctg ctgcccCtgc ggagaagaaa gaagccaaga 360
aggaagagaa agaagagtct gatgatgaca tgggattcac tctcttcgag taaggttttt 420
gtccccacgg aaaggagtcg agatttgatt tttgtgtctc ttagtgttgc tggbytttgc 480
tcctctttgt agttcgtgtt tattaaagat tcttgatta cgaattttac tcgttagata 540
atgaagcaag aagagttttt tc

```

(2) INFORMATION FOR SEQ ID NO:1708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1708:

```

Met Lys Val Ala Ala Ala Phe Leu Leu Ala Val Leu Gly Gly Asn Ala
 1 5 10 15
Asn Pro Ser Ala Glu Asn Ile Lys Asp Ile Ile Gly Ala Val Gly Ala
 20 25 30
Asp Val Asp Gly Glu Ser Ile Glu Leu Leu Lys Glu Val Ser Gly

```

(2) INFORMATION FOR SEQ ID NO:1709:

(A) LENGTH: 526 base pairs

(C) STRANDEDNESS: sing

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

```
(11) MOLECULE TYPE: DNA (genomic)
(18) FEATURE:
```

## (18) FEATURE: (B) NAME:

(A) NAME/KEY: -  
(B) LOCATION: 1

(B) LOCATION: 1.526

(D) OTHER INFORMATION: / Ceres Seq. ID 1570751  
SEQUENCE DESCRIPTION: SEQ. ID NO. 1700:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1709:

|             |             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| agagatatata | tgaatatcaag | gagacacaaaa | cttaagaaaa  | aaaacccaaa  | aaaaaaaagag | 60  |
| agaggtgaaa  | ttgattttct  | gtctgcgtcag | gtctatttcaa | ttttcttaata | gactttcttgg | 120 |
| tgtttttctc  | ccggcgtaat  | catacagaacc | ctaaaaagagc | tagcagacag  | gaagatttgag | 180 |
| ataattctca  | aaaaacattt  | aaagagagga  | tttgttcctg  | agaccaccac  | caagaaggcg  | 240 |
| aaggatctac  | ccgttgtgtc  | catctcttct  | ggctcttttg  | ttctttgttg  | cattggatca  | 300 |
| ttctcttttc  | agatcattag  | gactgcacat  | agcggaggca  | tggcctaatac | caaaaacacag | 360 |
| tcaagctaga  | agaagcagtt  | tttcaaatgt  | agaactttct  | tctgtctcct  | ttctttttct  | 420 |
| ctctcttata  | tgtagaattg  | gtccaacttt  | tgtttactat  | atcagtgaat  | gaagattatt  | 480 |
| tgaatttttc  | ataactccaag | tctcaaacgc  | tttaagtatg  | tDtttc      |             |     |

(2) INFORMATION FOR SEQ ID NO:1710:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..36

(D) OTHER INFORMATION: / Ceres Seq. ID 1570752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1710:

Arg Asp Ile Leu Lys Ser Arg Arg Gln Lys Leu Lys Lys Lys Asn Pro  
1 5 10 15  
Lys Lys Lys Glu Arg Gly Glu Ile Asp Phe Leu Leu Ala Ile Val Ile  
20 25 30  
Ser Ile Ser Asn  
35

(2) INFORMATION FOR SEQ ID NO:1711:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptic

(ix) FEATURE:

(A) NAM

(B) LOCATION: 1..68

(D) OTHER INFORMATION

(D) OTHER INFORMATION: / Series 303, 12 18, 1999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1711:

Met Thr Thr Ser Lys Arg Leu Ala Asp Arg Lys Ile Glu Lys Phe Asp  
1 5 10 15  
Lys Asn Ile Leu Lys Arg Gly Phe Val Pro Glu Thr Thr Thr Lys Lys  
20 25 30  
Gly Lys Asp Tyr Pro Val Gly Pro Ile Leu Leu Gly Phe Phe Val Phe  
35 40 45  
Val Val Ile Gly Ser Ser Leu Phe Gln Ile Ile Arg Thr Ala Thr Ser  
50 55 60  
Gly Gly Met Ala  
65

(2) INFORMATION FOR SEQ ID NO:1712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..664
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1712:

tcacctatct ctgcagcgga gcttcttctt ctcttagggc ttccacgcga ctacgcctgc 60  
caaaatcatt ctacaggaag catgaagcca gtcttctgtg ggaactttga gtatgatgcy 120  
cgcggaaggtg acctggaacg actattcagg aaatacggca aggttgagag ggttgatatg 180  
aaagctgggtg ttgcttttgt atacatggaa gatgaaaggg atgcggaaga tgccatccga 240  
gcacttgacc gctttgaatt tgggcgtaag ggacgcagac ttcgtgttga atggacaaaag 300  
agtgaacgtg gaggtgataa aagatctggt ggtggttcaa ggagatcctc atccagcatg 360  
agaccttcca agactctctt tgtgattaac ttgatgcggg ataatactag gaccocgggat 420  
ctagagaaac actttgagcc gtatggaaaac atcgtaaacg ttaggatcag gaggaatttt 480  
gcatttatcc agtacgaggc acaagaggat gccaccagag cattggatgc ttcaaaataac 540  
agtaagctga tggataaggt gatctcggtg gagtatgctg tgAaggatga tgatgctaga 600  
atcatataaa cctcaactta taattataga cacttttata tttaaatcag ctacgttttg 660  
tggc

(2) INFORMATION FOR SEQ ID NO:1713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..202
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1713:

Ser Pro Ile Ser Arg Arg Glu Leu Leu Leu Leu Gly Leu Pro Arg  
1 5 10 15  
Asp Tyr Ala Cys Gln Asn His Ser Thr Gly Ser Met Lys Pro Val Phe  
20 25 30  
Cys Gly Asn Phe Glu Tyr Asp Ala Arg Glu Gly Asp Leu Glu Arg Leu  
35 40 45  
Phe Arg Lys Tyr Gly Lys Val Glu Arg Val Asp Met Lys Ala Gly Phe  
50 55 60  
Ala Phe Val Tyr Met Glu Asp Glu Arg Asp Ala Glu Asp Ala Ile Arg  
65 70 75 80  
Ala Leu Asp Arg Phe Glu Phe Gly Arg Lys Gly Arg Arg Leu Arg Val  
85 90 95  
Glu Trp Thr Lys Ser Glu Arg Gly Gly Asp Lys Arg Ser Gly Gly Gly  
100 105 110

Ser Arg Arg Ser Ser Ser Ser Met Arg Pro Ser Lys Thr Leu Phe Val  
115 120 125  
Ile Asn Phe Asp Ala Asp Asn Thr Arg Thr Arg Asp Leu Glu Lys His  
130 135 140  
Phe Glu Pro Tyr Gly Lys Ile Val Asn Val Arg Ile Arg Arg Asn Phe  
145 150 155 160  
Ala Phe Ile Gln Tyr Glu Ala Gln Glu Asp Ala Thr Arg Ala Leu Asp  
165 170 175  
Ala Ser Asn Asn Ser Lys Leu Met Asp Lys Val Ile Ser Val Glu Tyr  
180 185 190  
Ala Val Lys Asp Asp Asp Ala Arg Ile Ile  
195 200

(2) INFORMATION FOR SEQ ID NO:1714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1714:

Met Lys Pro Val Phe Cys Gly Asn Phe Glu Tyr Asp Ala Arg Glu Gly  
1 5 10 15  
Asp Leu Glu Arg Leu Phe Arg Lys Tyr Gly Lys Val Glu Arg Val Asp  
20 25 30  
Met Lys Ala Gly Phe Ala Phe Val Tyr Met Glu Asp Glu Arg Asp Ala  
35 40 45  
Glu Asp Ala Ile Arg Ala Leu Asp Arg Phe Glu Phe Gly Arg Lys Gly  
50 55 60  
Arg Arg Leu Arg Val Glu Trp Thr Lys Ser Glu Arg Gly Gly Asp Lys  
65 70 75 80  
Arg Ser Gly Gly Gly Ser Arg Arg Ser Ser Ser Ser Met Arg Pro Ser  
85 90 95  
Lys Thr Leu Phe Val Ile Asn Phe Asp Ala Asp Asn Thr Arg Thr Arg  
100 105 110  
Asp Leu Glu Lys His Phe Glu Pro Tyr Gly Lys Ile Val Asn Val Arg  
115 120 125  
Ile Arg Arg Asn Phe Ala Phe Ile Gln Tyr Glu Ala Gln Glu Asp Ala  
130 135 140  
Thr Arg Ala Leu Asp Ala Ser Asn Asn Ser Lys Leu Met Asp Lys Val  
145 150 155 160  
Ile Ser Val Glu Tyr Ala Val Lys Asp Asp Asp Ala Arg Ile Ile  
165 170 175

(2) INFORMATION FOR SEQ ID NO:1715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1715:

Met Lys Ala Gly Phe Ala Phe Val Tyr Met Glu Asp Glu Arg Asp Ala  
1 5 10 15  
Glu Asp Ala Ile Arg Ala Leu Asp Arg Phe Glu Phe Gly Arg Lys Gly

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Tyr | Ile | Thr | Gln | Ser | Asn | Lys | His | Thr | His | Ile | Thr | Tyr | Arg | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Xaa | Xaa | Gln | Lys | Ile | Gly | Met | Ser | Met | Ala | Pro | Lys | Thr | Ser | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Leu | Ala | Leu | Phe | Leu | Val | Thr | Asn | Ile | Leu | Phe | Leu | Asn | Leu | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Thr | Leu | Ser | Cys | Ala | Asp | Asn | Thr | Cys | Pro | Arg | Asp | Val | Leu | Lys | Leu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Thr | Cys | Ser | Asn | Val | Leu | Asn | Leu | Ile | Asn | Leu | Lys | Leu | Gly | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Ala | Met | Arg | Pro | Cys | Cys | Ser | Ile | Leu | Phe | Gly | Leu | Ile | Asp | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Val | Ala | Val | Cys | Cys | Cys | Thr | Ala | Leu | Lys | Leu | Ser | Leu | Leu | Gly |

(2) INFORMATION FOR SEQ ID NO:1718:

(A) LENGTH: 117 amino acids

- (ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

- (B) LOCATION: 1..117

- (D) OTHER INFORMATION

- SEQUENCE DESCRIPTION: SEQ ID NO:1718:

(AI) SEQUENCE DESCRIPTION: SEQ ID NO:1718:  
Ser Met Ala Pro Lys Thr Ser Thr Thr Leu Al

(2) INFORMATION FOR SEO ID NO:1719:

(A) LENGTH: 115 amino acids

- (ix) FEATURE:

(1X) FEATURE.  
(2X) NAME.

- (B) LOCATION: 1 115

- (D) OTHER INFORMATION

- SEQUENCE DESCRIPTION: SEQ ID NO:1719:

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:17/19:  
Ala Pro Lys Thr Ser Thr Thr Leu Ala Leu Ph

[illegible]



(2) INFORMATION FOR SEQ ID NO:1720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..644
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1720:

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| atcgaaaagt | ctacgaattt | aggGtttaat | ttgtgttaat  | gagccaccgt  | gtttcgattc | 60  |
| tatcatctca | ttttccacot | gcctccgcgc | tcattggcttc | cgagaaagaa  | gctgctctcg | 120 |
| cgcgcacotc | ttccgattct | cccaccatat | ttgacaagat  | catcagcaaa  | gagattccat | 180 |
| ccaccgtggt | ttttgaggat | gacaaggctc | tagcttttag  | ggacataaac  | cccagggttc | 240 |
| ctgttcacat | cctccttatt | ccaaaagtga | gggatggcct  | aactggcctc  | tctaaggctg | 300 |
| aggaaggcca | catcgacatc | ttgggcgcgc | ttctctacac  | tgccaaagctt | gtagcaaaac | 360 |
| aagaaggcct | agcagagggt | ttcagaattg | ttatcaatga  | tggtcctcaa  | ggctgtcaat | 420 |
| cggtgtatca | cattcatgtt | catctcattg | gaggacgccca | aatgaactgg  | cctcctggtt | 480 |
| aaagatcatc | ttgaagtggg | ttgttttcc  | gatgataaga  | gggacgctta  | gagtttgctc | 540 |
| tctgtactca | atgtctctat | aaataaaaaa | acgtggggaca | tgacttttat  | gattgttatg | 600 |
| caaaacotta | ttttatgtta | tgaaaaggat | atttcactgt  | tttc        |            |     |

(2) INFORMATION FOR SEQ ID NO:1721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1721:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | His | Arg | Val | Ser | Ile | Leu | Ser | Ser | His | Phe | Ser | Pro | Ala | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Val | Met | Ala | Ser | Glu | Lys | Glu | Ala | Ala | Leu | Ala | Ala | Thr | Pro | Ser |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Ser | Pro | Thr | Ile | Phe | Asp | Lys | Ile | Ile | Ser | Lys | Glu | Ile | Pro | Ser |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Thr | Val | Val | Phe | Glu | Asp | Asp | Lys | Val | Leu | Ala | Phe | Arg | Asp | Ile | Thr |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Pro | Gln | Gly | Pro | Val | His | Ile | Leu | Leu | Ile | Pro | Lys | Val | Arg | Asp | Gly |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     | 80  |     |
| Leu | Thr | Gly | Leu | Ser | Lys | Ala | Glu | Glu | Arg | His | Ile | Asp | Ile | Leu | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Arg | Leu | Leu | Tyr | Thr | Ala | Lys | Leu | Val | Ala | Lys | Gln | Glu | Gly | Leu | Ala |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Gly | Phe | Arg | Ile | Val | Ile | Asn | Asp | Gly | Pro | Gln | Gly | Cys | Gln | Ser |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Val | Tyr | His | Ile | His | Val | His | Leu | Ile | Gly | Gly | Arg | Gln | Met | Asn | Trp |
|     |     |     |     | 130 |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Pro | Pro | Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..129  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570781  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1722:  
Met Ala Ser Glu Lys Glu Ala Ala Leu Ala Ala Thr Pro Ser Asp Ser  
1          5          10          15  
Pro Thr Ile Phe Asp Lys Ile Ile Ser Lys Glu Ile Pro Ser Thr Val  
          20          25          30  
Val Phe Glu Asp Asp Lys Val Leu Ala Phe Arg Asp Ile Thr Pro Gln  
          35          40          45  
Gly Pro Val His Ile Leu Leu Ile Pro Lys Val Arg Asp Gly Leu Thr  
          50          55          60  
Gly Leu Ser Lys Ala Glu Glu Arg His Ile Asp Ile Leu Gly Arg Leu  
65          70          75          80  
Leu Tyr Thr Ala Lys Leu Val Ala Lys Gln Glu Gly Leu Ala Glu Gly  
          85          90          95  
Phe Arg Ile Val Ile Asn Asp Gly Pro Gln Gly Cys Gln Ser Val Tyr  
          100         105         110  
His Ile His Val His Leu Ile Gly Gly Arg Gln Met Asn Trp Pro Pro  
          115         120         125  
Gly

(2) INFORMATION FOR SEQ ID NO:1723:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 521 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..521  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570782  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1723:  
acttaaacgg aacagatttg tcacgaagah gaaatcagtg tagcaaacac catccatccc 60  
tgagcaaaaga tagaagaaaa gctatgactg atttgcaaat ggaggtagag gtatatacca 120  
attcttcttt gcaggagctct ctcccgaagc cgcaagtcac gtacagatgt aagaaatgta 180  
gaaggatagt tgctattgag gaaaacatag tcccgcacatg accaggaaaag ggtgaagaat 240  
gctttgcttg gaaaaagaga agtggaacct ctgaacaagt gcaatgctct tccatctttg 300  
tcgagcctat gaaatggatg cagacaatac atgatggagt ggtggaagag aagcttctat 360  
gttttgatg taacgggaga ttagggttatt tcaactgggc tgggatgcaa tgtagctgtg 420  
gtgcatgggt taatccggct tttcagctta ataaaagccg aatagacgag tgtaaatccg 480  
agcccaaccc gaacctgaat atggaaactt gatgaaaaAg g

(2) INFORMATION FOR SEQ ID NO:1724:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 169 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..169  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570783  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1724:  
Leu Asn Arg Thr Asp Leu Ser Arg Arg Xaa Asn Gln Cys Ser Lys His  
1          5          10          15  
His Pro Ser Leu Ser Lys Asp Arg Arg Lys Ala Met Thr Asp Leu Gln  
          20          25          30

Met Glu Val Glu Val Asp Thr Asn Ser Ser Leu Gln Glu Ser Leu Pro  
35 40 45  
Lys Pro Gln Val Met Tyr Arg Cys Lys Lys Cys Arg Arg Ile Val Ala  
50 55 60  
Ile Glu Glu Asn Ile Val Pro His Glu Pro Gly Lys Gly Glu Glu Cys  
65 70 75 80  
Phe Ala Trp Lys Lys Arg Ser Gly Asn Ser Glu Gln Val Gln Cys Ser  
85 90 95  
Ser Ile Phe Val Glu Pro Met Lys Trp Met Gln Thr Ile His Asp Gly  
100 105 110  
Val Val Glu Glu Lys Leu Leu Cys Phe Gly Cys Asn Gly Arg Leu Gly  
115 120 125  
Tyr Phe Asn Trp Ala Gly Met Gln Cys Ser Cys Gly Ala Trp Val Asn  
130 135 140  
Pro Ala Phe Gln Leu Asn Lys Ser Arg Ile Asp Glu Cys Lys Ser Glu  
145 150 155 160  
Pro Asn Pro Asn Leu Asn Met Glu Thr  
165

(2) INFORMATION FOR SEQ ID NO:1725:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1570784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1725:

Met Thr Asp Leu Gln Met Glu Val Glu Val Asp Thr Asn Ser Ser Leu  
1 5 10 15  
Gln Glu Ser Leu Pro Lys Pro Gln Val Met Tyr Arg Cys Lys Lys Cys  
20 25 30  
Arg Arg Ile Val Ala Ile Glu Glu Asn Ile Val Pro His Glu Pro Gly  
35 40 45  
Lys Gly Glu Glu Cys Phe Ala Trp Lys Lys Arg Ser Gly Asn Ser Glu  
50 55 60  
Gln Val Gln Cys Ser Ser Ile Phe Val Glu Pro Met Lys Trp Met Gln  
65 70 75 80  
Thr Ile His Asp Gly Val Val Glu Glu Lys Leu Cys Phe Gly Cys  
85 90 95  
Asn Gly Arg Leu Gly Tyr Phe Asn Trp Ala Gly Met Gln Cys Ser Cys  
100 105 110  
Gly Ala Trp Val Asn Pro Ala Phe Gln Leu Asn Lys Ser Arg Ile Asp  
115 120 125  
Glu Cys Lys Ser Glu Pro Asn Pro Asn Leu Asn Met Glu Thr  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1726:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1570785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1726:

Met Glu Val Glu Val Asp Thr Asn Ser Ser Leu Gln Glu Ser Leu Pro

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Lys Pro Gln Val Met Tyr Arg Cys Lys Lys Cys Arg Arg Ile Val Ala | 20  | 25  | 30  |
| Ile Glu Glu Asn Ile Val Pro His Glu Pro Gly Lys Gly Glu Glu Cys | 35  | 40  | 45  |
| Phe Ala Trp Lys Lys Arg Ser Gly Asn Ser Glu Gln Val Gln Cys Ser | 50  | 55  | 60  |
| Ser Ile Phe Val Glu Pro Met Lys Trp Met Gln Thr Ile His Asp Gly | 65  | 70  | 75  |
| Val Val Glu Glu Lys Leu Leu Cys Phe Gly Cys Asn Gly Arg Leu Gly | 85  | 90  | 95  |
| Tyr Phe Asn Trp Ala Gly Met Gln Cys Ser Cys Gly Ala Trp Val Asn | 100 | 105 | 110 |
| Pro Ala Phe Gln Leu Asn Lys Ser Arg Ile Asp Glu Cys Lys Ser Glu | 115 | 120 | 125 |
| Pro Asn Pro Asn Leu Asn Met Glu Thr                             | 130 | 135 |     |

(2) INFORMATION FOR SEQ ID NO:1727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..744
- (D) OTHER INFORMATION: / Ceres Seq. ID 1507086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1727:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| ttcaactcac | aaagcatcac | ataacactca | cacacacact  | ttctcttctc | ttattttctc | 60  |
| agttctttta | actctttttc | ctacctatat | tcaaatggcc  | accgtcgagg | ttgaacaagt | 120 |
| gactccagta | gcagctgaga | acatcgaggt | gccaccacca  | aaggctgtgg | agtcggagga | 180 |
| agtcaccacc | gtctccgagt | ctcttccagg | tccggttaaca | gaatctcaag | cgcctgtcga | 240 |
| agtaacaact | aaagatttgg | tcgtggaaga | gacagagaaa  | ccaatcgagg | aaacagagga | 300 |
| agctcaagtt | gaaactccgg | aggttgtgga | gatcaagaaa  | gatgaagaag | ctccggttga | 360 |
| aactccgggt | gttgtggagg | atgagagcaa | aacagaggaa  | gttgtagagg | cgaagaagaa | 420 |
| ggaagaagta | gaagaaaaga | agacagagga | agctccagtg  | gttggtggag | aagagaagaa | 480 |
| gccagaggca | gaggaggaga | aAcccgccgt | ggaagcctcc  | gtgacagctc | cagtgagaaa | 540 |
| ggctgatgag | taaatgtgaa | gaaaaaaact | gtcttttgaa  | agacaaaaga | agaagaaaat | 600 |
| gttagcaagt | aatttatttg | ctactttaag | tactttgtgt  | cttgttatgt | ttttgagtct | 660 |
| atgactcttc | ttgtcttttg | tttttaactc | ttcttaagta  | ctattttcaa | tggttatcat | 720 |
| ttttaataag | atatacatta | tttt       |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183
- (D) OTHER INFORMATION: / Ceres Seq. ID 1507087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1728:

|                                                                 |    |    |    |    |
|-----------------------------------------------------------------|----|----|----|----|
| Ser Leu Thr Lys Ala Ser His Asn Thr His Thr His Thr Phe Ser Ser | 1  | 5  | 10 | 15 |
| Leu Ile Phe Ser Val Leu Leu Thr Leu Phe Ser Thr Tyr Ile Gln Met | 20 | 25 | 30 |    |
| Ala Thr Val Glu Val Glu Gln Val Thr Pro Val Ala Ala Glu Asn Ile | 35 | 40 | 45 |    |
| Glu Val Pro Pro Lys Ala Val Glu Ser Glu Glu Val Thr Thr Val     |    |    |    |    |

50 55 60  
Ser Glu Ser Leu Pro Ala Pro Val Thr Glu Ser Gln Ala Pro Val Glu  
65 70 75 80  
Val Thr Thr Lys Asp Leu Val Val Glu Glu Thr Glu Lys Pro Ile Glu  
85 90 95  
Glu Thr Glu Glu Ala Gln Val Glu Thr Pro Glu Val Val Glu Ile Lys  
100 105 110  
Lys Asp Glu Glu Ala Pro Val Glu Thr Pro Val Val Val Glu Asp Glu  
115 120 125  
Ser Lys Thr Glu Glu Val Val Glu Ala Lys Lys Glu Glu Glu Val Glu  
130 135 140  
Glu Lys Lys Thr Glu Glu Ala Pro Val Val Val Glu Glu Glu Lys Lys  
145 150 155 160  
Pro Glu Ala Glu Glu Glu Lys Pro Ala Val Glu Ala Ser Val Thr Ala  
165 170 175  
Pro Val Glu Lys Ala Asp Glu  
180

(2) INFORMATION FOR SEQ ID NO:1729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
  - (B) LOCATION: 1..152
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1570788
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1729:

Met Ala Thr Val Glu Val Glu Gln Val Thr Pro Val Ala Ala Glu Asn  
1 5 10 15  
Ile Glu Val Pro Pro Lys Ala Val Glu Ser Glu Glu Val Thr Thr  
20 25 30  
Val Ser Glu Ser Leu Pro Ala Pro Val Thr Glu Ser Gln Ala Pro Val  
35 40 45  
Glu Val Thr Thr Lys Asp Leu Val Val Glu Glu Thr Glu Lys Pro Ile  
50 55 60  
Glu Glu Thr Glu Glu Ala Gln Val Glu Thr Pro Glu Val Val Glu Ile  
65 70 75 80  
Lys Lys Asp Glu Glu Ala Pro Val Glu Thr Pro Val Val Val Glu Asp  
85 90 95  
Glu Ser Lys Thr Glu Glu Val Val Glu Ala Lys Lys Glu Glu Glu Val  
100 105 110  
Glu Glu Lys Lys Thr Glu Glu Ala Pro Val Val Val Glu Glu Glu Lys  
115 120 125  
Lys Pro Glu Ala Glu Glu Glu Lys Pro Ala Val Glu Ala Ser Val Thr  
130 135 140  
Ala Pro Val Glu Lys Ala Asp Glu  
145 150

(2) INFORMATION FOR SEQ ID NO:1730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
  - (B) LOCATION: 1..458
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1570793
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1730:

cattttcgac cgctacaacg attcctatct cagacgaatc ggatccaatg ttttctctta 60  
cgtgaacatg gtctgtgctg gcCtgcggaa ttcaatcccc aagtcacatg tatactgcc 120  
agtcogagaa gogaagcgCa Ngtctcctcg accatttctt tgcggagCtc ggtaccatgg 180  
atatgaagag gctctcgtcg ctattgaacg aagatccacg aatcatggag agacgcagtg 240  
ccatctcaaa goggctagaa ttgtatcgag cagcccaatc cgagatcgat gctgttgctt 300  
ggtccaagtg ataccggcat gtcattgtca ctgttttgcg cggttctggt cggtgtggct 360  
cagactcgga gcagagattt agggctctga atttgtataa gatgatcttc ccgataccat 420  
gcagtatcgt ttatataaac atccacattg ttgtcccc

(2) INFORMATION FOR SEQ ID NO:1731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1570794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1731:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Phe | Asp | Arg | Tyr | Asn | Asp | Ser | Tyr | Leu | Arg | Arg | Ile | Gly | Ser | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Leu | Ser | Tyr | Val | Asn | Met | Val | Cys | Ala | Gly | Leu | Arg | Asn | Ser | Ile |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Lys | Ser | Ile | Val | Tyr | Cys | Gln | Val | Arg | Glu | Ala | Lys | Arg | Xaa | Ser |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Pro | Arg | Pro | Phe | Leu | Cys | Gly | Ala | Arg | Tyr | His | Gly | Tyr | Glu | Glu | Ala |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Leu | Val | Ala | Ile | Glu | Arg | Arg | Ser | Ser | Asn | His | Gly | Glu | Thr | Gln | Cys |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     | 75  |     | 80  |
| His | Leu | Lys | Ala | Ala | Arg | Ile | Val | Ser | Ser | Ser | Pro | Ile | Arg | Asp | Arg |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Cys | Cys | Cys | Leu | Val | Gln | Val | Ile | Pro | Ala | Cys | His | Val | His | Cys | Phe |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Arg | Phe | Trp | Ser | Val | Trp | Leu | Arg | Leu | Gly | Ala | Glu | Ile |     |     |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |

(2) INFORMATION FOR SEQ ID NO:1732:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1570795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1732:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Cys | Ala | Gly | Leu | Arg | Asn | Ser | Ile | Pro | Lys | Ser | Ile | Val | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Gln | Val | Arg | Glu | Ala | Lys | Arg | Xaa | Ser | Pro | Arg | Pro | Phe | Leu | Cys |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ala | Arg | Tyr | His | Gly | Tyr | Glu | Glu | Ala | Leu | Val | Ala | Ile | Glu | Arg |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Arg | Ser | Ser | Asn | His | Gly | Glu | Thr | Gln | Cys | His | Leu | Lys | Ala | Ala | Arg |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Ile | Val | Ser | Ser | Ser | Pro | Ile | Arg | Asp | Arg | Cys | Cys | Cys | Leu | Val | Gln |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     | 75  |     | 80  |
| Val | Ile | Pro | Ala | Cys | His | Val | His | Cys | Phe | Ala | Arg | Phe | Trp | Ser | Val |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |

Trp Leu Arg Leu Gly Ala Glu Ile

100

(2) INFORMATION FOR SEQ ID NO:1733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..527

(D) OTHER INFORMATION: / Ceres Seq. ID 1507096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1733:

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| aattttgctt  | tgagacgacg | aaacgaagdg | agaaagagac  | aagccctaaa | aatcgctttg | 60  |
| agacgataaa  | tcttataaat | cttcgattcg | tccacgatga  | tctccctgtg | tgtgtgtttt | 120 |
| acttgtggaa  | aggtgattgg | gaacaaatgg | gacacatata  | ttagaactct | ccaggctgat | 180 |
| tacgctgaag  | gggatgctct | tgacgcgctt | ggatttagcc  | gttactgctg | caggcgatg  | 240 |
| cttatgactc  | atgtcgatct | aatcgaaaag | cttctaact   | acaacactat | ggagaaatcc | 300 |
| gaccccaatt  | aaagaaagat | gctataatga | atacaaatc   | atcaagagct | aaagtgtagg | 360 |
| agtgagggcat | ctcattcatg | tgaaagtctt | aataaaaacca | caatgtttca | gaaattttgt | 420 |
| tgaattttaga | aactaggaat | gttgataatt | caatgttttc  | tgatgttctt | gttcggtttt | 480 |
| agaagacaac  | ttttcgagct | acaaataaag | ctcaagcttg  | tagagcc    |            |     |

(2) INFORMATION FOR SEQ ID NO:1734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1507097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1734:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ile | Val | Pro | Val | Arg | Cys | Phe | Thr | Cys | Gly | Lys | Val | Ile | Gly | Asn |  |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |  |
| Lys | Trp | Asp | Thr | Tyr | Leu | Glu | Leu | Leu | Gln | Ala | Asp | Tyr | Ala | Glu | Gly |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asp | Ala | Leu | Asp | Ala | Leu | Gly | Leu | Val | Arg | Tyr | Cys | Cys | Arg | Arg | Met |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu | Met | Thr | His | Val | Asp | Leu | Ile | Glu | Lys | Leu | Leu | Asn | Tyr | Asn | Thr |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |  |
| Met | Glu | Lys | Ser | Asp | Pro | Asn |     |     |     |     |     |     |     |     |     |  |
| 65  |     |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..605

(D) OTHER INFORMATION: / Ceres Seq. ID 1507098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1735:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| aaaaataaaaa | cctttactta | tcttctttct | tctcacttct | cagacctcaa | tttccaagca | 60  |
| gagatgacgg  | tgaagataag | gCtcgcgcgt | cttggttgta | aacaccgacc | cttctatcgt | 120 |
| gtagtgtgct  | ccgatgaaaa | atcgcgcgag | gacggtaaac | aaatcgaggt | gttaggcttt | 180 |
| tatgatccac  | tccaaggcaa | agaagatgcg | gatagagtga | gcctcaaat  | cgacagaatc | 240 |
| aagtactggt  | tatctgttgg | agctcaacca | acagacacag | tggaaagcat | gcttttcagg | 300 |

gccggtttga taccacaaaa gcctatggta gtggtcggtt caaaaaatgg gcagaagtct 360  
acgagccaac atgtttcacc cattacaggt gaaatcttga actaagagtg ttgatgcggt 420  
gagcaagaaa gagccttttg tgtctgtgtg aaaggagttt atgtaatggt gttaaagact 480  
tttctgttta tgtgaaagga gttaatgtaa tgttgtttaa gacttttgct ttctatgtga 540  
aagcagttta atgttatggt ggtaaagact tttctgcaac agagtttggt gaatttttaw 600  
tcytt

(2) INFORMATION FOR SEQ ID NO:1736:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1570799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1736:

Lys Ile Lys Thr Phe Thr Tyr Leu Leu Ser Ser His Phe Ser Asp Leu  
1 5 10 15  
Asn Phe Gln Ala Glu Met Thr Val Lys Ile Arg Leu Ala Arg Leu Gly  
20 25 30  
Cys Lys His Arg Pro Phe Tyr Arg Val Val Val Ala Asp Glu Lys Ser  
35 40 45  
Arg Arg Asp Gly Lys Gln Ile Glu Val Leu Gly Phe Tyr Asp Pro Leu  
50 55 60  
Gln Gly Lys Glu Asp Ala Asp Arg Val Ser Leu Lys Phe Asp Arg Ile  
65 70 75 80  
Lys Tyr Trp Leu Ser Val Gly Ala Gln Pro Thr Asp Thr Val Glu Ser  
85 90 95  
Met Leu Phe Arg Ala Gly Leu Ile Pro Pro Lys Pro Met Val Val Val  
100 105 110  
Gly Ser Lys Asn Gly Gln Lys Ser Thr Ser Gln His Val Ser Pro Ile  
115 120 125  
Thr Gly Glu Ile Leu Asn  
130

(2) INFORMATION FOR SEQ ID NO:1737:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1570800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1737:

Met Thr Val Lys Ile Arg Leu Ala Arg Leu Gly Cys Lys His Arg Pro  
1 5 10 15  
Phe Tyr Arg Val Val Val Ala Asp Glu Lys Ser Arg Arg Asp Gly Lys  
20 25 30  
Gln Ile Glu Val Leu Gly Phe Tyr Asp Pro Leu Gln Gly Lys Glu Asp  
35 40 45  
Ala Asp Arg Val Ser Leu Lys Phe Asp Arg Ile Lys Tyr Trp Leu Ser  
50 55 60  
Val Gly Ala Gln Pro Thr Asp Thr Val Glu Ser Met Leu Phe Arg Ala  
65 70 75 80  
Gly Leu Ile Pro Pro Lys Pro Met Val Val Val Gly Ser Lys Asn Gly  
85 90 95  
Gln Lys Ser Thr Ser Gln His Val Ser Pro Ile Thr Gly Glu Ile Leu



Asn 100 105 110

(2) INFORMATION FOR SEQ ID NO:1738:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 511 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..511

(D) OTHER INFORMATION: / Ceres Seq. ID 1570805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1738:

|             |             |            |             |             |            |     |
|-------------|-------------|------------|-------------|-------------|------------|-----|
| atttgaacga  | gattgtatta  | agaagtaac  | tatatggaNa  | cGcgaacgc   | gCttatttgt | 60  |
| gtccaagggtc | ctggatatata | aactgctcga | gacattattt  | taccgcccctc | tgtggaaatc | 120 |
| attgataata  | cacagcatat  | agctacctta | acagaaccaa  | tagattttgtg | tattgaatta | 180 |
| aaaattgaga  | ggaatcgcg   | atatagtcta | aaaatgtcaa  | ataaactttga | agacagaagt | 240 |
| tatcctatcg  | atgctgtatt  | catgcctgtt | gaaaaatgcca | atcatagtat  | tcattcttat | 300 |
| gggaatggga  | atgaaaaaca  | agagattctt | ttctagaaa   | tatggacaaa  | tggagttta  | 360 |
| actcctaag   | aagcacttca  | tcaagcctcc | cggaatttga  | ttaattttatt | tattcctttt | 420 |
| ctacatatag  | aagaagaaac  | gttctattta | gagaacaatc  | aacatcaagt  | tactttacc  | 480 |
| ttttttcctt  | ttcataatcg  | attagttaac | c           |             |            |     |

(2) INFORMATION FOR SEQ ID NO:1739:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1570806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1739:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Xaa | Thr | Arg | Asn | Ala | Leu | Ile | Cys | Val | Gln | Gly | Pro | Gly | Tyr | Ile |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Thr | Ala | Arg | Asp | Ile | Ile | Leu | Pro | Pro | Ser | Val | Glu | Ile | Ile | Asp | Asn |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |  |
| Thr | Gln | His | Ile | Ala | Thr | Leu | Thr | Glu | Pro | Ile | Asp | Leu | Cys | Ile | Glu |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Leu | Lys | Ile | Glu | Arg | Asn | Arg | Gly | Tyr | Ser | Leu | Lys | Met | Ser | Asn | Asn |  |
|     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Phe | Glu | Asp | Arg | Ser | Tyr | Pro | Ile | Asp | Ala | Val | Phe | Met | Pro | Val | Glu |  |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Asn | Ala | Asn | His | Ser | Ile | His | Ser | Tyr | Gly | Asn | Gly | Asn | Glu | Lys | Gln |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Glu | Ile | Leu | Phe | Leu | Glu | Ile | Trp | Thr | Asn | Gly | Ser | Leu | Thr | Pro | Lys |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Glu | Ala | Leu | His | Gln | Ala | Ser | Arg | Asn | Leu | Ile | Asn | Leu | Phe | Ile | Pro |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Phe | Leu | His | Val | Glu | Glu | Glu | Thr | Phe | Tyr | Leu | Glu | Asn | Asn | Gln | His |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |  |
| Gln | Val | Thr | Leu | Pro | Phe | Phe | Pro | Phe | His | Asn | Arg | Leu | Val | Asn |     |  |
|     |     | 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1740:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..99  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570807  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1740:  
Met Ser Asn Asn Phe Glu Asp Arg Ser Tyr Pro Ile Asp Ala Val Phe  
1 5 10 15  
Met Pro Val Glu Asn Ala Asn His Ser Ile His Ser Tyr Gly Asn Gly  
20 25 30  
Asn Glu Lys Gln Glu Ile Leu Phe Leu Glu Ile Trp Thr Asn Gly Ser  
35 40 45  
Leu Thr Pro Lys Glu Ala Leu His Gln Ala Ser Arg Asn Leu Ile Asn  
50 55 60  
Leu Phe Ile Pro Phe Leu His Val Glu Glu Thr Phe Tyr Leu Glu  
65 70 75 80  
Asn Asn Gln His Gln Val Thr Leu Pro Phe Phe Pro Phe His Asn Arg  
85 90 95  
Leu Val Asn

(2) INFORMATION FOR SEQ ID NO:1741:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 83 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..83  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570808  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1741:  
Met Pro Val Glu Asn Ala Asn His Ser Ile His Ser Tyr Gly Asn Gly  
1 5 10 15  
Asn Glu Lys Gln Glu Ile Leu Phe Leu Glu Ile Trp Thr Asn Gly Ser  
20 25 30  
Leu Thr Pro Lys Glu Ala Leu His Gln Ala Ser Arg Asn Leu Ile Asn  
35 40 45  
Leu Phe Ile Pro Phe Leu His Val Glu Glu Thr Phe Tyr Leu Glu  
50 55 60  
Asn Asn Gln His Gln Val Thr Leu Pro Phe Phe Pro Phe His Asn Arg  
65 70 75 80  
Leu Val Asn

(2) INFORMATION FOR SEQ ID NO:1742:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 475 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..475  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570816  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1742:  
gttgatcgga aaggaaaagt aaaaaagaga gatctgagaa atgggaaatg agacgaagac 60  
caacgggtgt cctgcaagta tggccggagg Cggaggattc agagctaaaa tggaaacatta 120  
cgtttacagt ggtgaaaaga agcacgtctt ggtcgggattc ggaatcgtca ccatcatctt 180  
cggagttcct tggattttga tgactcaagg gtcaaagcat caatctcacc aagattacat 240

ggacaaggcc gataaagctc gaaaagcagc cctctcatcg tcttcatcag ctaacaagta 300  
gtctgtctga aggattgagt catttgcaca ctgttatctc atactcattt tccacacaaa 360  
gttaaaactt agtcaaaatc tgagcttttt ttgtgattta gattcaaaat catttccatt 420  
ttcatgcacc atgttttggt atccgttttt taataaaaag atcaaagatt ctatc

(2) INFORMATION FOR SEQ ID NO:1743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1570817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1743:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Asn | Glu | Thr | Lys | Thr | Asn | Gly | Gly | Pro | Ala | Ser | Met | Ala | Gly |  |
| 1   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |  |
| Gly | Gly | Gly | Phe | Arg | Ala | Lys | Met | Glu | His | Tyr | Val | Tyr | Ser | Gly | Glu |  |
|     |     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |  |
| Lys | Lys | His | Val | Leu | Val | Gly | Ile | Gly | Ile | Val | Thr | Ile | Ile | Phe | Gly |  |
|     |     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |  |
| Val | Pro | Trp | Tyr | Leu | Met | Thr | Gln | Gly | Ser | Lys | His | Gln | Ser | His | Gln |  |
|     |     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |  |
| Asp | Tyr | Met | Asp | Lys | Ala | Asp | Lys | Ala | Arg | Lys | Ala | Arg | Leu | Ser | Ser |  |
|     |     |     |     |     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |  |
| Ser | Ser | Ser | Ala | Asn | Lys |     |     |     |     |     |     |     |     | 80  |     |  |
|     |     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73

(D) OTHER INFORMATION: / Ceres Seq. ID 1570818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1744:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Gly | Gly | Phe | Arg | Ala | Lys | Met | Glu | His | Tyr | Val | Tyr |     |
| 1   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Gly | Glu | Lys | Lys | His | Val | Leu | Val | Gly | Ile | Gly | Ile | Val | Thr | Ile |
|     |     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |
| Ile | Phe | Gly | Val | Pro | Trp | Tyr | Leu | Met | Thr | Gln | Gly | Ser | Lys | His | Gln |
|     |     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |
| Ser | His | Gln | Asp | Tyr | Met | Asp | Lys | Ala | Asp | Lys | Ala | Arg | Lys | Ala | Arg |
|     |     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |
| Leu | Ser | Ser | Ser | Ser | Ser | Ala | Asn | Lys |     |     |     |     |     |     |     |
|     |     |     |     |     | 65  |     |     |     | 70  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1570819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1745:

Met Glu His Tyr Val Tyr Ser Gly Glu Lys Lys His Val Leu Val Gly  
1 5 10 15  
Ile Gly Ile Val Thr Ile Ile Phe Gly Val Pro Trp Tyr Leu Met Thr  
20 25 30  
Gln Gly Ser Lys His Gln Ser His Gln Asp Tyr Met Asp Lys Ala Asp  
35 40 45  
Lys Ala Arg Lys Ala Arg Leu Ser Ser Ser Ser Ala Asn Lys  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..805
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1746:

aaagtaaccc caaaagaaaa aaagcaaaaa gagaggaaaa gaaaaaaaat gacgaagacg 60  
atgatgatct tcgcgcgacg gatgacggcg atggctttgc ttacagttcc tgcgattgaa 120  
gcacaaaactg agtgcgtgag Caagctagtc ccttgcttca acgacctgaa cagcaacaa 180  
acgcgggtga aagaatgttg cgactcgata aaagaagcgg tggagaagga acttacatgt 240  
ctctgtacaa tctacaccag tccaggtttg ctgcgtcagt tcaacgtcac cactgagaaa 300  
gctctcggtc tttagcgtgc ttgcaacgtc accactgac tcctccgcttg taccgctaaa 360  
ggagctccat cgccaaaagc ttctttacct cctccagctc cagcagggaa taccaaaaaa 420  
gacgcggagc ctgggaacaa gctcgcgggt tatggagtca ccaccgtgat cttgtctttt 480  
atctcatoca tctctctctg aattccttta cccggtttta ttattattag ctcaataaat 540  
tctsgagagt tgyttgtctt ttggtcttaac ttatttaata ttttaagaaa aacaaaGaaG 600  
tattttttgt tcaatgttta tgtattatca ttgattcatc attgagtc cc atgttagtat 660  
atttaccgggt ttcaatcgga cctatcatct tgcatactgt ttttgagtgt ggatgtgtgt 720  
tggttttatgt aactctctac tctatgggac ttaattattc tactgtgtga ctggatttaa 780  
ttgatgtaaa aactgtCgtt ggttt

(2) INFORMATION FOR SEQ ID NO:1747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..166
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1747:

Lys Val Thr Pro Lys Glu Lys Lys Gln Arg Glu Arg Lys Arg Lys Lys  
1 5 10 15  
Met Thr Lys Thr Met Met Ile Phe Ala Ala Thr Met Thr Ala Met Ala  
20 25 30  
Leu Leu Ser Val Pro Ala Ile Glu Ala Gln Thr Glu Cys Val Ser Lys  
35 40 45  
Leu Val Pro Cys Phe Asn Asp Leu Asn Thr Thr Thr Thr Pro Val Lys  
50 55 60  
Glu Cys Cys Asp Ser Ile Lys Glu Ala Val Glu Lys Glu Leu Thr Cys  
65 70 75 80  
Leu Cys Thr Ile Tyr Thr Ser Pro Gly Leu Leu Ala Gln Phe Asn Val  
85 90 95  
Thr Thr Glu Lys Ala Leu Gly Leu Ser Arg Arg Cys Asn Val Thr Thr  
100 105 110

Asp Leu Ser Ala Cys Thr Ala Lys Gly Ala Pro Ser Pro Lys Ala Ser  
115 120 125  
Leu Pro Pro Pro Ala Pro Ala Gly Asn Thr Lys Lys Asp Ala Gly Ala  
130 135 140  
Gly Asn Lys Leu Ala Gly Tyr Gly Val Thr Thr Val Ile Leu Ser Leu  
145 150 155 160  
Ile Ser Ser Ile Phe Phe  
165

(2) INFORMATION FOR SEQ ID NO:1748:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1570825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1748:

Met Thr Lys Thr Met Met Ile Phe Ala Ala Thr Met Thr Ala Met Ala  
1 5 10 15  
Leu Leu Ser Val Pro Ala Ile Glu Ala Gln Thr Glu Cys Val Ser Lys  
20 25 30  
Leu Val Pro Cys Phe Asn Asp Leu Asn Thr Thr Thr Thr Pro Val Lys  
35 40 45  
Glu Cys Cys Asp Ser Ile Lys Glu Ala Val Glu Lys Glu Leu Thr Cys  
50 55 60  
Leu Cys Thr Ile Tyr Thr Ser Pro Gly Leu Leu Ala Gln Phe Asn Val  
65 70 75 80  
Thr Thr Glu Lys Ala Leu Gly Leu Ser Arg Arg Cys Asn Val Thr Thr  
85 90 95  
Asp Leu Ser Ala Cys Thr Ala Lys Gly Ala Pro Ser Pro Lys Ala Ser  
100 105 110  
Leu Pro Pro Pro Ala Pro Ala Gly Asn Thr Lys Lys Asp Ala Gly Ala  
115 120 125  
Gly Asn Lys Leu Ala Gly Tyr Gly Val Thr Thr Val Ile Leu Ser Leu  
130 135 140  
Ile Ser Ser Ile Phe Phe  
145 150

(2) INFORMATION FOR SEQ ID NO:1749:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1570826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1749:

Met Met Ile Phe Ala Ala Thr Met Thr Ala Met Ala Leu Leu Ser Val  
1 5 10 15  
Pro Ala Ile Glu Ala Gln Thr Glu Cys Val Ser Lys Leu Val Pro Cys  
20 25 30  
Phe Asn Asp Leu Asn Thr Thr Thr Thr Pro Val Lys Glu Cys Cys Asp  
35 40 45  
Ser Ile Lys Glu Ala Val Glu Lys Glu Leu Thr Cys Leu Cys Thr Ile  
50 55 60  
Tyr Thr Ser Pro Gly Leu Leu Ala Gln Phe Asn Val Thr Thr Glu Lys

(2) INFORMATION FOR SEQ ID NO:1750:

(A) LENGTH: 659 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(1x) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..659  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1750:

|             |             |             |             |            |            |     |
|-------------|-------------|-------------|-------------|------------|------------|-----|
| aaaaaacac   | gcgcgtagagt | ttcttaagaa  | caacagctgac | gaaaaggttt | ttagggtttc | 60  |
| ataatctcc   | agaatctccg  | caagatgaac  | attcttcgaat | gaaagacag  | caaggttcaa | 120 |
| ttatcttcgc  | aactgtaac   | tggcggcaac  | tactggactt  | gagacccctc | tcgatcagat | 180 |
| ttattcttggt | attacaaagt  | agcaggaacca | gtctctggga  | gttcttaaac | gtttgagcca | 240 |
| ggctacaaat  | atgaactctg  | atgaatctca  | tgaactgtgt  | ttttccaca  | agaaagagt  | 300 |
| acaaacaact  | gtgtctgggt  | tgtacatcat  | cagagggagc  | aacatgagtg | ttatcgggga | 360 |
| ctgtcgagag  | gactgtgatg  | ctagctctgga | tttttccgaac | ctagagagcc | atcogtga   | 420 |
| accctgagt   | cattgattga  | atataagttg  | ggtgagaaaa  | tcatattctc | tcattcaaac | 480 |
| ctataaaac   | aagagaagat  | tigtattgt   | acaattctgg  | tagttatttc | tgtgtctgt  | 540 |
| agtttctcta  | tttgtgtcat  | ctatagacaa  | aaagctatga  | atatatttat | tttcaaacgt | 600 |
| tttgtctgta  | aaCCTtaaat  | caaCQCCaa   | CcttttgatAa | caqAacctag | gtttctCct  |     |

(2) INFORMATION FOR SEQ ID NO:1751:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..98  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1751:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1752:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 543 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..543  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570829  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1752:

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| ataaaatcga | ttttctctca  | caaattctat  | tctctttcga | cttcagtgcc | ggcgcatcca | 60  |
| gagattcaaa | ctcagagaaa  | atggtggcga  | caggcttatt | cgtggggcta | aacaaaggac | 120 |
| acgttggtac | caaacgcgag  | caacctctcc  | gccttaacaa | cagaaaagg  | aaaacaagca | 180 |
| aaaggactat | ttttatcagg  | aattctcatca | aggaagttgc | gggtcaagct | ccctatgaga | 240 |
| agaggatcac | tgagcttttg  | aaggttggtta | aagacaagag | agctctttaa | gttgccaagc | 300 |
| gaaagtgtgg | aactcacaca  | agagctaaac  | gaaagagaga | ggagatgtct | agtgttctcc | 360 |
| gcaagatgag | gtctggtggt  | gctggtgcac  | ccgagaagaa | gaagtgatgc | gctgactctg | 420 |
| gttcagcgct | ctgtttcttc  | taaaccagtt  | ttctgttttt | tgaatttttt | gGcagtacct | 480 |
| tgtgtttcct | ttggatatatt | tgtagcagag  | ataattaaat | gttaaaacga | aaccattatg | 540 |

acg

(2) INFORMATION FOR SEQ ID NO:1753:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 134 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..134  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570830  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1753:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ile | Asp | Phe | Leu | Ser | Gln | Ile | Leu | Phe | Ser | Phe | Asp | Phe | Ser | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ala | Phe | Arg | Asp | Ser | Asn | Ser | Glu | Lys | Met | Val | Ala | Thr | Gly | Leu |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Val | Gly | Leu | Asn | Lys | Gly | His | Val | Val | Thr | Lys | Arg | Glu | Gln | Pro |
|     |     |     |     | 35  |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Pro | Arg | Pro | Asn | Asn | Arg | Lys | Gly | Lys | Thr | Ser | Lys | Arg | Thr | Ile | Phe |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ile | Arg | Asn | Leu | Ile | Lys | Glu | Val | Ala | Gly | Gln | Ala | Pro | Tyr | Glu | Lys |
|     |     |     |     | 65  |     | 70  |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Ile | Thr | Glu | Leu | Leu | Lys | Val | Gly | Lys | Asp | Lys | Arg | Ala | Leu | Lys |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Ala | Lys | Arg | Lys | Leu | Gly | Thr | His | Lys | Arg | Ala | Lys | Arg | Lys | Arg |
|     |     |     |     | 100 |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Glu | Glu | Met | Ser | Ser | Val | Leu | Arg | Lys | Met | Arg | Ser | Gly | Gly | Ala | Gly |
|     |     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Ser | Glu | Lys | Lys | Lys |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 130 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1754:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 108 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1570831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1754:

```
Met Val Ala Thr Gly Leu Phe Val Gly Leu Asn Lys Gly His Val Val
1 5 10 15
Thr Lys Arg Glu Gln Pro Pro Arg Pro Asn Asn Arg Lys Gly Lys Thr
 20 25 30
Ser Lys Arg Thr Ile Phe Ile Arg Asn Leu Ile Lys Glu Val Ala Gly
 35 40 45
Gln Ala Pro Tyr Glu Lys Arg Ile Thr Glu Leu Leu Lys Val Gly Lys
 50 55 60
Asp Lys Arg Ala Leu Lys Val Ala Lys Arg Lys Leu Gly Thr His Lys
65 70 75 80
Arg Ala Lys Arg Lys Arg Glu Glu Met Ser Ser Val Leu Arg Lys Met
 85 90 95
Arg Ser Gly Gly Ala Gly Ala Ser Glu Lys Lys
100 105
```

(2) INFORMATION FOR SEQ ID NO:1755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..552
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1755:

```
agatcagtgga ttgttcgatg aacgaagagg agccagacaa agaacacgtg gcggattota 60
ctatgtcggc ggcgcgcgatt gatgtgtgtg cggtctgag atcggtgttt cagcgggttaa 120
accaggcggc ggagaaagcg ggtcgtgggt cggtacgat acgggtcgta gcggtgagta 180
agacgaaacc agtttctctg attgcgcaag tatacgacgc ttgtcagagg tcttttgag 240
agaattatgt gcaagagatc attgagaagg cacctcagct tccagaagat atagagtggc 300
atttcatttg gaatttgcag agcaacaaag tgaagccttt gctatgtaaa ttgactttgc 360
tatttcaaag tcttcatctt tagttttttt gtattgagtt actaaattgg gtgtaaaact 420
ccacacttga gttctattct taattctttg gtttgatcag ctggtgttcc taacctgttg 480
accgtggaag gtgttgatga tgaaaaggta aaagtctctc tttgttatat ttaaagagRa 540
aattggtttg tt
```

(2) INFORMATION FOR SEQ ID NO:1756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1756:

```
Ile Ser Asp Cys Ser Met Asn Glu Glu Glu Pro Asp Lys Glu His Val
1 5 10 15
Ala Asp Ser Thr Met Ser Ala Ala Ala Ile Asp Gly Val Ala Ala Leu
 20 25 30
Arg Ser Val Phe Gln Arg Val Asn Gln Ala Ala Glu Lys Ala Gly Arg
 35 40 45
Gly Ser Asp Gln Ile Arg Val Val Ala Val Ser Lys Thr Lys Pro Val
 50 55 60
Ser Leu Ile Arg Gln Val Tyr Asp Ala Gly Gln Arg Ser Phe Gly Glu
65 70 75 80
Asn Tyr Val Gln Glu Ile Ile Glu Lys Ala Pro Gln Leu Pro Glu Asp
```



(2) INFORMATION FOR SEO ID NO:1757:

(A) LENGTH: 121 amino ac

- (ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

- (B) LOCATION: 1..121

- (D) OTHER INFORMATION

- SEQUENCE DESCRIPTION: SEO ID NO:1757:

Asp Glu Glu Glu Pro Asp Lys Glu His Val Al

(2) INFORMATION FOR SEQ ID NO:1758:

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..106

- (D) OTHER INFORMATION: / Ceres Seq. ID 1570839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1758:

(2) INFORMATION FOR SEQ ID NO:1759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..676  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1759:

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| aacaatccct  | acacgggcta | catctacact | tcttttcaag | agagagcaac  | ttttatctcc  | 60  |
| cacgccaaaca | cggcgaaGct | agccacgaca | tacggcgaca | caactctcgc  | caaaatctgt  | 120 |
| ggaacaatcg  | cggcgatga  | gaagcggcac | gagatggcgt | atcgcgggat  | cgtcgagaag  | 180 |
| ctattcgaga  | ttgatccga  | tggatccgta | caagctctag | cgagtatgat  | gaggaagcga  | 240 |
| atcacgatgc  | cggctcagct | gatgcacgac | ggtcgcgatg | acaatctgtt  | cgatcattac  | 300 |
| gctgcgtgtg  | cgcagagaat | cggagtgtat | accgcgacgg | attacgcagg  | gattttggag  | 360 |
| tttttgttgc  | ggcgggtgga | ggtggagaag | ttagggatgg | gtttgtccgg  | tgaagggaagg | 420 |
| agagcacagg  | attatctgtg | taccttgccg | cagaggatca | ggaggtttaga | ggaaagagct  | 480 |
| gacgatagag  | tcaaacgtgc | gtcaaatgtc | aaacctctcg | tttcgttcag  | ctggatttac  | 540 |
| gggagagaag  | ttgaactata | aacgacaatg | gttggtgCgt | ttcactgtat  | tagactctta  | 600 |
| aacgttatgg  | gccttactaa | tgtaatatgg | gaagtaaatg | taataaagaa  | acgctaaaaa  | 660 |
| atcttgcggt  | ttagtctc   |            |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..186  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1760:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Asn | Pro | Tyr | Asn | Gly | Tyr | Ile | Tyr | Thr | Ser | Phe | Gln | Glu | Arg | Ala |  |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |  |
| Thr | Phe | Ile | Ser | His | Ala | Asn | Thr | Ala | Lys | Leu | Ala | Thr | Thr | Tyr | Gly |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asp | Thr | Thr | Leu | Ala | Lys | Ile | Cys | Gly | Thr | Ile | Ala | Ala | Asp | Glu | Lys |  |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | His | Glu | Met | Ala | Tyr | Thr | Arg | Ile | Val | Glu | Lys | Leu | Phe | Glu | Ile |  |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Asp | Pro | Asp | Gly | Thr | Val | Gln | Ala | Leu | Ala | Ser | Met | Met | Arg | Lys | Arg |  |
|     |     |     |     | 65  |     | 70  |     |     |     | 75  |     |     |     | 80  |     |  |
| Ile | Thr | Met | Pro | Ala | Gln | Leu | Met | His | Asp | Gly | Arg | Asp | Asp | Asn | Leu |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Phe | Asp | His | Tyr | Ala | Ala | Val | Ala | Gln | Arg | Ile | Gly | Val | Tyr | Thr | Ala |  |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Thr | Asp | Tyr | Ala | Gly | Ile | Leu | Glu | Phe | Leu | Leu | Arg | Arg | Trp | Glu | Val |  |
|     |     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Glu | Lys | Leu | Gly | Met | Gly | Leu | Ser | Gly | Glu | Gly | Arg | Arg | Ala | Gln | Asp |  |
|     |     |     |     | 130 |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Tyr | Leu | Cys | Thr | Leu | Pro | Gln | Arg | Ile | Arg | Arg | Leu | Glu | Glu | Arg | Ala |  |
|     |     |     |     | 145 |     | 150 |     |     |     | 155 |     |     |     | 160 |     |  |
| Asp | Asp | Arg | Val | Lys | Arg | Ala | Ser | Lys | Ser | Lys | Pro | Ser | Val | Ser | Phe |  |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Ser | Trp | Ile | Tyr | Gly | Arg | Glu | Val | Glu | Leu |     |     |     |     |     |     |  |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..135
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1570854
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1761:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Tyr | Thr | Arg | Ile | Val | Glu | Lys | Leu | Phe | Glu | Ile | Asp | Pro | Asp |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Gly | Thr | Val | Gln | Ala | Leu | Ala | Ser | Met | Met | Arg | Lys | Arg | Ile | Thr | Met |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Pro | Ala | Gln | Leu | Met | His | Asp | Gly | Arg | Asp | Asp | Asn | Leu | Phe | Asp | His |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Tyr | Ala | Ala | Val | Ala | Gln | Arg | Ile | Gly | Val | Tyr | Thr | Ala | Thr | Asp | Tyr |  |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Ala | Gly | Ile | Leu | Glu | Phe | Leu | Leu | Arg | Arg | Trp | Glu | Val | Glu | Lys | Leu |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Gly | Met | Gly | Leu | Ser | Gly | Glu | Gly | Arg | Arg | Ala | Gln | Asp | Tyr | Leu | Cys |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Thr | Leu | Pro | Gln | Arg | Ile | Arg | Arg | Leu | Glu | Glu | Arg | Ala | Asp | Asp | Arg |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Val | Lys | Arg | Ala | Ser | Lys | Ser | Lys | Pro | Ser | Val | Ser | Phe | Ser | Trp | Ile |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |
| Tyr | Gly | Arg | Glu | Val | Glu | Leu |     |     |     |     |     |     |     |     |     |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1762:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 111 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1762:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Met | Arg | Lys | Arg | Ile | Thr | Met | Pro | Ala | Gln | Leu | Met | His | Asp | Gly |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Arg | Asp | Asp | Asn | Leu | Phe | Asp | His | Tyr | Ala | Ala | Val | Ala | Gln | Arg | Ile |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Gly | Val | Tyr | Thr | Ala | Thr | Asp | Tyr | Ala | Gly | Ile | Leu | Glu | Phe | Leu | Leu |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Arg | Trp | Glu | Val | Glu | Lys | Leu | Gly | Met | Gly | Leu | Ser | Gly | Glu | Gly |  |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Arg | Arg | Ala | Gln | Asp | Tyr | Leu | Cys | Thr | Leu | Pro | Gln | Arg | Ile | Arg | Arg |  |
| 65  |     |     |     | 70  |     |     | 75  |     |     |     |     |     | 80  |     |     |  |
| Leu | Glu | Glu | Arg | Ala | Asp | Asp | Arg | Val | Lys | Arg | Ala | Ser | Lys | Ser | Lys |  |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |  |
| Pro | Ser | Val | Ser | Phe | Ser | Trp | Ile | Tyr | Gly | Arg | Glu | Val | Glu | Leu |     |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1763:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 646 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..646  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1763:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| tctcgagtac  | acctcatcat | tcttcttcgt | gtgagagaga | tctttttgga | aaacgaaaac | 60  |
| Gggatttagc  | gtatagcagc | ttccaccgtt | tcgccaatt  | tcactgagct | tcaagtgaac | 120 |
| atgagtaaac  | caatggaaga | ggataccaac | cagggaaaga | ctgaggagga | ggagttcaac | 180 |
| actggaccac  | tctctgtttt | gatgatgagt | gttaagaata | acactcaggt | gttgatcaat | 240 |
| tgccgtaaca  | acaggaacct | ccttggccga | gttagggcct | ttgacaggca | ctgcaacatg | 300 |
| gttctttgaa  | atgtcagaga | aatgtggact | gaggttccga | aaaccggaaa | aggaagaaga | 360 |
| aaagctcttc  | ctgttaacag | agatcgattc | atcagcaaga | tgttctgcg  | tggagactca | 420 |
| gtcattatcg  | tcttcaggaa | ccccaagtga | gagaagctct | tcttatgata | attctcgctt | 480 |
| cttcttgta   | aatctaat   | gttgcatcaa | cagtgagaac | atgttttgat | tatgagcttt | 540 |
| aaatctacta  | gtgttgCctt | gtatttttca | ctgtctctct | atctttgact | tgaacgcag  | 600 |
| ccagtgaaact | ttgtaatact | aaaagagaag | ttctttwttt | cttttt     |            |     |

(2) INFORMATION FOR SEQ ID NO:1764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1570863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1764:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Lys | Pro | Met | Glu | Glu | Asp | Thr | Asn | Gln | Gly | Lys | Thr | Glu | Glu |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Glu | Phe | Asn | Thr | Gly | Pro | Leu | Ser | Val | Leu | Met | Met | Ser | Val | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Asn | Thr | Gln | Val | Leu | Ile | Asn | Cys | Arg | Asn | Asn | Arg | Lys | Leu | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Arg | Val | Arg | Ala | Phe | Asp | Arg | His | Cys | Asn | Met | Val | Leu | Glu | Asn |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Arg | Glu | Met | Trp | Thr | Glu | Val | Pro | Lys | Thr | Gly | Lys | Gly | Lys | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Ala | Leu | Pro | Val | Asn | Arg | Asp | Arg | Phe | Ile | Ser | Lys | Met | Phe | Leu |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Gly | Asp | Ser | Val | Ile | Ile | Val | Leu | Arg | Asn | Pro | Lys |     |     |     |
|     |     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1570864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1765:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Glu | Asp | Thr | Asn | Gln | Gly | Lys | Thr | Glu | Glu | Glu | Phe | Asn |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |
| Thr | Gly | Pro | Leu | Ser | Val | Leu | Met | Met | Ser | Val | Lys | Asn | Asn | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Val | Leu | Ile | Asn | Cys | Arg | Asn | Asn | Arg | Lys | Leu | Leu | Gly | Arg | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ala | Phe | Asp | Arg | His | Cys | Asn | Met | Val | Leu | Glu | Asn | Val | Arg | Glu |
|     |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |

Trp Thr Glu Val Pro Lys Thr Gly Lys Gly Lys Lys Lys Ala Leu Pro  
65 70 75 80  
Val Asn Arg Asp Arg Phe Ile Ser Lys Met Phe Leu Arg Gly Asp Ser  
65 90 95  
Val Ile Ile Val Leu Arg Asn Pro Lys  
100 105

(2) INFORMATION FOR SEQ ID NO:1766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1570865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1766:

Met Met Ser Val Lys Asn Asn Thr Gln Val Leu Ile Asn Cys Arg Asn  
1 5 10 15  
Asn Arg Lys Leu Leu Gly Arg Val Arg Ala Phe Asp Arg His Cys Asn  
20 25 30  
Met Val Leu Glu Asn Val Arg Glu Met Trp Thr Glu Val Pro Lys Thr  
35 40 45  
Gly Lys Gly Lys Lys Lys Ala Leu Pro Val Asn Arg Asp Arg Phe Ile  
50 55 60  
Ser Lys Met Phe Leu Arg Gly Asp Ser Val Ile Val Leu Arg Asn  
65 70 75 80  
Pro Lys

(2) INFORMATION FOR SEQ ID NO:1767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..502

(D) OTHER INFORMATION: / Ceres Seq. ID 1570869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1767:

atcagaaaaac acaaatcttta aaactttctg gaaaaacaaa aatgttcagga agaggaaaaag 60  
gaggaaaaagg gttaggcaaa ggaggagcaa agagacacag aaaggttcta agagacaaca 120  
ttcaaggaat cacaaagcca gcgattcgct gtcttgctcg tagaggaggt gtgaagagaa 180  
tcagtgatt gatctatgaa gaaacgagag gtgtgttgaa gatctttctg gagaatgtga 240  
ttagagatgc tgttaacttac actgagcatg cgaggaggaa gacggtgact gctatggatg 300  
ttgtttatgc cttgaagaga caaggaagaa ctctatatgg atttggtggt tgatcaattt 360  
gagatctggg tttctgtggt aatgatgata atttaagtct tgcgatcaag aaattccaga 420  
aattgggttg aattttaggg tttcgttttg tgttgtaatt agggcagcat tgtaattggat 480  
taatgataag tacCatttgc cc

(2) INFORMATION FOR SEQ ID NO:1768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1570870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1768:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Gln | Lys | Thr | Gln | Ile | Leu | Lys | Leu | Ser | Gly | Lys | Thr | Lys | Met | Ser | Gly |  |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Arg | Gly | Lys | Gly | Gly | Lys | Gly | Leu | Gly | Lys | Gly | Gly | Ala | Lys | Arg | His |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Arg | Lys | Val | Leu | Arg | Asp | Asn | Ile | Gln | Gly | Ile | Thr | Lys | Pro | Ala | Ile |  |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Arg | Arg | Leu | Ala | Arg | Arg | Gly | Gly | Val | Lys | Arg | Ile | Ser | Gly | Leu | Ile |  |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |  |
| Tyr | Glu | Glu | Thr | Arg | Gly | Val | Leu | Lys | Ile | Phe | Leu | Glu | Asn | Val | Ile |  |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |     |  |  |
| Arg | Asp | Ala | Val | Thr | Tyr | Thr | Glu | His | Ala | Arg | Arg | Lys | Thr | Val | Thr |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |  |
| Ala | Met | Asp | Val | Val | Tyr | Ala | Leu | Lys | Arg | Gln | Gly | Arg | Thr | Leu | Tyr |  |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |  |
| Gly | Phe | Gly | Gly |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:1769:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1570871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1769:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Ser | Gly | Arg | Gly | Lys | Gly | Gly | Lys | Gly | Leu | Gly | Lys | Gly | Gly | Ala |  |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |  |
| Lys | Arg | His | Arg | Lys | Val | Leu | Arg | Asp | Asn | Ile | Gln | Gly | Ile | Thr | Lys |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Pro | Ala | Ile | Arg | Arg | Leu | Ala | Arg | Arg | Gly | Gly | Val | Lys | Arg | Ile | Ser |  |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Gly | Leu | Ile | Tyr | Glu | Glu | Thr | Arg | Gly | Val | Leu | Lys | Ile | Phe | Leu | Glu |  |  |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |  |  |
| Asn | Val | Ile | Arg | Asp | Ala | Val | Thr | Tyr | Thr | Glu | His | Ala | Arg | Arg | Lys |  |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |     |  |  |
| Thr | Val | Thr | Ala | Met | Asp | Val | Val | Tyr | Ala | Leu | Lys | Arg | Gln | Gly | Arg |  |  |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |     |  |  |
| Thr | Leu | Tyr | Gly | Phe | Gly | Gly |     |     |     |     |     |     |     |     |     |  |  |
|     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:1770:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 634 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..634

(D) OTHER INFORMATION: / Ceres Seq. ID 1570895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1770:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| atttgcaga  | ttgggttggga | tggtcttcgt | atgcttgatc | caagtactag | ccgaactttg | 60  |
| agaatatatc | ctcttgagaa  | catcacaaga | tgcgaaaaac | tagattcgtc | tattctggct | 120 |
| ttctggctca | agactccggt  | agacattgaa | gctaaacgta | tcagattgca | atcaaatagt | 180 |
| tacaccacca | acacccctct  | ggacactgtg | acggctgcac | tgtttcagcg | caaggagatc | 240 |
| gggggaagta | gcaggcctcc  | cacctctgga | aaactggttg | aacaaactcg | tgagaagaaa | 300 |

aaaggattgg gtgattggat gaacattata aagcctgtta atgaggagaa agatcattgg 360  
gtacctgatg aagctgttcc taagtgcaca tcatgtggtt cagatttcgg tgcatttata 420  
cgaaggcacc actgcaggaa ttgtggtgaa gtcttctgtg acaagtgtac tcaaggcagg 480  
attgctctca ctgctgagga taatgtctct caagtccgtg tttgtgaccg gtgcatggca 540  
gaagtgtcac aaaggttgag taatgCcaag gaaaccactg gcaggaatgt gagCctgcag 600  
agccatgaag accttgctag aaagttwcag gagg

(2) INFORMATION FOR SEQ ID NO:1771:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..211

(D) OTHER INFORMATION: / Ceres Seq. ID 1570896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1771:

Ile Cys Gln Ile Gly Leu Asp Gly Leu Arg Met Leu Asp Pro Ser Thr  
1 5 10 15  
Ser Arg Thr Leu Arg Ile Tyr Pro Leu Glu Asn Ile Thr Arg Cys Glu  
20 25 30  
Lys Leu Asp Ser Ser Ile Leu Ala Phe Trp Ser Lys Thr Pro Val Asp  
35 40 45  
Ile Glu Ala Lys Arg Ile Arg Leu Gln Ser Asn Ser Tyr Thr Thr Asn  
50 55 60  
Thr Leu Leu Asp Thr Val Thr Ala Ala Met Phe Gln Ala Lys Glu Ile  
65 70 75 80  
Gly Gly Ser Ser Arg Pro Pro Thr Ser Gly Lys Leu Val Glu Gln Thr  
85 90 95  
Ala Glu Lys Lys Lys Gly Leu Gly Asp Trp Met Asn Ile Ile Lys Pro  
100 105 110  
Val Asn Glu Glu Lys Asp His Trp Val Pro Asp Glu Ala Val Ser Lys  
115 120 125  
Cys Thr Ser Cys Gly Ser Asp Phe Gly Ala Phe Ile Arg Arg His His  
130 135 140  
Cys Arg Asn Cys Gly Glu Val Phe Cys Asp Lys Cys Thr Gln Gly Arg  
145 150 155 160  
Ile Ala Leu Thr Ala Glu Asp Asn Ala Pro Gln Val Arg Val Cys Asp  
165 170 175  
Arg Cys Met Ala Glu Val Ser Gln Arg Leu Ser Asn Ala Lys Glu Thr  
180 185 190  
Thr Gly Arg Asn Val Ser Leu Gln Ser His Glu Asp Leu Ala Arg Lys  
195 200 205  
Xaa Gln Glu  
210

(2) INFORMATION FOR SEQ ID NO:1772:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..201

(D) OTHER INFORMATION: / Ceres Seq. ID 1570897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1772:

Met Leu Asp Pro Ser Thr Ser Arg Thr Leu Arg Ile Tyr Pro Leu Glu  
1 5 10 15  
Asn Ile Thr Arg Cys Glu Lys Leu Asp Ser Ser Ile Leu Ala Phe Trp

(1x) FEATURE:



(A) NAME/KEY: -

(B) LOCATION: 1..525

(D) OTHER INFORMATION: / Ceres Seq. ID 1570913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1774:

|            |             |             |             |            |            |     |
|------------|-------------|-------------|-------------|------------|------------|-----|
| aagatggcca | agtaacaaga  | gattgcgaag  | aagaagagag  | aggctaaagc | cgatagaaaa | 60  |
| cgagccattc | acggcgatcc  | tctaccaaat  | aaattgaaga  | ccagaactcc | ggtccctccc | 120 |
| gtctccggca | aacgtcagag  | aaagctcctt  | cgcaaattgc  | gcagagagca | gaaagatatg | 180 |
| gtggagaagg | gtcttgttac  | tatggaagat  | gtggagatgg  | cttctgctca | agctgcatca | 240 |
| gaagactcca | agaaatcccc  | cagaaaaattt | agcgttaaga  | agagcttgaa | gttgaacaaa | 300 |
| ctaaataata | aaggcaaaaa  | gaagaaaaaac | cagaaaagcca | gtggtgaaaa | atctgctgat | 360 |
| tgtatgctag | aatgagtgct  | gtgtatacct  | gtaaacccat  | tctctctaac | ggatgataga | 420 |
| ggtttctcaa | tgtctgggtta | gattctttcca | aaaatgtgaa  | acgtgtgttt | ttgcatccgg | 480 |
| aggatGcgNa | aGcagaggaa  | tggagggttt  | gatatgattt  | tattt      |            |     |

(2) INFORMATION FOR SEQ ID NO:1775:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1570914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1775:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Met | Ala | Lys | Tyr | Asn | Glu | Ile | Ala | Lys | Lys | Lys | Arg | Glu | Ala | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Asp | Arg | Lys | Arg | Ala | Ile | His | Gly | Asp | Pro | Leu | Thr | Asn | Lys | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Thr | Arg | Thr | Pro | Val | Pro | Ser | Val | Ser | Gly | Lys | Arg | Gln | Arg | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Leu | Arg | Lys | Trp | Arg | Arg | Glu | Gln | Lys | Asp | Met | Val | Glu | Lys | Gly |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Leu | Val | Thr | Met | Glu | Asp | Val | Glu | Met | Ala | Ser | Ala | Gln | Ala | Ala | Ser |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Glu | Asp | Ser | Lys | Lys | Ser | Pro | Arg | Lys | Phe | Ser | Val | Lys | Lys | Ser | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Leu | Asn | Lys | Leu | Asn | Asn | Lys | Gly | Lys | Lys | Lys | Lys | Asn | Gln | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Ala | Ser | Gly | Gly | Lys | Ser | Ala | Asp | Cys | Met | Leu | Glu |     |     |     |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1776:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1570915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1776:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Tyr | Asn | Glu | Ile | Ala | Lys | Lys | Arg | Glu | Ala | Lys | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |
| Asp | Arg | Lys | Arg | Ala | Ile | His | Gly | Asp | Pro | Leu | Thr | Asn | Lys | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Thr | Arg | Thr | Pro | Val | Pro | Ser | Val | Ser | Gly | Lys | Arg | Gln | Arg | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Leu | Arg | Lys | Trp | Arg | Arg | Glu | Gln | Lys | Asp | Met | Val | Glu | Lys | Gly |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |

Val Thr Met Glu Asp Val Glu Met Ala Ser Ala Gln Ala Ala Ser Glu  
65 70 75 80  
Asp Ser Lys Lys Ser Pro Arg Lys Phe Ser Val Lys Lys Ser Leu Lys  
85 90 95  
Leu Asn Lys Leu Asn Asn Lys Gly Lys Lys Lys Asn Gln Lys Ala  
100 105 110  
Ser Gly Glu Lys Ser Ala Asp Cys Met Leu Glu  
115 120

(2) INFORMATION FOR SEQ ID NO:1777:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1570916

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1777:

Met Val Glu Lys Gly Leu Val Thr Met Glu Asp Val Glu Met Ala Ser  
1 5 10 15  
Ala Gln Ala Ala Ser Glu Asp Ser Lys Lys Ser Pro Arg Lys Phe Ser  
20 25 30  
Val Lys Lys Ser Leu Lys Leu Asn Lys Leu Asn Asn Lys Gly Lys Lys  
35 40 45  
Lys Lys Asn Gln Lys Ala Ser Gly Glu Lys Ser Ala Asp Cys Met Leu  
50 55 60

Glu

65

(2) INFORMATION FOR SEQ ID NO:1778:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 475 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..475

(D) OTHER INFORMATION: / Ceres Seq. ID 1570931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1778:

aattttcaaaa aaaagcagat taaaacagag attagcgagt gagagagaga gacaaagata 60  
tagagcttct cgtgaagcaa cagtgaagaa aaggaaagt aatcgccat gatgatcgcc 120  
ttcgcttaag ccgcagaatc cgctttcttc ttcttgcttg gctccgctgt tctcgctccg 180  
gaagaataga gtttatcaga cgatttggat acaaggaaaat aatcaaaagca acagaaggtt 240  
tccgtaaggt tatttacacc aactatcacg ggtctgcata cagagctaaa ttcaaaggtg 300  
gtgaggttgc ttgtgtcaaa gaactcacgt ctcttgatct tggacgagaa aggtttgatg 360  
aggaagttca gcttttgggt cgcttacgtc accgtcatct ccttacActt cgtgggtttt 420  
gcatttttagt cttgaacaat catctcagtc tgtattttga atttggttca ctctct

(2) INFORMATION FOR SEQ ID NO:1779:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1570932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1779:

Met Asp Asp Arg Leu Arg Leu Ser Arg Arg Ile Arg Phe Leu Leu Leu  
1 5 10 15  
Ala Trp Leu Arg Arg Ser Arg Ser Gly Arg Ile Glu Phe Ile Arg Arg  
20 25 30  
Phe Gly Tyr Lys Glu Ile Ile Lys Ala Thr Glu Gly Phe Arg Lys Val  
35 40 45  
Ile Tyr Thr Asn Tyr His Gly Ser Ala Tyr Arg Ala Lys Phe Lys Gly  
50 55 60  
Gly Glu Val Ala Leu Val Lys Glu Leu Thr Ala Leu Asp Leu Gly Arg  
65 70 75 80  
Glu Arg Phe Asp Glu Glu Val Gln Leu Leu Gly Arg Leu Arg His Arg  
85 90 95  
His Leu Leu Thr Leu Arg Gly Phe Cys Ile Leu Val Leu Asn His  
100 105 110  
Leu Ser Leu Tyr Phe Glu Phe Gly Ser Leu  
115 120

(2) INFORMATION FOR SEQ ID NO:1780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..850
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1780:

acacacacac acatgttctt cgttgctgct tcgttgggtt aaaaactttt ttAtttgttt 60  
cttgcttttt gtaaagtcac agataacaaa taaataagaa aaatggagaa tctaccacct 120  
ggttatcgct ccaatgttgg tgtttgtcta atcaactcgg ataattogtt attttagact 180  
tctagattga atgttccagg agcatggcag atgccacagg gaggcattga agatggggag 240  
gatccaaagt cagcagccat gagagaatta caagaagaaa ctggtgttgt ttacgctgaa 300  
atcgctcagc aggtcccaaa ttggttgaca tatgattttc caccagcagt aaaagcaaaa 360  
gttaaccgct ttgtgggcgg tgaatggcat ggtcaagctc agaaaatggta tttagtgaga 420  
ctgaggaacg atgaggacga gaaagagatc aatctagcga acaacgaagc ggattcagag 480  
tttgcggagt ggaatgggac gaagccagaa gaagtggtag agcaagcagt ggattacaaa 540  
aggccaacct atgaagaagt catcaagact ttgtgttcgt tcttaaacga cacaggaaga 600  
gctgctaaat gtaaatcagc caagtgggtga tataagatac caagaaccaa tgtttgtctt 660  
tttatttttt ttgttaactg ttgtttttct ttttttgggc gttctctttt agtagaaccc 720  
ttttggaatg caaaagcttt ctctaggggt tttttacttt catttttgta aattgtttat 780  
tggtacgtag aaagtttttt gggttttatt taacgtgggg gtcattgtaa taaagtctgt 840  
gtctggattc

(2) INFORMATION FOR SEQ ID NO:1781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1781:

Met Glu Asn Leu Pro Pro Gly Tyr Arg Pro Asn Val Gly Val Cys Leu  
1 5 10 15  
Ile Asn Ser Asp Asn Cys Val Phe Val Ala Ser Arg Leu Asn Val Pro  
20 25 30  
Gly Ala Trp Gln Met Pro Gln Gly Gly Ile Glu Asp Gly Gly Asp Pro

(2) INFORMATION FOR SEQ ID NO:1782:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1570938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1782:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Gln | Gly | Gly | Ile | Glu | Asp | Gly | Glu | Asp | Pro | Lys | Ser | Ala | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Arg | Glu | Leu | Gln | Glu | Glu | Thr | Gly | Val | Val | Ser | Ala | Glu | Ile | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Glu | Val | Pro | Asn | Trp | Leu | Thr | Tyr | Asp | Phe | Pro | Pro | Ala | Val | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Lys | Val | Asn | Arg | Leu | Trp | Gly | Glu | Trp | His | Gly | Gln | Ala | Gln |     |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Lys | Trp | Tyr | Leu | Val | Arg | Leu | Arg | Asn | Asp | Glu | Asp | Glu | Lys | Glu | Ile |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Asn | Leu | Ala | Asn | Asn | Glu | Ala | Asp | Ser | Glu | Phe | Ala | Glu | Trp | Lys | Trp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Lys | Pro | Glu | Glu | Val | Val | Glu | Gln | Ala | Val | Asp | Tyr | Lys | Arg | Pro |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Tyr | Glu | Glu | Val | Ile | Lys | Thr | Phe | Gly | Ser | Phe | Leu | Asn | Asp | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Arg | Ala | Ala | Lys | Cys | Lys | Ser | Ala | Lys | Trp |     |     |     |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1783:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(IX) FEATURE.  
(A) NAME

(B) LOCATION: 1..123

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:1783:

Arg Glu Leu Gln Glu Glu Thr Gly Val Val Se

| Met | Ala | Glu | Leu | Gln | Gly | Val | Val | Ser | Asa | Glu | Thr | Val |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   |     |     |     | 5   |     | 10  |     |     |     |     |     | 15  |

Ser Glu Val Pro Asn Trp Leu Thr Tyr Asp Phe Pro Pro Ala Val Lys  
20 25 30  
Ala Lys Val Asn Arg Leu Trp Gly Gly Glu Trp His Gly Gln Ala Gln  
35 40 45  
Lys Trp Tyr Leu Val Arg Leu Arg Asn Asp Glu Asp Glu Lys Glu Ile  
50 55 60  
Asn Leu Ala Asn Asn Glu Ala Asp Ser Glu Phe Ala Glu Trp Lys Trp  
65 70 75 80  
Ala Lys Pro Glu Glu Val Val Glu Gln Ala Val Asp Tyr Lys Arg Pro  
85 90 95  
Thr Tyr Glu Glu Val Ile Lys Thr Phe Gly Ser Phe Leu Asn Asp Thr  
100 105 110  
Gly Arg Ala Ala Lys Cys Lys Ser Ala Lys Trp  
115 120

(2) INFORMATION FOR SEQ ID NO:1784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..651

(D) OTHER INFORMATION: / Ceres Seq. ID 1570951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1784:

```

cttttttgc gaccattttt gtttctgagt tgttcttctt gattagcttt gtccgcttg 60
aaccacaacat ggcgagtcctt ggccatatag ccagagaatc atcagacatc acacgcctcg 120
cccagtttta caaagaggtg tttgggttcg aggagatcga aagtccctgat tttggagacc 180
taaaagtggt gtggctaaac ttaccaggtg cttttgcaat gcacattatc cagagaaacc 240
cttcaacaaa tcttcagaa ggtccttaca gtgtacctc agcggttaag gatcctagcc 300
atctcccaat gggtcatcat atctgtttct ctgtcccaaa ttctgactct ttctctcatt 360
ctctcaagga gaaagggata gaaacttttc agaagtctct gcctgatgga aaagtcaagc 420
aagttttctt ctttgatcct gatggaaacg gattagaggt agcaagtgcg tcatgagcct 480
tgaacctgaa atatgtggta tcactactta tagaatgaaa taaagtatt gtataataa 540
tcagtttgtt gaaataaaaat ctatatgtat aggtttgatg ttaactttgt acaGcttacg 600
cctcaaaagt cgtgtcatgt gctttgaatg ktggatgtaw cgrattttatg c

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(2) INFORMATION FOR SEQ ID NO:1785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1570952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1785:

Phe Leu Ser Thr Ile Phe Val Ser Glu Leu Phe Phe Leu Ile Ser Phe  
1 5 10 15  
Val Arg Leu Glu Pro Asn Met Ala Ser Leu Gly His Ile Ala Arg Glu  
20 25 30  
Ser Ser Asp Ile Thr Arg Leu Ala Gln Phe Tyr Lys Glu Val Phe Gly  
35 40 45  
Phe Glu Glu Ile Glu Ser Pro Asp Phe Gly Asp Leu Lys Val Val Trp  
50 55 60  
Leu Asn Leu Pro Gly Ala Phe Ala Met His Ile Gln Arg Asn Pro  
65 70 75 80  
Ser Thr Asn Leu Pro Glu Gly Pro Tyr Ser Ala Thr Ser Ala Val Lys  
85 90 95

Asp Pro Ser His Leu Pro Met Gly His His Ile Cys Phe Ser Val Pro  
100 105 110  
Asn Phe Asp Ser Phe Leu His Ser Leu Lys Glu Lys Gly Ile Glu Thr  
115 120 125  
Phe Gln Lys Ser Leu Pro Asp Gly Lys Val Lys Gln Val Phe Phe Phe  
130 135 140  
Asp Pro Asp Gly Asn Gly Leu Glu Val Ala Ser Arg Ser  
145 150 155

(2) INFORMATION FOR SEQ ID NO:1786:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1570953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1786:

Met Ala Ser Leu Gly His Ile Ala Arg Glu Ser Ser Asp Ile Thr Arg  
1 5 10 15  
Leu Ala Gln Phe Tyr Lys Glu Val Phe Gly Phe Glu Glu Ile Glu Ser  
20 25 30  
Pro Asp Phe Gly Asp Leu Lys Val Val Trp Leu Asn Leu Pro Gly Ala  
35 40 45  
Phe Ala Met His Ile Ile Gln Arg Asn Pro Ser Thr Asn Leu Pro Glu  
50 55 60  
Gly Pro Tyr Ser Ala Thr Ser Ala Val Lys Asp Pro Ser His Leu Pro  
65 70 75 80  
Met Gly His His Ile Cys Phe Ser Val Pro Asn Phe Asp Ser Phe Leu  
85 90 95  
His Ser Leu Lys Glu Lys Gly Ile Glu Thr Phe Gln Lys Ser Leu Pro  
100 105 110  
Asp Gly Lys Val Lys Gln Val Phe Phe Phe Asp Pro Asp Gly Asn Gly  
115 120 125  
Leu Glu Val Ala Ser Arg Ser  
130 135

(2) INFORMATION FOR SEQ ID NO:1787:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1570954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1787:

Met His Ile Ile Gln Arg Asn Pro Ser Thr Asn Leu Pro Glu Gly Pro  
1 5 10 15  
Tyr Ser Ala Thr Ser Ala Val Lys Asp Pro Ser His Leu Pro Met Gly  
20 25 30  
His His Ile Cys Phe Ser Val Pro Asn Phe Asp Ser Phe Leu His Ser  
35 40 45  
Leu Lys Glu Lys Gly Ile Glu Thr Phe Gln Lys Ser Leu Pro Asp Gly  
50 55 60  
Lys Val Lys Gln Val Phe Phe Phe Asp Pro Asp Gly Asn Gly Leu Glu  
65 70 75 80  
Val Ala Ser Arg Ser

85

(2) INFORMATION FOR SEQ ID NO:1788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1092
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1788:

```
aacttttggc gagaaaaatca gagacagaag aagaagaaaaa gcaaaaaaaa gcaaaacatg 60
aaggcgacga cgaagactcc gatccacgtg gtgtgggtcat gggttaggag acaacctccg 120
aaggtgaagg cttttctcgc cgtgggtcact ggcattggcg ctttggttct tctcagattc 180
attgttaacg atcacgacaa tctcttcgtt gccgctgagg ctgttcattc catcgggatc 240
tgtgtgtcta tctacaaact catgaaggag aagacctgtg ccggattgtc actgaaatct 300
caggagctta cggcgatat tttagctgtt aggcgtgtatt gtacgattgt aatggaatat 360
gatatacata ccaattcttga cttggctact ttgggaacaa ctctctgggt tatatttatg 420
attcgttttca agttaagagc tagttacatg gaggacaaaag acaactttcc tctctattat 480
gtgcttggcg cctgtgttgc attagctgtg ttcattccat catcgacctc tcataacata 540
ataaacagaa ttctcatgggc tttatgtgta taacctgaag ctgtttcagt actacctcag 600
ctacgagtga tgcagaacac aaagattgtt gaacctgtca cggctcatta tgtttttgca 660
cttggagtag caaggttccct cagctgtgcc cactgggttt tacaggttgt ggacacgcgg 720
ggacgggttc ttgtagcatt gggttatgga ttgtggccat caatggttct gatctcagaa 780
attgttcaaa ctttcatctt gccagatttc tgttactact acgtcaaaa gcttttcgga 840
ggccagctgt tctctcggct accgtctgga gtagNtataa gttcaaaaaga tagaaatact 900
ccaacagatg cctgcgatga gcttgacgga aattctaatt gggaaagata gctcaatttt 960
tctttacctc tgatttcatc gtttatgtgt cttgagggtt ccccaagagt ctcggttaacg 1020
aattaatttt acagtgttgt atatittgcc tatcaaggga tttaacgtct ttcagggtcga 1080
taagttatct tt
```

(2) INFORMATION FOR SEQ ID NO:1789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..316
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1789:

```
Asn Phe Cys Arg Glu Asn Gln Arg Gln Lys Lys Lys Ser Glu Lys
1 5 10 15
Lys Gln Asn Met Lys Ala Thr Thr Lys Thr Pro Ile His Val Val Trp
 20 25 30
Ser Trp Val Arg Arg Gln Pro Lys Val Lys Ala Phe Leu Ala Val
 35 40 45
Val Thr Gly Met Ala Ala Leu Val Leu Leu Arg Phe Ile Val His Asp
 50 55 60
His Asp Asn Leu Phe Val Ala Ala Glu Ala Val His Ser Ile Gly Ile
 65 70 75 80
Cys Val Leu Ile Tyr Lys Leu Met Lys Glu Lys Thr Cys Ala Gly Leu
 85 90 95
Ser Leu Lys Ser Gln Glu Leu Thr Ala Ile Phe Leu Ala Val Arg Leu
 100 105 110
Tyr Cys Ser Ile Val Met Glu Tyr Asp Ile His Thr Ile Leu Asp Leu
 115 120 125
Ala Thr Leu Gly Thr Thr Leu Trp Val Ile Phe Met Ile Arg Phe Lys
```

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 130                                                             | 135 | 140 |
| Leu Arg Ala Ser Tyr Met Glu Asp Lys Asp Asn Phe Pro Leu Tyr Tyr |     |     |
| 145                                                             | 150 | 155 |
| Val Leu Ala Pro Cys Val Ala Leu Ala Val Phe Ile His Pro Ser Thr |     | 160 |
|                                                                 | 165 | 170 |
| Ser His Asn Ile Ile Asn Arg Ile Ser Trp Ala Leu Cys Val Tyr Leu |     | 175 |
|                                                                 | 180 | 185 |
| Glu Ala Val Ser Val Leu Pro Gln Leu Arg Val Met Gln Asn Thr Lys |     | 190 |
|                                                                 | 195 | 200 |
| Ile Val Glu Pro Phe Thr Ala His Tyr Val Phe Ala Leu Gly Val Ala |     | 205 |
|                                                                 | 210 | 215 |
| Arg Phe Leu Ser Cys Ala His Trp Val Leu Gln Val Val Asp Thr Arg |     | 220 |
| 225                                                             | 230 | 235 |
| Gly Arg Leu Leu Val Ala Leu Gly Tyr Gly Leu Trp Pro Ser Met Val |     | 240 |
|                                                                 | 245 | 250 |
| Leu Ile Ser Glu Ile Val Gln Thr Phe Ile Leu Ala Asp Phe Cys Tyr |     | 255 |
|                                                                 | 260 | 265 |
| Tyr Tyr Val Lys Ser Val Phe Gly Gly Gln Leu Val Leu Arg Leu Pro |     | 270 |
|                                                                 | 275 | 280 |
| Ser Gly Val Xaa Ile Ser Ser Lys Asp Arg Asn Thr Pro Thr Met Ser |     | 285 |
|                                                                 | 290 | 295 |
| Cys Asp Glu Leu Asp Gly Asn Ser Asn Trp Glu Arg                 |     | 300 |
| 305                                                             | 310 | 315 |

(2) INFORMATION FOR SEQ ID NO:1790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..297

(D) OTHER INFORMATION: / Ceres Seq. ID 1570976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1790:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Lys Ala Thr Thr Lys Thr Pro Ile His Val Val Trp Ser Trp Val |     |
| 1                                                               | 5   |
| Arg Arg Gln Pro Pro Lys Val Lys Ala Phe Leu Ala Val Val Thr Gly |     |
|                                                                 | 20  |
| Met Ala Ala Leu Val Leu Leu Arg Phe Ile Val His Asp His Asp Asn |     |
|                                                                 | 35  |
| Leu Phe Val Ala Ala Glu Ala Val His Ser Ile Gly Ile Cys Val Leu |     |
| 50                                                              | 55  |
| Ile Tyr Lys Leu Met Lys Glu Lys Thr Cys Ala Gly Leu Ser Leu Lys |     |
| 65                                                              | 70  |
| Ser Gln Glu Leu Thr Ala Ile Phe Leu Ala Val Arg Leu Tyr Cys Ser |     |
|                                                                 | 85  |
| Ile Val Met Glu Tyr Asp Ile His Thr Ile Leu Asp Leu Ala Thr Leu |     |
|                                                                 | 100 |
| Gly Thr Thr Leu Trp Val Ile Phe Met Ile Arg Phe Lys Leu Arg Ala |     |
|                                                                 | 115 |
| Ser Tyr Met Glu Asp Lys Asp Asn Phe Pro Leu Tyr Trp Val Leu Ala |     |
|                                                                 | 130 |
| Pro Cys Val Ala Leu Ala Val Phe Ile His Pro Ser Thr Ser His Asn |     |
| 145                                                             | 150 |
| Ile Ile Asn Arg Ile Ser Trp Ala Leu Cys Val Tyr Leu Glu Ala Val |     |
|                                                                 | 165 |
| Ser Val Leu Pro Gln Leu Arg Val Met Gln Asn Thr Lys Ile Val Glu |     |
|                                                                 | 180 |
| Pro Phe Thr Ala His Tyr Val Phe Ala Leu Gly Val Ala Arg Phe Leu |     |
|                                                                 | 195 |
|                                                                 | 200 |
|                                                                 | 205 |



Ser Cys Ala His Trp Val Leu Gln Val Val Asp Thr Arg Gly Arg Leu  
210 215 220  
Leu Val Ala Leu Gly Tyr Gly Leu Trp Pro Ser Met Val Leu Ile Ser  
225 230 235 240  
Glu Ile Val Gln Thr Phe Ile Leu Ala Asp Phe Cys Tyr Tyr Tyr Val  
245 250 255  
Lys Ser Val Phe Gly Gly Gln Leu Val Leu Arg Leu Pro Ser Gly Val  
260 265 270  
Xaa Ile Ser Ser Lys Asp Arg Asn Thr Pro Thr Met Ser Cys Asp Glu  
275 280 285  
Leu Asp Gly Asn Ser Asn Trp Glu Arg  
290 295

(2) INFORMATION FOR SEQ ID NO:1791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..265
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1791:

Met Ala Ala Leu Val Leu Leu Arg Phe Ile Val His Asp His Asp Asn  
1 5 10 15  
Leu Phe Val Ala Ala Glu Ala Val His Ser Ile Gly Ile Cys Val Leu  
20 25 30  
Ile Tyr Lys Leu Met Lys Glu Lys Thr Cys Ala Gly Leu Ser Leu Lys  
35 40 45  
Ser Gln Glu Leu Thr Ala Ile Phe Leu Ala Val Arg Leu Tyr Cys Ser  
50 55 60  
Ile Val Met Glu Tyr Asp Ile His Thr Ile Leu Asp Leu Ala Thr Leu  
65 70 75 80  
Gly Thr Thr Leu Trp Val Ile Phe Met Ile Arg Phe Lys Leu Arg Ala  
85 90 95  
Ser Tyr Met Glu Asp Lys Asp Asn Phe Pro Leu Tyr Tyr Val Leu Ala  
100 105 110  
Pro Cys Val Ala Leu Ala Val Phe Ile His Pro Ser Thr Ser His Asn  
115 120 125  
Ile Ile Asn Arg Ile Ser Trp Ala Leu Cys Val Tyr Leu Glu Ala Val  
130 135 140  
Ser Val Leu Pro Gln Leu Arg Val Met Gln Asn Thr Lys Ile Val Glu  
145 150 155 160  
Pro Phe Thr Ala His Tyr Val Phe Ala Leu Gly Val Ala Arg Phe Leu  
165 170 175  
Ser Cys Ala His Trp Val Leu Gln Val Val Asp Thr Arg Gly Arg Leu  
180 185 190  
Leu Val Ala Leu Gly Tyr Gly Leu Trp Pro Ser Met Val Leu Ile Ser  
195 200 205  
Glu Ile Val Gln Thr Phe Ile Leu Ala Asp Phe Cys Tyr Tyr Tyr Val  
210 215 220  
Lys Ser Val Phe Gly Gly Gln Leu Val Leu Arg Leu Pro Ser Gly Val  
225 230 235 240  
Xaa Ile Ser Ser Lys Asp Arg Asn Thr Pro Thr Met Ser Cys Asp Glu  
245 250 255  
Leu Asp Gly Asn Ser Asn Trp Glu Arg  
260 265

(2) INFORMATION FOR SEQ ID NO:1792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1710 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..1710  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1792:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| tatcaagaat  | ttggacgagt  | coatcgacca  | caaagcactg  | catgatactt  | tttcatcggt  | 60   |
| ttggaacatt  | gtgtcgtgca  | aggtagctgt  | cgattcttca  | ggccagtcac  | aaggctatgg  | 120  |
| gtttgtgcga  | tacgccaatt  | aagaatctgc  | ccagaaagct  | atagagaaac  | tgaacggcatc | 180  |
| gttgctcaat  | gacaagcaag  | tgtatgtggg  | tcctttcctg  | aggagacaag  | aaagagacttc | 240  |
| cactgctaac  | aaaacgaat   | tcaccaatgt  | gtatgtgaag  | aatctcggcg  | aaagtaactac | 300  |
| cgatgatgac  | ttgaagaatg  | cttttggcga  | gtatggaaag  | ataacaagtg  | ctgtcgtgat  | 360  |
| gaaagatgga  | gaagggaagt  | ccaagggtct  | tgggtttgtc  | aactttgaaa  | atgctgatga  | 420  |
| tgctcgtagg  | gctgtggagt  | ctctcaatgg  | gcacaaatct  | gatgataagg  | agtggatagt  | 480  |
| tggtagagcc  | cagaagaagt  | cagagaggga  | aacakaacta  | agggtccggt  | atgaacagaa  | 540  |
| tttgaaggaa  | gctgcagaca  | agtttaaaag  | ttcaaacctg  | tatgttaaga  | atttggatcc  | 600  |
| tagcatctca  | gagagaagac  | tttaagagat  | ctttctctct  | tttggtaacc  | ttacatctag  | 660  |
| caaggtgatg  | cgggatccta  | atggaacaa   | caaaggctca  | ggttttgttg  | ctttcgcaac  | 720  |
| tcocgaagaa  | gcaactgaag  | ctatgtcaca  | gttgagcggt  | aaaatgatcg  | aaagcaagcc  | 780  |
| actctatgtg  | gctattgcac  | agcgggaagg  | agacagaagg  | ctcagactac  | aggctcagtt  | 840  |
| ttcccaagtg  | aggccagttg  | caatgcagcc  | gtctgttggg  | cccccgcagc  | cagtttatcc  | 900  |
| cccggtgtgt  | ctcgttatgt  | gacaaacaa   | gttctatgtg  | caggcccccct | ctgcaatgat  | 960  |
| tcctcccgag  | cctgggttatg | gataccaaca  | gcagcttggg  | ccctggaatga | gaactgggtgg | 1020 |
| gggtcctgtga | cccagtttct  | tcagtgcctat | gggttcagcca | cagcagcagc  | gtcctggagg  | 1080 |
| aggaagacgt  | cctgggggaa  | tcacaacact  | ccagcagcga  | aatcccatga  | tcagcacaaca | 1140 |
| gatgcaccca  | aggggtcgga  | tgttcocgta  | tcoccaaagg  | cgtggttgta  | gtgggtgatgt | 1200 |
| gcctccatcat | gatattggca  | acaaactgcc  | attgactatt  | ggagctttgg  | cttcaaatct  | 1260 |
| gtctaatgct  | actccagagc  | aacagaggac  | gatgctgggt  | gaggtgctgt  | accctgttgg  | 1320 |
| ggagcagagt  | gaggcagagt  | ctgcagccaa  | agtgaactgg  | atgcttttgg  | agatggacca  | 1380 |
| gactgaagtg  | ctccatctgt  | tggagtcaac  | agaagctctc  | aaggccaaag  | ttgcagaggg  | 1440 |
| tatggatggt  | ctcaggagtg  | tcgctgctgg  | tgctgcaaac  | gagcagctcg  | cttccttgaa  | 1500 |
| ctctctctaa  | attgcttttt  | atcatttgat  | ctttggcttt  | tgctctctcc  | atacaattgg  | 1560 |
| agttgtttct  | ttgtctattg  | ttttctccct  | gggaatttgg  | attcctccac  | ataaCtggct  | 1620 |
| ttgtgtttat  | ttaaaccttc  | gtttttaaac  | cacaaaggaa  | aaacctatct  | gctttgttct  | 1680 |
| tttgatttag  | ttgcgtgttc  | tacgttgttc  |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1793:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..502  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1793:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Lys | Asn | Leu | Asp | Glu | Ser | Ile | Asp | His | Lys | Ala | Leu | His | Asp | Thr |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Phe | Ser | Ser | Phe | Gly | Asn | Ile | Val | Ser | Cys | Lys | Val | Ala | Val | Asp | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Gly | Gln | Ser | Lys | Gly | Tyr | Gly | Phe | Val | Gln | Tyr | Ala | Asn | Glu | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Ser | Ala | Gln | Lys | Ala | Ile | Glu | Lys | Leu | Asn | Gly | Met | Leu | Leu | Asn | Asp |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Lys | Gln | Val | Tyr | Val | Gly | Pro | Phe | Leu | Arg | Arg | Gln | Glu | Arg | Asp | Ser |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     | 80  |     |     |
| Thr | Ala | Asn | Lys | Thr | Lys | Phe | Thr | Asn | Val | Tyr | Val | Lys | Asn | Leu | Ala |

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1.443

(D) OTHER INFORMATION: / Ceres Seq. ID 1571000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1794:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Leu | Asn | Asp | Lys | Gln | Val | Tyr | Val | Gly | Pro | Phe | Leu | Arg | Arg |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Glu | Arg | Asp | Ser | Thr | Ala | Asn | Lys | Thr | Lys | Phe | Thr | Asn | Val | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Lys | Asn | Leu | Ala | Glu | Ser | Thr | Asp | Asp | Asp | Leu | Lys | Asn | Ala |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Phe | Gly | Glu | Tyr | Gly | Lys | Ile | Thr | Ser | Ala | Val | Val | Met | Lys | Asp | Gly |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Gly | Lys | Ser | Lys | Gly | Phe | Gly | Phe | Val | Asn | Phe | Glu | Asn | Ala | Asp |
|     |     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Ala | Ala | Arg | Ala | Val | Glu | Ser | Leu | Asn | Gly | His | Lys | Phe | Asp | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Glu | Trp | Tyr | Val | Gly | Arg | Ala | Gln | Lys | Lys | Ser | Glu | Arg | Glu | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Xaa | Leu | Arg | Val | Arg | Tyr | Glu | Gln | Asn | Leu | Lys | Glu | Ala | Ala | Asp | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Lys | Ser | Ser | Asn | Leu | Tyr | Val | Lys | Asn | Leu | Asp | Pro | Ser | Ile | Ser |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Asp | Glu | Lys | Leu | Lys | Glu | Ile | Phe | Ser | Pro | Phe | Gly | Thr | Val | Thr | Ser |
|     |     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Lys | Val | Met | Arg | Asp | Pro | Asn | Gly | Thr | Ser | Lys | Gly | Ser | Gly | Phe |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Ala | Phe | Ala | Thr | Pro | Glu | Glu | Ala | Thr | Glu | Ala | Met | Ser | Gln | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Gly | Lys | Met | Ile | Glu | Ser | Lys | Pro | Leu | Tyr | Val | Ala | Ile | Ala | Gln |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Lys | Glu | Asp | Arg | Arg | Val | Arg | Leu | Gln | Ala | Gln | Phe | Ser | Gln | Val |
|     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Arg | Pro | Val | Ala | Met | Gln | Pro | Ser | Val | Gly | Pro | Arg | Met | Pro | Val | Tyr |
|     |     | 225 |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Pro | Pro | Gly | Gly | Pro | Gly | Ile | Gly | Gln | Gln | Met | Phe | Tyr | Gly | Gln | Ala |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Pro | Ala | Met | Ile | Pro | Pro | Gln | Pro | Gly | Tyr | Gly | Tyr | Gln | Gln | Gln |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Leu | Val | Pro | Gly | Met | Arg | Pro | Gly | Gly | Gly | Pro | Val | Pro | Ser | Phe | Phe |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Met | Pro | Met | Val | Gln | Pro | Gln | Gln | Gln | Arg | Pro | Gly | Gly | Gly | Arg | Arg |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Pro | Gly | Gly | Ile | Gln | His | Ser | Gln | Gln | Gln | Asn | Pro | Met | Met | Gln | Gln |
|     |     |     | 310 |     |     |     |     |     |     | 315 |     |     |     | 320 |     |
| Gln | Met | His | Pro | Arg | Gly | Arg | Met | Phe | Arg | Tyr | Pro | Gln | Gly | Arg | Gly |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Gly | Ser | Gly | Asp | Val | Pro | Pro | Tyr | Asp | Met | Gly | Asn | Asn | Met | Pro | Leu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Thr | Ile | Gly | Ala | Leu | Ala | Ser | Asn | Leu | Ser | Asn | Ala | Thr | Pro | Glu | Gln |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Gln | Arg | Thr | Met | Leu | Gly | Glu | Val | Leu | Tyr | Pro | Leu | Val | Glu | Gln | Val |
|     |     | 370 |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |
| Glu | Ala | Glu | Ser | Ala | Ala | Lys | Val | Thr | Gly | Met | Leu | Leu | Glu | Met | Asp |
|     |     | 385 |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |     |
| Gln | Thr | Glu | Val | Leu | His | Leu | Leu | Glu | Ser | Pro | Glu | Ala | Leu | Lys | Ala |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Lys | Val | Ala | Glu | Ala | Met | Asp | Val | Leu | Arg | Ser | Val | Ala | Ala | Gly | Ala |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Ala | Thr | Glu | Gln | Leu | Ala | Ser | Leu | Asn | Leu | Ser |     |     |     |     |     |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1795:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 383 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:  
 (A) NAME/KEY: peptide  
 (B) LOCATION: 1..383  
 (D) OTHER INFORMATION: / Ceres Seq. ID 1571001  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1795:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Asp | Gly | Glu | Gly | Lys | Ser | Lys | Gly | Phe | Val | Asn | Phe |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Glu | Asn | Ala | Asp | Asp | Ala | Ala | Arg | Ala | Val | Glu | Ser | Leu | Asn |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  | Gly |
| Lys | Phe | Asp | Asp | Lys | Glu | Trp | Tyr | Val | Gly | Arg | Ala | Gln | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  | Lys |
| Glu | Arg | Glu | Thr | Xaa | Leu | Arg | Val | Arg | Tyr | Glu | Gln | Asn | Leu |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     | Lys |
| Ala | Ala | Asp | Lys | Phe | Lys | Ser | Ser | Asn | Leu | Tyr | Val | Lys | Asn |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |
| Pro | Ser | Ile | Ser | Asp | Glu | Lys | Leu | Lys | Glu | Ile | Phe | Ser | Pro |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | Phe |
| Thr | Val | Thr | Ser | Ser | Lys | Val | Met | Arg | Asp | Pro | Asn | Gly | Thr |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 | Ser |
| Gly | Ser | Gly | Phe | Val | Ala | Phe | Ala | Thr | Pro | Glu | Glu | Ala | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 | Glu |
| Met | Ser | Gln | Leu | Ser | Gly | Lys | Met | Ile | Glu | Ser | Lys | Pro | Leu |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     | Tyr |
| Ala | Ile | Ala | Gln | Arg | Lys | Glu | Asp | Arg | Arg | Val | Arg | Leu | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     | 160 |
| Phe | Ser | Gln | Val | Arg | Pro | Val | Ala | Met | Gln | Pro | Ser | Val | Gly |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |
| Met | Pro | Val | Tyr | Pro | Pro | Gly | Gly | Pro | Gly | Ile | Gly | Gln | Met |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 | Phe |
| Tyr | Gly | Gln | Ala | Pro | Pro | Ala | Met | Ile | Pro | Pro | Gln | Pro | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 | Tyr |
| Tyr | Gln | Gln | Gln | Leu | Val | Pro | Gly | Met | Arg | Pro | Gly | Gly | Pro |
|     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 | Val |
| Pro | Ser | Phe | Phe | Met | Pro | Met | Val | Gln | Pro | Gln | Gln | Gln | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     | 240 |
| Gly | Gly | Arg | Arg | Pro | Gly | Gly | Ile | Gln | His | Ser | Gln | Gln | Gln |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     | 255 |
| Met | Met | Gln | Gln | Gln | Met | His | Pro | Arg | Gly | Arg | Met | Phe | Arg |
|     |     |     | 260 |     |     |     |     |     | 265 |     |     |     | 270 |
| Gln | Gly | Arg | Gly | Gly | Ser | Gly | Asp | Val | Pro | Pro | Tyr | Asp | Met |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 | Gly |
| Asn | Met | Pro | Leu | Thr | Ile | Gly | Ala | Leu | Ala | Ser | Asn | Leu | Ser |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     | Asn |
| Thr | Pro | Glu | Gln | Gln | Arg | Thr | Met | Leu | Gly | Glu | Val | Leu | Tyr |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     | 320 |
| Val | Glu | Gln | Val | Glu | Ala | Glu | Ser | Ala | Ala | Lys | Val | Thr | Gly |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     | 335 |
| Leu | Glu | Met | Asp | Gln | Thr | Glu | Val | Leu | His | Leu | Leu | Glu | Ser |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 | Pro |
| Ala | Leu | Lys | Ala | Lys | Val | Ala | Glu | Ala | Met | Asp | Val | Leu | Arg |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 | Ser |
| Ala | Ala | Gly | Ala | Ala | Thr | Glu | Gln | Leu | Ala | Ser | Leu | Asn | Leu |
|     |     | 370 |     |     |     |     | 375 |     |     |     |     |     | Ser |

- (2) INFORMATION FOR SEQ ID NO:1796:  
 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..862

(D) OTHER INFORMATION: / Ceres Seq. ID 1571014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1796:

|             |            |             |            |             |            |     |
|-------------|------------|-------------|------------|-------------|------------|-----|
| agttttctctt | tacttccctc | tttctctgag  | ctatggagat | tactgtaac   | gctttctcct | 60  |
| caatcgatga  | aggaattgga | agttgggata  | tcaaaacggg | gacagagcag  | cttcaattca | 120 |
| agccgtgtgc  | ttctccggcg | catgggtctca | ccgcgcgtcg | caaaaaattc  | tcgcctctct | 180 |
| tcagctctcg  | gcgagaaata | cttctggctc  | gattttttac | tggtcttgga  | ctaagcctca | 240 |
| agctgaagt   | aagagctacc | cagtggaaac  | aataaaggct | cttgacagca  | acaatgaagg | 300 |
| aacttattta  | gttgggtggg | gaatctctgg  | agatatttac | ctttggggag  | ttgcgactgg | 360 |
| gaagttgctt  | aagaagtggc | atgggttcaag | gcgggttcac | agatcttcag  | cgacggagga | 420 |
| ttggactact  | tgggcaaccc | gagcttggtc  | cacgctcaga | gcattcttag  | catttgggct | 480 |
| actcaagtta  | ttctcatggg | agctgttgaa  | ggctacagag | tcgcccggag  | tggtccattg | 540 |
| ggagaaacag  | aggacttgct | ttaccacagg  | ggcagcttcg | acccattggg  | cctcgctact | 600 |
| gaccccagg   | ctttcgacga | gttgaagggt  | aaggagctca | agaacgggaag | gttggctatg | 660 |
| ttctctatgt  | ttggattctt | cggtcaagcc  | atcgtcaccc | gaaagggacc  | tttggagaac | 720 |
| ctcgccgacc  | atttgccgga | cccagtcac   | aacaacgctt | gggccttcgc  | caccaacttc | 780 |
| gtccccggaa  | agtgagcgcc | tgcttattat  | gtgaatgaga | gcagagaaag  | agagtttggt | 840 |
| tgtygtctat  | tctatgtaaa | ac          |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:1797:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1571015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1797:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ile | Thr | Val | Ile | Ala | Ser | Ser | Ser | Ile | Asp | Glu | Gly | Ile | Gly |
| 1   |     |     | 5   |     |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Ser | Trp | Asp | Leu | Lys | Thr | Gly | Thr | Gly | Gln | Leu | Gln | Phe | Lys | Pro | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ser | Pro | Ala | His | Gly | Leu | Thr | Ala | Val | Gly | Lys | Asn | Phe | Ser | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Leu | Ser | Ser | Arg | Arg | Glu | Ile | Leu | Leu | Ala | Arg | Phe | Phe | Thr | Gly |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Gly | Leu | Ser | Leu | Lys | Leu | Lys |     |     |     |     |     |     |     |     |
|     |     | 65  |     |     |     | 70  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1798:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..55

(D) OTHER INFORMATION: / Ceres Seq. ID 1571016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1798:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Glu | Leu | Glu | Val | Gly | Ile | Ser | Lys | Pro | Gly | Gln | Ser | Ser | Phe |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |

Asn Ser Ser Arg Val Leu Leu Arg Arg Met Val Ser Pro Pro Ser Ala  
20 25 30  
Lys Ile Ser Arg Leu Leu Ser Ala Leu Gly Glu Lys Tyr Phe Trp Leu  
35 40 45  
Asp Phe Leu Leu Val Leu Asp  
50 55

(2) INFORMATION FOR SEQ ID NO:1799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1571017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1799:

Met Gly Ala Val Glu Gly Tyr Arg Val Ala Gly Asp Gly Pro Leu Gly  
1 5 10 15  
Glu Ala Glu Asp Leu Leu Tyr Pro Gly Gly Ser Phe Asp Pro Leu Gly  
20 25 30  
Leu Ala Thr Asp Pro Glu Ala Phe Ala Glu Leu Lys Val Lys Glu Leu  
35 40 45  
Lys Asn Gly Arg Leu Ala Met Phe Ser Met Phe Gly Phe Phe Val Gln  
50 55 60  
Ala Ile Val Thr Gly Lys Gly Pro Leu Glu Asn Leu Ala Asp His Leu  
65 70 75 80  
Ala Asp Pro Val Asn Asn Asn Ala Trp Ala Phe Ala Thr Asn Phe Val  
85 90 95  
Pro Gly Lys

(2) INFORMATION FOR SEQ ID NO:1800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1244

(D) OTHER INFORMATION: / Ceres Seq. ID 1571021

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1800:

acaSRcatat acattcacat tactaatctc tcaagatttc acaattttct tgtgattttc 60  
tctcagtttc ttatttctgt tcataacatg gatgccatga gtacgctaga cgagagctct 120  
acaaactacag attccattcc ggcgagaaag tcatcgcttc cggcgagttt actatataga 180  
atgggaagcgt gaacaagcgt ggtacttgat tcagagaacg gtgtcgaagt cgaagtgcga 240  
gccgaatcaa gaagacttcc ttcttcaaga ttcaaaagtg ttgttcccta accaaatgga 300  
agatggggag ctacagattta cgagaaaacat caacgcgtgt ggcttggtag ttccaacgag 360  
gaagaacgaag cagctcgctgc ttacgcgctc gcggctcacc gtttccgtgg ccgcgatgcc 420  
gttactaatt tcaaaagacac gaaggttcgaa gaagaggttg agttctttaa ttccgatgtg 480  
aaatcagaga tcgtagatat gttgagaaaa cacacttaca aagaagagtt agaccaaaagg 540  
aaacgtacac gtgacggttaa cggaaaagag acgacggcgt ttgctttggc ttgatgggtg 600  
gttatgacgg ggttttaaac ggccgagttta ctgtttgaga aaacggtaac gccaaagtac 660  
gtcgggaaac taaacccgtt agttatacca aaacaccaag cggagaaaaa ttttccgcta 720  
ccgttaggta ataataacgt tcccgattaa ggtatgctgt tgaatttoga agacgttaac 780  
gggaaagtgt ggaggtttccg ttactcttat tggaatagta gtcaaatgta tgtgttgacg 840  
aaaggttggg gtatgattcgt taaagagaag agactttgtg ctggtgattt gatcagtttt 900  
aaaagatcca acgatcaaga tcaaaaattc tttatcgggt ggaaatcgaa atccgggttg 960  
gatctagaga cgggtcgggt tatgagattt tttgggggtg atatttcttt aaacgccgtc 1020

gttgtagtga aggaacaac ggaggtgtta atgtcgtcgt taaggtgttaa gaatacaacga 1080  
gttttgaat aacaatttaa caacttggga aagaaaaaaa aagctttttg attttaattt 1140  
ctcttcaacg ttaattcttg tgagattatt tatgtgttaa gttgtaacaa gtggaaaaaa 1200  
ttaattaggt gtcaacaaa tcttgtgtta atattctttg tatg

(2) INFORMATION FOR SEQ ID NO:1801:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..362

(D) OTHER INFORMATION: / Ceres Seq. ID 1571022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1801:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Xaa | Ile | Tyr | Ile | His | Ile | Thr | Asn | Leu | Ser | Arg | Phe | His | Asn | Phe |
| 1   |     |     |     | 5   |     |     |     |     |     |     |     |     |     | 10  | 15  |
| Leu | Val | Ile | Phe | Ser | Gln | Phe | Leu | Ile | Ser | Phe | His | Asn | Met | Asp | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Ser | Ser | Val | Asp | Glu | Ser | Ser | Thr | Thr | Asp | Ser | Ile | Pro | Ala |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Arg | Lys | Ser | Ser | Ser | Pro | Ala | Ser | Leu | Leu | Tyr | Arg | Met | Gly | Ser | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Ser | Val | Val | Leu | Asp | Ser | Glu | Asn | Gly | Val | Glu | Val | Glu | Val | Glu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| Ala | Glu | Ser | Arg | Lys | Leu | Pro | Ser | Ser | Arg | Phe | Lys | Gly | Val | Val | Pro |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Gln | Pro | Asn | Gly | Arg | Trp | Gly | Ala | Gln | Ile | Tyr | Glu | Lys | His | Gln | Arg |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Val | Trp | Leu | Gly | Thr | Phe | Asn | Glu | Glu | Asp | Glu | Ala | Ala | Arg | Ala | Tyr |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Asp | Val | Ala | Ala | His | Arg | Phe | Arg | Gly | Arg | Asp | Ala | Val | Thr | Asn | Phe |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Lys | Asp | Thr | Thr | Phe | Glu | Glu | Glu | Val | Glu | Phe | Leu | Asn | Ala | His | Ser |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Lys | Ser | Glu | Ile | Val | Asp | Met | Leu | Arg | Lys | His | Thr | Tyr | Lys | Glu | Glu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Asp | Gln | Arg | Lys | Arg | Asn | Arg | Asp | Gly | Asn | Gly | Lys | Glu | Thr | Thr |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ala | Phe | Ala | Leu | Ala | Ser | Met | Val | Val | Met | Thr | Gly | Phe | Lys | Thr | Ala |
|     |     |     | 195 |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Glu | Leu | Leu | Phe | Glu | Lys | Thr | Val | Thr | Pro | Ser | Asp | Val | Gly | Lys | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asn | Arg | Leu | Val | Ile | Pro | Lys | His | Gln | Ala | Glu | Lys | His | Phe | Pro | Leu |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Pro | Leu | Gly | Asn | Asn | Asn | Val | Ser | Val | Lys | Gly | Met | Leu | Leu | Asn | Phe |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Asp | Val | Asn | Gly | Lys | Val | Trp | Arg | Phe | Arg | Tyr | Ser | Tyr | Trp | Asn |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Ser | Ser | Gln | Ser | Tyr | Val | Leu | Thr | Lys | Gly | Trp | Ser | Arg | Phe | Val | Lys |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Glu | Lys | Arg | Leu | Cys | Ala | Gly | Asp | Leu | Ile | Ser | Phe | Lys | Arg | Ser | Asn |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asp | Gln | Asp | Gln | Lys | Phe | Phe | Ile | Gly | Trp | Lys | Ser | Lys | Ser | Gly | Leu |
|     | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Asp | Leu | Glu | Thr | Gly | Arg | Val | Met | Arg | Leu | Phe | Gly | Val | Asp | Ile | Ser |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Asn | Ala | Val | Val | Val | Lys | Glu | Thr | Thr | Glu | Val | Leu | Met | Ser |     |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Ser | Leu | Arg | Cys | Lys | Asn | Gln | Arg | Val | Leu |     |     |     |     |     |     |



355 360  
(2) INFORMATION FOR SEQ ID NO:1802:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 333 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..333  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571023  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1802:  
Met Asp Ala Met Ser Ser Val Asp Glu Ser Ser Thr Thr Thr Asp Ser  
1 5 10 15  
Ile Pro Ala Arg Lys Ser Ser Ser Pro Ala Ser Leu Leu Tyr Arg Met  
20 25 30  
Gly Ser Gly Thr Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Val  
35 40 45  
Glu Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Arg Phe Lys Gly  
50 55 60  
Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys  
65 70 75 80  
His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala  
85 90 95  
Arg Ala Tyr Asp Val Ala Ala His Arg Phe Arg Gly Arg Asp Ala Val  
100 105 110  
Thr Asn Phe Lys Asp Thr Thr Phe Glu Glu Val Glu Phe Leu Asn  
115 120 125  
Ala His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr  
130 135 140  
Lys Glu Glu Leu Asp Gln Arg Lys Arg Asn Asp Gly Asn Gly Lys  
145 150 155 160  
Glu Thr Thr Ala Phe Ala Leu Ala Ser Met Val Val Met Thr Gly Phe  
165 170 175  
Lys Thr Ala Glu Leu Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val  
180 185 190  
Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His Gln Ala Glu Lys His  
195 200 205  
Phe Pro Leu Pro Leu Gly Asn Asn Asn Val Ser Val Lys Gly Met Leu  
210 215 220  
Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg Phe Arg Tyr Ser  
225 230 235 240  
Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg  
245 250 255  
Phe Val Lys Glu Lys Arg Leu Cys Ala Gly Asp Leu Ile Ser Phe Lys  
260 265 270  
Arg Ser Asn Asp Gln Asp Gln Lys Phe Phe Ile Gly Trp Lys Ser Lys  
275 280 285  
Ser Gly Leu Asp Leu Glu Thr Gly Arg Val Met Arg Leu Phe Gly Val  
290 295 300  
Asp Ile Ser Leu Asn Ala Val Val Val Lys Glu Thr Thr Glu Val  
305 310 315 320  
Leu Met Ser Ser Leu Arg Cys Lys Asn Gln Arg Val Leu  
325 330

(2) INFORMATION FOR SEQ ID NO:1803:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 330 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..330  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571024  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1803:

```
Met Ser Ser Val Asp Glu Ser Ser Thr Thr Asp Ser Ile Pro Ala
1 5 10 15
Arg Lys Ser Ser Ser Pro Ala Ser Leu Leu Tyr Arg Met Gly Ser Gly
 20 25 30
Thr Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Val Glu Val Glu
 35 40 45
Ala Glu Ser Arg Lys Leu Pro Ser Ser Arg Phe Lys Gly Val Val Pro
 50 55 60
Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg
 65 70 75
Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala Arg Ala Tyr
 85 90 95
Asp Val Ala Ala His Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe
 100 105 110
Lys Asp Thr Thr Phe Glu Glu Glu Val Glu Phe Leu Asn Ala His Ser
 115 120 125
Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Lys Glu Glu
 130 135 140
Leu Asp Gln Arg Lys Arg Asn Arg Asp Gly Asn Gly Lys Glu Thr Thr
 145 150 155
Ala Phe Ala Leu Ala Ser Met Val Val Met Thr Gly Phe Lys Thr Ala
 165 170 175
Glu Leu Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu
 180 185 190
Asn Arg Leu Val Ile Pro Lys His Gln Ala Glu Lys His Phe Pro Leu
 195 200 205
Pro Leu Gly Asn Asn Asn Val Ser Val Lys Gly Met Leu Leu Asn Phe
 210 215 220
Glu Asp Val Asn Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn
 225 230 235
Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys
 245 250 255
Glu Lys Arg Leu Cys Ala Gly Asp Leu Ile Ser Phe Lys Arg Ser Asn
 260 265 270
Asp Gln Asp Gln Lys Phe Phe Ile Gly Trp Lys Ser Lys Ser Gly Leu
 275 280 285
Asp Leu Glu Thr Gly Arg Val Met Arg Leu Phe Gly Val Asp Ile Ser
 290 295 300
Leu Asn Ala Val Val Val Lys Glu Thr Thr Glu Val Leu Met Ser
 305 310 315
Ser Leu Arg Cys Lys Asn Gln Arg Val Leu
 325 330
```

(2) INFORMATION FOR SEQ ID NO:1804:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1140 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1140  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1804:

ctttctcaga ttctctcttt cccgagaaaa ttggaagaaa cagagattca tcattttctc

|             |             |            |            |            |            |      |
|-------------|-------------|------------|------------|------------|------------|------|
| ttctctcaca  | aatcagatc   | tgcaaaactc | tcagatcact | catgggttgg | atttcaaac  | 120  |
| ctaccggttt  | gattctcgtc  | gccaccatct | tcttctcgtt | ttcttcaatc | tcgggtcagg | 180  |
| attctcgtcgt | tqagaacaat  | gagagacaag | aatctgaagg | atctggtaaa | gagcttggtc | 240  |
| gtcgtggaat  | gggttggtact | gaacgaattg | gagttgtatc | tgttgtagac | aatattggtg | 300  |
| ctcttggttt  | gaactctagac | cttgatgcta | ctgctcctag | tgtatttgat | gctttgtttt | 360  |
| cgagtttctc  | gatgatactt  | gtcaccgaga | tgggggatga | aacttttata | atagcgcat  | 420  |
| tgtatggctat | gcgacatcct  | aaagctactg | ttttatctgg | tgcactctca | gctttgtttg | 480  |
| tkakgactat  | actGttctac  | tggacttggt | aggatagtgc | caaacttgat | atcgaggaa  | 540  |
| cacaccaata  | gtgctgtcac  | agtgcctat  | gcattttttg | gtttgagact | actctacatt | 600  |
| gcttgagggt  | ctactgattc  | aaagtcaaat | cagaagaaa  | aaatggagga | agttgaagag | 660  |
| aagctcgagt  | caggtcaagg  | gaagacaccc | ttccgtcgtt | tattctcaag | attttgtacc | 720  |
| ccaatatttc  | tggagtctct  | catcttaacc | ttctagctg  | aatggggtga | ccgtgaccag | 780  |
| atcgctacaa  | tagctttggc  | gactcacaag | aacgccaatg | gagtgccat  | tggggcaagt | 840  |
| attggacaca  | ctgtgtgtac  | ttcactagca | gttggtggag | gaagcatggt | ggcttcaagg | 900  |
| atctcgcaac  | gtacgggtcgc | aactgttgga | gcttactct  | tcttcggctt | ttcagttctc | 960  |
| tcctattttc  | atctccattt  | gtagttaagt | tgcttcttct | gaaaatgggt | gttagagaca | 1020 |
| atttctaagt  | aaagtttcaa  | tttttttttt | gattttaatt | taagtttgat | ttttgtttaa | 1080 |
| tatcaatggc  | caaatggccc  | aaaccaaa   | atccaacgcc | tatgctttta | caatttactt | 1140 |

(2) INFORMATION FOR SEQ ID NO:1805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1805:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Leu | Ile | Ser | Asn | Pro | Thr | Arg | Leu | Ile | Leu | Val | Ala | Thr | Ile |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Phe | Phe | Leu | Val | Ser | Ser | Ile | Ser | Gly | Gln | Asp | Ser | Val | Val | Glu | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Asn | Glu | Arg | Gln | Glu | Ser | Glu | Gly | Ser | Gly | Lys | Glu | Leu | Gly | Arg | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Met | Val | Gly | Thr | Glu | Arg | Ile | Gly | Val | Asp | Thr | Val | Val | Asp | Asn |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ile | Gly | Ala | Leu | Gly | Leu | Asn | Leu | Asp | Leu | Asp | Ala | Thr | Ala | Pro | Ser |
| 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Val | Phe | Asp | Ala | Leu | Phe | Ser | Ser | Phe | Ser | Met | Ile | Leu | Val | Thr | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ile | Gly | Asp | Glu | Thr | Phe | Ile | Ile | Ala | Ala | Leu | Met | Ala | Met | Arg | His |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Pro | Lys | Ala | Thr | Val | Leu | Ser | Gly | Ala | Leu | Ser | Ala | Leu | Phe | Xaa | Xaa |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     | 125 |     |
| Thr | Ile | Leu | Phe | Tyr | Trp | Thr | Trp |     |     |     |     |     |     |     |     |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1806:

Met Val Gly Thr Glu Arg Ile Gly Val Asp Thr Val Val Asp Asn Ile  
1 5 10 15  
Gly Ala Leu Gly Leu Asn Leu Asp Leu Asp Ala Thr Ala Pro Ser Val  
20 25 30  
Phe Asp Ala Leu Phe Ser Ser Phe Ser Met Ile Leu Val Thr Glu Ile  
35 40 45  
Gly Asp Glu Thr Phe Ile Ile Ala Ala Leu Met Ala Met Arg His Pro  
50 55 60  
Lys Ala Thr Val Leu Ser Gly Ala Leu Ser Ala Leu Phe Xaa Xaa Thr  
65 70 75 80  
Ile Leu Phe Tyr Trp Thr Trp  
85

(2) INFORMATION FOR SEQ ID NO:1807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1807:

Met Glu Glu Val Glu Glu Lys Leu Glu Ser Gly Gln Gly Lys Thr Pro  
1 5 10 15  
Phe Arg Arg Leu Phe Ser Arg Phe Cys Thr Pro Ile Phe Leu Glu Ser  
20 25 30  
Phe Ile Leu Thr Phe Leu Ala Glu Trp Gly Asp Arg Ser Gln Ile Ala  
35 40 45  
Thr Ile Ala Leu Ala Thr His Lys Asn Ala Ile Gly Val Ala Ile Gly  
50 55 60  
Ala Ser Ile Gly His Thr Val Cys Thr Ser Leu Ala Val Val Gly Gly  
65 70 75 80  
Ser Met Leu Ala Ser Arg Ile Ser Gln Arg Thr Val Ala Thr Val Gly  
85 90 95  
Gly Leu Leu Phe Leu Gly Phe Ser Val Ser Ser Tyr Phe Tyr Pro Pro  
100 105 110  
Leu

(2) INFORMATION FOR SEQ ID NO:1808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..782
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1808:

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| atcaaccacaa | acaaaacata  | aaaaacaagt | ggaagcttta | aaacgagagg | gagagagcaa  | 60  |
| aaatggcgac  | gtcgggaacg  | tacgtgacgg | aaagtccgct | aaaaggatcg | gccgagaaat  | 120 |
| actacaagag  | gtggaagaac  | gagaaccatg | tcttccctga | tgctatcgcg | caccacatcc  | 180 |
| aaaatgttac  | cgttcacgaa  | ggcgaacatg | actctcacgg | Gtctatcagg | agtttggaact | 240 |
| acacatggga  | tggaaaaggag | gaggtgttca | aggagagaag | agagatagac | gatgagacca  | 300 |
| aaacgttgac  | gttaagagga  | cttgagggtc | acgtgatgga | gcagctcaaa | gtgtacgacg  | 360 |
| tcgtctacca  | attcatctcc  | aaatctgagg | atacctgcac | cggcaaaaac | actttaatat  | 420 |
| gggagaagcg  | caacgatgat  | tccccagaac | caagcggcta | catgaaattc | gtcaagagct  | 480 |
| tggttgctga  | catgggaaac  | cacgttagca | aaacttaatc | atcattccca | cagtcgctcg  | 540 |

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| catcatcatc atcatcatca tcatcatcat catcatcatc atcatcatca tcatcatcat | 600 |
| catcatcatc atcatcatca tctctgatga taagttaaga tgttttcagt ataataaatg | 660 |
| gggtcttggt gatcggtcat tctcatgtgt aaaccgtttg gttctgtagt atgcttcgat | 720 |
| atattgttat gttcatgac atagtctggg ttcatataa tgattcttaa gattaattta   | 780 |

ct

(2) INFORMATION FOR SEQ ID NO:1809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1809:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ala Thr Ser Gly Thr Tyr Val Thr Glu Val Pro Leu Lys Gly Ser |  |
| 1 5 10 15                                                       |  |
| Ala Glu Lys Tyr Tyr Lys Arg Trp Lys Asn Glu Asn His Val Phe Pro |  |
| 20 25 30                                                        |  |
| Asp Ala Ile Gly His His Ile Gln Asn Val Thr Val His Glu Gly Glu |  |
| 35 40 45                                                        |  |
| His Asp Ser His Gly Ser Ile Arg Ser Trp Asn Tyr Thr Trp Asp Gly |  |
| 50 55 60                                                        |  |
| Lys Glu Glu Val Phe Lys Glu Arg Arg Glu Ile Asp Asp Glu Thr Lys |  |
| 65 70 75 80                                                     |  |
| Thr Leu Thr Leu Arg Gly Leu Glu Gly His Val Met Glu Gln Leu Lys |  |
| 85 90 95                                                        |  |
| Val Tyr Asp Val Val Tyr Gln Phe Ile Pro Lys Ser Glu Asp Thr Cys |  |
| 100 105 110                                                     |  |
| Ile Gly Lys Ile Thr Leu Ile Trp Glu Lys Arg Asn Asp Ser Pro     |  |
| 115 120 125                                                     |  |
| Glu Pro Ser Gly Tyr Met Lys Phe Val Lys Ser Leu Val Ala Asp Met |  |
| 130 135 140                                                     |  |
| Gly Asn His Val Ser Lys Thr                                     |  |
| 145 150                                                         |  |

(2) INFORMATION FOR SEQ ID NO:1810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 682 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..682
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1810:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| agtgaagtga agaagaatca gagaaaatgc cgccgaaatt ggatccatct caaatcgctgc  | 60  |
| acgtctacgt ccgagtcacc ggaggKgaN gtccggagcag cgtcttcaact cgctccaaag  | 120 |
| atcggtccac tgggtctggtg accaaagaag atcggagaag acatcgccaa agagacagcg  | 180 |
| aaagaatgga aaggtcttcg agtcaccgtg aagcttacgg tacagaatcg tcaagctaag   | 240 |
| gtcacagtgg ttccatccgc agcggtctcta gtcacaaag ccctcaagga gccagagaga   | 300 |
| gataggaaga aagtgaagaa catcaaacat atgggcaaca tttcgtttga tgatgtgatt   | 360 |
| gagattgcta agataatgct tctatagatt atcgctaagg aattgagtg aacagtgaag    | 420 |
| gagattttag gaactttggt ctctgttggt tgcactgttg atggtaaga cctaaggat     | 480 |
| cttcaggaag aaattaacag tgggtgacatt gatattccta acgagtgaata aaggttttta | 540 |
| cttttgagtt ctctatcggt ttattttttg tatttgatt tgaggatttg gtattagtaa    | 600 |
| tactatattt cggaagtga gaattgttg cttttgccca tttgaatctt tctttgggat     | 660 |
| taatcaaat gttcaatttt ct                                             |     |

(2) INFORMATION FOR SEQ ID NO:1811:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1571045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1811:

```
Val Ser Glu Arg Arg Ile Arg Glu Asn Ala Ala Glu Ile Gly Ser Ile
1 5 10 15
Ser Asn Arg Arg Arg Leu Arg Pro Ser His Arg Arg Xaa Xaa Ser Glu
 20 25 30
Gln Arg Leu His Ser Leu Gln Arg Ser Val His Ser Val Trp His Gln
 35 40 45
Arg Arg Ser Glu Lys Thr Ser Pro Lys Arg Gln Arg Lys Asn Gly Lys
50 55 60
Val Phe Glu Ser Pro
65
```

(2) INFORMATION FOR SEQ ID NO:1812:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1571046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1812:

```
Met Pro Pro Lys Leu Asp Pro Ser Gln Ile Val Asp Val Tyr Val Arg
1 5 10 15
Val Thr Gly Xaa Glu Xaa Arg Ser Ser Val Phe Thr Arg Ser Lys Asp
 20 25 30
Arg Ser Thr Arg Ser Gly Thr Lys Glu Asp Arg Arg Arg His Arg Gln
 35 40 45
Arg Asp Ser Glu Arg Met Glu Arg Ser Ser Ser His Arg Glu Ala Tyr
50 55 60
Gly Thr Glu Ser Ser Ser
65 70
```

(2) INFORMATION FOR SEQ ID NO:1813:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1571047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1813:

```
Met Arg Pro Arg Ser Ile Ala Lys Glu Leu Ser Gly Thr Val Lys Glu
1 5 10 15
Ile Leu Gly Thr Cys Val Ser Val Gly Cys Thr Val Asp Gly Lys Asp
 20 25 30
Pro Lys Asp Leu Gln Glu Glu Ile Asn Ser Gly Asp Ile Asp Ile Pro
```

35 40 45

Asn Glu  
50

(2) INFORMATION FOR SEQ ID NO:1814:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 585 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..585  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1814:

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| ataaacacaaa | agaatttgaa | ccaacaaagc | aaaacatgaa | aggcacattc  | actaacttgc  | 60  |
| ttgtgtctct  | ctctattgca | cttggtttgt | ccaatgtcgg | tgctaggaaa  | gttatctccg  | 120 |
| aagataccca  | attcaaggat | gaaaaatctt | tcctcggagg | cagtgggcagc | ggtgatggct  | 180 |
| tagggccttg  | ccttggttga | ggagctggtc | ttggtgggct | tgggattggg  | gctgggatcg  | 240 |
| gcgcgggagc  | cggactaggg | ttaggtggag | gcggttttgg | gggaggagcc  | ggtggcgggac | 300 |
| tcggtggcct  | tccttgaacg | tattgacaag | tgtgcgtgtg | agagctgatt  | ctcagcttat  | 360 |
| tactaattaa  | ttaagttact | ttcattctct | taataaaatc | tagaggggtt  | gaatttcgga  | 420 |
| tttcttcagc  | tttaatttaa | acttcaatat | ttgaaccaaa | aaaggtctta  | gctactagag  | 480 |
| gtaatgctcg  | taatcgtatt | atgtgtAacg | cgggttctga | tattcttatg  | tgcaagtgtg  | 540 |
| gaacgtttct  | cttttattca | ctatatagca | ttactttctt | ttttt       |             |     |

(2) INFORMATION FOR SEQ ID NO:1815:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..104  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1815:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Lys | Gln | Lys | Glu | Phe | Glu | Pro | Thr | Lys | Gln | Asn | Met | Lys | Gly | Thr | Phe |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Thr | Asn | Leu | Leu | Val | Leu | Leu | Leu | Ile | Ala | Leu | Val | Cys | Ala | Asn | Val |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gly | Ala | Arg | Lys | Val | Ile | Ser | Glu | Asp | Thr | Gln | Phe | Lys | Asp | Glu | Lys |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Phe | Leu | Gly | Gly | Ser | Gly | Ser | Gly | Asp | Gly | Leu | Gly | Leu | Gly | Leu |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gly | Gly | Gly | Ala | Gly | Leu | Gly | Gly | Leu | Gly | Ile | Gly | Ala | Gly | Ile | Gly |  |
|     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |  |
| Ala | Gly | Ala | Gly | Leu | Gly | Leu | Gly | Gly | Gly | Phe | Gly | Gly | Gly | Ala |     |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |     |  |
| Gly | Gly | Gly | Leu | Gly | Gly | Leu | Pro |     |     |     |     |     |     |     |     |  |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1816:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1571064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1816:

Met Lys Gly Thr Phe Thr Asn Leu Leu Val Leu Leu Leu Ile Ala Leu  
1 5 10 15  
Val Cys Ala Asn Val Gly Ala Arg Lys Val Ile Ser Glu Asp Thr Gln  
20 25 30  
Phe Lys Asp Glu Lys Ser Phe Leu Gly Gly Ser Gly Ser Gly Asp Gly  
35 40 45  
Leu Gly Leu Gly Leu Gly Gly Ala Gly Leu Gly Gly Leu Gly Ile  
50 55 60  
Gly Ala Gly Ile Gly Ala Gly Ala Gly Leu Gly Leu Gly Gly Gly Gly  
65 70 75 80  
Phe Gly Gly Gly Ala Gly Gly Gly Leu Gly Gly Leu Pro  
85 90

(2) INFORMATION FOR SEQ ID NO:1817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..718

(D) OTHER INFORMATION: / Ceres Seq. ID 1571079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1817:

attcaaaagac atacaaaata attgagtttt ttttttttaa ttgaaacaa atgggggttga 60  
gtgggtgttct tcaatgtggag gttgaggtta agtctccggc tgaaaagtgc tgggttagccc 120  
tcggcgacagg catacaatctc ttccccaaga ctttccctaa cgactacaaa accatccaag 180  
ttctagccgg cgacggccaac gctcctggct ccattcgccct cattacttat ggagaaggat 240  
tccactgggt gaagatatgc gcggagagga tcgaagcagt ggatttggag aacaaaagca 300  
tgtcatacag tcattattgc ggcgaatgt tggagtacta caaacgttc aaaggaacca 360  
tcaccgttat tcttaagaac ggtggcagcc ttctgaaatg gtctgggtgag tttagaaga 420  
cggcccatga gattgatgac ccacacgtca tcaaggactt tgcgtgcaag aacttcaag 480  
agatagatga gtatctcctt aagcaaaacta gtgcctaaca ctagaacctt taaattatat 540  
Maagaggggt cgatcgctct tataagattt ttctaattaa gaagttaga aaagtggaaac 600  
ctctttatga atatccaagt ttgtgatttc ggagtttatg cagcctagta ggccataaag 660  
tttttacaac agccaattta gtcgaacatt ttgaaaaaat cgaacctttt ggtaaagc

(2) INFORMATION FOR SEQ ID NO:1818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1571080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1818:

Met Gly Leu Ser Gly Val Leu His Val Glu Val Glu Val Lys Ser Pro  
1 5 10 15  
Ala Glu Lys Phe Trp Val Ala Leu Gly Asp Gly Ile Asn Leu Phe Pro  
20 25 30  
Lys Ala Phe Pro Asn Asp Tyr Lys Thr Ile Gln Val Leu Ala Gly Asp  
35 40 45  
Gly Asn Ala Pro Gly Ser Ile Arg Leu Ile Thr Tyr Gly Glu Gly Ser  
50 55 60  
Pro Leu Val Lys Ile Ser Ala Glu Arg Ile Glu Ala Val Asp Leu Glu  
65 70 75 80  
Asn Lys Ser Met Ser Tyr Ser Ile Ile Gly Gly Glu Met Leu Glu Tyr



(2) INFORMATION FOR SEQ ID NO:1819:

(2) INFORMATION FOR SEQ ID NO:1821:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..76  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571087  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1821:  
Met Gly Leu Asp Lys Asn Thr Lys Thr Pro Cys Gly Phe Cys Phe Val  
1 5 10 15  
Leu Phe Tyr Ser Arg Glu Asp Thr Glu Asp Ala Val Lys Tyr Ile Ser  
20 25 30  
Gly Thr Ile Leu Asp Asp Arg Pro Ile Arg Val Asp Phe Asp Trp Gly  
35 40 45  
Phe Gln Glu Gly Arg Gln Trp Gly Arg Gly Arg Ser Gly Gly Gln Val  
50 55 60  
Arg Asp Glu Tyr Arg Thr Asp Tyr Asp Pro Gly His  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1822:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 756 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..756  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571092  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1822:

aaacaactac aaacaacatt tctgagattg cgccggagtc aaggagaggg agagagcgat 60  
ccaacggttg agatgtttct acgggcaatc ggacggccat tattggctaa agtgaagcag 120  
acgacgggga tcgtcgggct tgacgttggt cccaacgcga gagcgggtgt gatcgatctc 180  
tacagcaaaa ccctaaaggga gatccaagct gtgccggagg atgaagggta ccgtNaaagc 240  
ggtggaatca ttacgcgcgc aacgtotcaa tgtgtgcaa gaagaagaag attggggagat 300  
gattgagaag cggcttggtt gtggctcaag cgaagagctt atcgaagagg ctgcgcatga 360  
gctcacacac attgggaaaa tgatcgagtg ggaatccttg ggtgtaccag atgattacga 420  
gtgtgaagtg attgagaatg atgcgccgat tccaaagcat gttcctcagc accgacctgg 480  
tcctcttctc gagcagttct ataaaacgct tgaaggtcta attgcagagt ctaaaacaga 540  
gatccacgct gctacaccca gogatccgca gttgaaggag taacttccag tttttacAYa 600  
tatbCgtRvt GcTtTgttgc tttttggcta gagttgtttc cgaatcagtg gtaacgcctc 660  
tgaaataaatt gcttaataat ttccataacg atacaatatg ctgttcacaa atgtttttac 720  
actcttatta aacaaatgat gttcttctcc ttttgc

(2) INFORMATION FOR SEQ ID NO:1823:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 101 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..101  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571093  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1823:

Lys Gln Leu Gln Thr Thr Phe Leu Arg Leu Arg Arg Ser Gln Gly Glu  
1 5 10 15  
Gly Glu Ser Asp Pro Thr Val Glu Met Phe Leu Arg Ala Ile Gly Arg

20 25 30  
Pro Leu Leu Ala Lys Val Lys Gln Thr Thr Gly Ile Val Gly Leu Asp  
35 40 45  
Val Val Pro Asn Ala Arg Ala Val Leu Ile Asp Leu Tyr Ser Lys Thr  
50 55 60  
Leu Lys Glu Ile Gln Ala Val Pro Glu Asp Glu Gly Tyr Arg Xaa Ser  
65 70 75 80  
Gly Gly Ile Ile His Ala Pro Thr Ser Gln Cys Val Gln Gly Arg Arg  
85 90 95  
Arg Leu Gly Asp Asp  
100

(2) INFORMATION FOR SEQ ID NO:1824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1824:

Met Lys Gly Thr Xaa Lys Ala Val Glu Ser Phe Thr Arg Gln Arg Leu  
1 5 10 15  
Asn Val Cys Lys Glu Glu Glu Asp Trp Glu Met Ile Glu Lys Arg Leu  
20 25 30  
Gly Cys Gly Gln Val Glu Glu Leu Ile Glu Glu Ala Arg Asp Glu Leu  
35 40 45  
Thr Leu Ile Gly Lys Met Ile Glu Trp Asp Pro Trp Gly Val Pro Asp  
50 55 60  
Asp Tyr Glu Cys Glu Val Ile Glu Asn Asp Ala Pro Ile Pro Lys His  
65 70 75 80  
Val Pro Gln His Arg Pro Gly Pro Leu Pro Glu Gln Phe Tyr Lys Thr  
85 90 95  
Leu Glu Gly Leu Ile Ala Glu Ser Lys Thr Glu Ile Pro Ala Ala Thr  
100 105 110  
Pro Ser Asp Pro Gln Leu Lys Glu  
115 120

(2) INFORMATION FOR SEQ ID NO:1825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1825:

Met Ile Glu Lys Arg Leu Gly Cys Gly Gln Val Glu Glu Leu Ile Glu  
1 5 10 15  
Glu Ala Arg Asp Glu Leu Thr Leu Ile Gly Lys Met Ile Glu Trp Asp  
20 25 30  
Pro Trp Gly Val Pro Asp Asp Tyr Glu Cys Glu Val Ile Glu Asn Asp  
35 40 45  
Ala Pro Ile Pro Lys His Val Pro Gln His Arg Pro Gly Pro Leu Pro  
50 55 60  
Glu Gln Phe Tyr Lys Thr Leu Glu Gly Leu Ile Ala Glu Ser Lys Thr  
65 70 75 80

Glu Ile Pro Ala Ala Thr Pro Ser Asp Pro Gln Leu Lys Glu  
85 90

(2) INFORMATION FOR SEQ ID NO:1826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1219
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1826:

|              |             |             |            |             |             |      |
|--------------|-------------|-------------|------------|-------------|-------------|------|
| aaaaaaaaactt | gcaaaaactct | cgctccgagat | atatcgactc | cgcgaccctc  | cactactctt  | 60   |
| ctgctgatct   | acacacacac  | acacaaaaaa  | aaaaaaactc | aatcgccagc  | acaactggcg  | 120  |
| aagctcacac   | tctctctctt  | cccttctctt  | ctcatctctt | cctcatccat  | cgtcttccaa  | 180  |
| tcagacgagc   | tctctggtga  | cgacgacgaa  | tttggcttag | aaggagcaaa  | gccccgctcc  | 240  |
| accgatcttt   | acacatcttc  | ttcttctctg  | ccacagcagc | agcaacagac  | tccaactatc  | 300  |
| cgagagaagat  | actcagatcc  | taccgatttg  | gattcaaaa  | tccaatttac  | tctcgaacat  | 360  |
| gccttcgggtg  | actctgattt  | ctccccgcgc  | ggtaactttt | ccgctcgctc  | caaaaacctgg | 420  |
| agtcattggcg  | gaaagacatt  | aacgaagctg  | cgattctcta | ggaatgattt  | ttctgtctaaa | 480  |
| gagaaagatg   | cattcaagaa  | tctgtgtaaa  | ggagatgact | tttatcggtt  | tcggctctca  | 540  |
| tttaaatgtg   | ttagtccacc  | agggagagag  | ttTgtgattg | catcagtgag  | agctagatgt  | 600  |
| ctaccacggg   | atggccttga  | tgagcatctt  | attatacaca | tggaaggtgc  | taacatcttg  | 660  |
| gcagttagtt   | atggttctcc  | tggggcggtg  | caatatctct | gccaaattgaa | acttcacaga  | 720  |
| aaatgggtcgt  | ttaactctca  | cacaattctg  | aaaagcagtg | agcaggcgcc  | aagaactcca  | 780  |
| atattcactg   | aggagattct  | aggcagtgag  | aatgtagagg | gagaagttga  | accaccacca  | 840  |
| gagagatcat   | tttggcgcaa  | atattggatg  | tatttgatac | cgcctgggact | cgtagtgtat  | 900  |
| aatgccttta   | cacaagcatc  | aaacatggct  | gaagaaccgc | cggttggaac  | ggcaggaggg  | 960  |
| gcacaagtgc   | aaccagctgc  | caggagaaga  | tgattccact | tttactcttc  | ccaaagcaat  | 1020 |
| gaaagctgca   | gctggttaga  | gatgatgatt  | caacagatct | tcagtataac  | catcttgcca  | 1080 |
| tcatttgggt   | ttatgtaacc  | tttaatttta  | atcctcgatc | gggtgtgttt  | tgtactcaac  | 1140 |
| aatcgggaaa   | tcaaaaatct  | tgtcttcatg  | acatatcaag | aacaaagaca  | tttagcagct  | 1200 |
| tcctatctct   | gttttgatc   |             |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..330
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1827:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Lys | Thr | Cys | Lys | Thr | Leu | Val | Arg | Asp | Ile | Ser | Thr | Pro | Arg | Pro |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Thr | Thr | Leu | Leu | Ile | Tyr | Thr | His | Thr | His | Lys | Lys | Lys | Lys |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Thr | Gln | Ser | Pro | Ala | Thr | Met | Ala | Lys | Leu | Thr | Leu | Leu | Phe | Phe | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Phe | Leu | Ile | Phe | Ser | Ser | Ser | Ile | Ala | Phe | Gln | Ser | Asp | Glu | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Leu | Val | Asp | Asp | Asp | Glu | Phe | Gly | Leu | Glu | Gly | Ala | Lys | Pro | Arg | Ser |
|     |     |     |     |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Thr | Asp | Leu | Tyr | Thr | Ser | Ser | Ser | Ser | Ser | Pro | Gln | Gln | Gln | Gln |     |
|     |     |     |     |     |     |     | 85  |     |     |     |     | 90  |     | 95  |     |
| Thr | Pro | Thr | Ile | Arg | Arg | Arg | Tyr | Ser | Asp | Pro | Thr | Asp | Leu | Asp | Ser |
|     |     |     |     |     |     |     | 100 |     |     |     |     | 105 |     | 110 |     |

Lys Val Gln Phe Thr Leu Glu His Ala Phe Gly Asp Ser Asp Phe Ser  
115 120 125  
Pro Ala Gly Thr Phe Ser Ala Arg Leu Lys Thr Trp Ser His Gly Gly  
130 135 140  
Lys Thr Leu Thr Lys Leu Arg Phe Ser Arg Asn Asp Phe Ser Ala Lys  
145 150 155 160  
Glu Lys Asp Ala Phe Lys Asn Leu Leu Lys Gly Asp Asp Phe Tyr Arg  
165 170 175  
Ile Arg Leu Pro Ser Asn Val Val Ser Pro Pro Gly Arg Glu Phe Val  
180 185 190  
Ile Ala Ser Val Arg Ala Arg Cys Leu Pro Arg Asp Gly Leu Asp Glu  
195 200 205  
His Phe Ile Ile His Met Glu Gly Ala Asn Ile Leu Ala Val Ser Tyr  
210 215 220  
Gly Ser Pro Gly Ala Cys Gln Tyr Pro Arg Gln Leu Lys Leu Pro Ala  
225 230 235 240  
Lys Trp Ser Phe Asn Ser His Thr Ile Leu Lys Ser Ser Glu Gln Ala  
245 250 255  
Pro Arg Thr Pro Ile Phe Thr Glu Glu Ile Leu Gly Ser Glu Asn Val  
260 265 270  
Glu Gly Glu Val Glu Pro Pro Pro Glu Arg Ser Phe Trp Ala Lys Tyr  
275 280 285  
Trp Met Tyr Leu Ile Pro Leu Gly Leu Val Val Met Asn Ala Val Thr  
290 295 300  
Gln Ala Ser Asn Met Ala Glu Glu Pro Ala Gly Gly Gln Ala Gly Gly  
305 310 315 320  
Ala Gln Val Gln Pro Ala Ala Arg Arg Arg  
325 330

(2) INFORMATION FOR SEQ ID NO:1828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..292

(B) OTHER INFORMATION: / Ceres Seq. ID 1571118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1828:

Met Ala Lys Leu Thr Leu Leu Phe Phe Leu Ser Phe Leu Ile Phe Ser  
1 5 10 15  
Ser Ser Ile Ala Phe Gln Ser Asp Glu Leu Val Asp Asp Asp Glu  
20 25 30  
Phe Gly Leu Glu Gly Ala Lys Pro Arg Ser Thr Asp Leu Tyr Thr Ser  
35 40 45  
Ser Ser Ser Ser Pro Gln Gln Gln Gln Thr Pro Thr Ile Arg Arg  
50 55 60  
Arg Tyr Ser Asp Pro Thr Asp Leu Asp Ser Lys Val Gln Phe Thr Leu  
65 70 75 80  
Glu His Ala Phe Gly Asp Ser Asp Phe Ser Pro Ala Gly Thr Phe Ser  
85 90 95  
Ala Arg Leu Lys Thr Trp Ser His Gly Gly Lys Thr Leu Thr Lys Leu  
100 105 110  
Arg Phe Ser Arg Asn Asp Phe Ser Ala Lys Glu Lys Asp Ala Phe Lys  
115 120 125  
Asn Leu Leu Lys Gly Asp Asp Phe Tyr Arg Ile Arg Leu Pro Ser Asn  
130 135 140  
Val Val Ser Pro Pro Gly Arg Glu Phe Val Ile Ala Ser Val Arg Ala  
145 150 155 160  
Arg Cys Leu Pro Arg Asp Gly Leu Asp Glu His Phe Ile Ile His Met

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Thr | Lys | Thr | Asn | Met | Ala | Leu | Gln | Lys | Phe | Pro | Leu | Leu | Gly | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Phe | Leu | Val | Leu | Thr | Ile | Leu | Val | Ser | Ser | Ala | Thr | Ala | Asp | Gly | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Val | Cys | Pro | Pro | Ser | Thr | Lys | Leu | Ser | Arg | Arg | Cys | Asn | Asn | Asp | Lys |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Glu | Asn | Val | Val | Val | Ser | Phe | Phe | His | Arg | Tyr | Lys | Val | Ile | Ser | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Pro | Val | Ser | Ile | Lys | Tyr | Leu | Leu | Met | Phe | Phe | Val | Phe | Val | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Tyr | Phe | Leu | Phe | Val | Asp | Asn | Gln | Glu | Pro | Met | Asp | Tyr | Trp | Ser | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

Ile Pro Leu Gly Arg Gly Pro Lys Asn Leu Leu Val Phe Ser Ile Leu  
100 105 110  
Phe Tyr Phe Asn Phe Tyr Ile Leu  
115 120

(2) INFORMATION FOR SEQ ID NO:1831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1831:

Met Ala Leu Gln Lys Phe Pro Leu Leu Gly Leu Phe Leu Val Leu Thr  
1 5 10 15  
Ile Leu Val Ser Ser Ala Thr Ala Asp Gly His Val Cys Pro Pro Ser  
20 25 30  
Thr Lys Leu Ser Arg Arg Cys Asn Asn Asp Lys Glu Asn Val Val Val  
35 40 45  
Ser Phe Phe His Arg Tyr Lys Val Ile Ser Glu Tyr Pro Val Ser Ile  
50 55 60  
Lys Tyr Leu Leu Met Phe Phe Val Phe Val Phe Tyr Phe Leu Phe Val  
65 70 75 80  
Asp Asn Gln Glu Pro Met Asp Tyr Trp Ser Ile Ile Pro Leu Gly Arg  
85 90 95  
Gly Pro Lys Asn Leu Leu Val Phe Ser Ile Leu Phe Tyr Phe Asn Phe  
100 105 110  
Tyr Ile Leu  
115

(2) INFORMATION FOR SEQ ID NO:1832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1832:

aatatttttc gttccaaacg aaaaccctaa aagagaaaaa tgggtgcagcg 60  
tcttgtttac cgtctggagc acagCtaacg caccaaatcg aaccagcacc gtatcgtcaa 120  
gactccaggga ggtaaaattgg tgtatcaaac cacaaagaag aaagctagtgt gccccaaatg 180  
tcctgtttact ggcaagcgta ttcaaggaat cctcacttg aggcctctgt agtacaagag 240  
gtcaagatta tcaagaaaca ggaggactgt aaaccgagca tacggtggag tcttgtctgg 300  
ttctgcagtc agggaaaagga tcatttcgggc attccttgtc gaagagcaaa agatgtgtgaa 360  
gaaagtgttg aaactccaaa aggcataagga gaaagtagcc cccaaggcctt aagcttttat 420  
gttttattct tctctgtttt ggaattatgg ctatgttcaa gtgataggac ttgggtgcagt 480  
catgtgagga catctatggt actcgcacaa ttttt

(2) INFORMATION FOR SEQ ID NO:1833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..136  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1833:

Ile Phe Phe Val Pro Asn Glu Asn Pro Lys Arg Glu Lys Glu Ala Lys  
1 5 10 15  
Met Val Gln Arg Leu Val Tyr Arg Ser Arg His Ser Tyr Ala Thr Lys  
20 25 30  
Ser Asn Gln His Arg Ile Val Lys Thr Pro Gly Gly Lys Leu Val Tyr  
35 40 45  
Gln Thr Thr Lys Lys Lys Ala Ser Gly Pro Lys Cys Pro Val Thr Gly  
50 55 60  
Lys Arg Ile Gln Gly Ile Pro His Leu Arg Pro Ser Glu Tyr Lys Arg  
65 70 75 80  
Ser Arg Leu Ser Arg Asn Arg Arg Thr Val Asn Arg Ala Tyr Gly Gly  
85 90 95  
Val Leu Ser Gly Ser Ala Val Arg Glu Arg Ile Ile Arg Ala Phe Leu  
100 105 110  
Val Glu Glu Gln Lys Ile Val Lys Lys Val Leu Lys Leu Gln Lys Ala  
115 120 125  
Lys Glu Lys Val Ala Pro Lys Ala  
130 135

(2) INFORMATION FOR SEQ ID NO:1834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..72  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1834:

Tyr Ser Ser Phe Gln Thr Lys Thr Leu Lys Glu Lys Arg Arg Arg Lys  
1 5 10 15  
Trp Cys Ser Val Leu Phe Thr Gly Arg Asp Thr Ala Thr Pro Pro Asn  
20 25 30  
Arg Thr Ser Thr Val Ser Ser Arg Leu Gln Glu Val Asn Trp Cys Ile  
35 40 45  
Lys Pro Gln Arg Arg Lys Leu Val Ala Pro Asn Val Leu Leu Leu Ala  
50 55 60  
Ser Val Phe Lys Glu Ser Leu Thr  
65 70

(2) INFORMATION FOR SEQ ID NO:1835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..120  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1835:

Met Val Gln Arg Leu Val Tyr Arg Ser Arg His Ser Tyr Ala Thr Lys  
1 5 10 15  
Ser Asn Gln His Arg Ile Val Lys Thr Pro Gly Gly Lys Leu Val Tyr  
20 25 30  
Gln Thr Thr Lys Lys Lys Ala Ser Gly Pro Lys Cys Pro Val Thr Gly



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 35                                                              | 40  | 45  |
| Lys Arg Ile Gln Gly Ile Pro His Leu Arg Pro Ser Glu Tyr Lys Arg |     |     |
| 50                                                              | 55  | 60  |
| Ser Arg Leu Ser Arg Asn Arg Arg Thr Val Asn Arg Ala Tyr Gly Gly |     |     |
| 65                                                              | 70  | 75  |
| Val Leu Ser Gly Ser Ala Val Arg Glu Arg Ile Ile Arg Ala Phe Leu |     |     |
| 85                                                              | 90  | 95  |
| Val Glu Glu Gln Lys Ile Val Lys Lys Val Leu Lys Leu Gln Lys Ala |     |     |
| 100                                                             | 105 | 110 |
| Lys Glu Lys Val Ala Pro Lys Ala                                 |     |     |
| 115                                                             | 120 |     |

(2) INFORMATION FOR SEQ ID NO:1836:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 705 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..705

(D) OTHER INFORMATION: / Ceres Seq. ID 1571134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1836:

|             |             |             |            |             |             |     |
|-------------|-------------|-------------|------------|-------------|-------------|-----|
| acatctcact  | gctcactact  | ctcactgtaa  | tccttagat  | cttcttttca  | aatttcaatg  | 60  |
| gcgtccgggtg | atgtttgagta | tccgtgtcttc | gttggaggtc | tagcatgggc  | cactgatgac  | 120 |
| agagctctctg | agactgcctt  | cgctcaatac  | ggcgacgtta | ttgattccaa  | gatcattaac  | 180 |
| gatcgctgaga | ctggaagatc  | aaggggattc  | ggattcgtca | ccttcaagga  | tgagaaagcc  | 240 |
| atgaaggatg  | cgattgaggg  | aatgaacgga  | caagatctcg | atggccgtgag | catcactgtt  | 300 |
| aacgaggctc  | agtcacgagg  | aagcgggtgg  | ggcggaggcc | accgtggagg  | tgggtggcgtg | 360 |
| ggataCgcga  | gcggcgggtg  | tggaggttac  | tccggtggag | gtggtagcta  | cgaggtgtggc | 420 |
| ggcggtagac  | Gcgaggggtg  | aggaggatac  | agcggcggcg | gcggttactc  | ctcaagaggt  | 480 |
| ggtgtgtgcg  | gaagctacgg  | tgggtgaaga  | cgtgaggagg | gaggaggata  | cgggtgtgtgt | 540 |
| gaaggaggag  | gttacggagg  | aagcgggtgt  | ggtggaggat | ggtaattcct  | ttaataggt   | 600 |
| ttgggattac  | caatgaatgt  | tctctctctc  | gcttgttatg | ctctactctg  | gttttgtgtg  | 660 |
| ttctctattt  | tggtattctt  | ccgttaatgt  | aatgaagag  | ttgttt      |             |     |

(2) INFORMATION FOR SEQ ID NO:1837:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1571135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1837:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Ala Ser Gly Asp Val Glu Tyr Arg Cys Phe Val Gly Gly Leu Ala |     |     |
| 1                                                               | 5   | 10  |
| Trp Ala Thr Asp Asp Arg Ala Leu Glu Thr Ala Phe Ala Gln Tyr Gly |     |     |
| 20                                                              | 25  | 30  |
| Asp Val Ile Asp Ser Lys Ile Ile Asn Asp Arg Glu Thr Gly Arg Ser |     |     |
| 35                                                              | 40  | 45  |
| Arg Gly Phe Gly Phe Val Thr Phe Lys Asp Glu Lys Ala Met Lys Asp |     |     |
| 50                                                              | 55  | 60  |
| Ala Ile Glu Gly Met Asn Gly Gln Asp Leu Asp Gly Arg Ser Ile Thr |     |     |
| 65                                                              | 70  | 75  |
| Val Asn Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Gly His Arg     |     |     |
| 85                                                              | 90  | 95  |
| Gly Gly Gly Gly Gly Gly Tyr Arg Ser Gly Gly Gly Gly Gly Tyr Ser |     |     |
| 100                                                             | 105 | 110 |

Gly Gly Gly Gly Ser Tyr Gly Gly Gly Gly Gly Arg Arg Glu Gly Gly  
115 120 125  
Gly Gly Tyr Ser Gly Gly Gly Tyr Ser Ser Arg Gly Gly Gly Gly  
130 135 140  
Gly Ser Tyr Gly Gly Gly Arg Arg Glu Gly Gly Gly Tyr Gly Gly  
145 150 155 160  
Gly Glu Gly Gly Gly Tyr Gly Gly Ser Gly Gly Gly Gly Trp  
165 170 175

(2) INFORMATION FOR SEQ ID NO:1838:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1571136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1838:

Met Lys Asp Ala Ile Glu Gly Met Asn Gly Gln Asp Leu Asp Gly Arg  
1 5 10 15  
Ser Ile Thr Val Asn Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Gly  
20 25 30  
Gly His Arg Gly Gly Gly Gly Tyr Arg Ser Gly Gly Gly Gly  
35 40 45  
Gly Tyr Ser Gly Gly Gly Gly Ser Tyr Gly Gly Gly Arg Arg  
50 55 60  
Glu Gly Gly Gly Gly Tyr Ser Gly Gly Gly Gly Tyr Ser Ser Arg Gly  
65 70 75 80  
Gly Gly Gly Gly Ser Tyr Gly Gly Gly Arg Arg Glu Gly Gly Gly  
85 90 95  
Tyr Gly Gly Gly Glu Gly Gly Gly Tyr Gly Gly Ser Gly Gly Gly  
100 105 110  
Gly Trp

(2) INFORMATION FOR SEQ ID NO:1839:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1571137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1839:

Met Asn Gly Gln Asp Leu Asp Gly Arg Ser Ile Thr Val Asn Glu Ala  
1 5 10 15  
Gln Ser Arg Gly Ser Gly Gly Gly Gly His Arg Gly Gly Gly Gly  
20 25 30  
Gly Gly Tyr Arg Ser Gly Gly Gly Gly Tyr Ser Gly Gly Gly Gly  
35 40 45  
Ser Tyr Gly Gly Gly Gly Gly Arg Arg Glu Gly Gly Gly Tyr Ser  
50 55 60  
Gly Gly Gly Gly Tyr Ser Ser Arg Gly Gly Gly Gly Ser Tyr Gly  
65 70 75 80  
Gly Gly Arg Arg Glu Gly Gly Gly Tyr Gly Gly Gly Glu Gly  
85 90 95  
Gly Tyr Gly Gly Ser Gly Gly Gly Gly Trp

100 105

(2) INFORMATION FOR SEQ ID NO:1840:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 873 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..873

(D) OTHER INFORMATION: / Ceres Seq. ID 1571138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1840:

|            |             |             |             |             |             |     |
|------------|-------------|-------------|-------------|-------------|-------------|-----|
| gaaacacaaa | caaacacaaa  | aatcaaaaagg | ggatcatttac | tatcttttaa  | gagacgacat  | 60  |
| atatagtctt | cgaccaagaa  | aagaaaaagg  | ggtagacctga | gttctctcaac | acataaacata | 120 |
| atggcgagg  | ttttcaaaaac | gggtacgttt  | cttgtttttg  | ttttgcgtgc  | cggtgtgttc  | 180 |
| ttcgcgagg  | actacgatgt  | tggtagatgt  | acggaatgga  | cgagacctat  | ggaccgccgag | 240 |
| ttctatacta | cttgggctac  | cggtaaaaact | ttcgtgttag  | gcgacgagct  | cgaattttgat | 300 |
| ttcgtctgtg | ggaggcatga  | tgtggcagtt  | gtatcagaag  | ctgcatttga  | aaactgtgag  | 360 |
| aaagagaaac | ccattagcca  | catgaccgtt  | cTcccggtca  | aaattatgct  | aaacaccact  | 420 |
| ggaccacaat | actttatctg  | caccgtcggt  | gaccattgtc  | gttttggtca  | aaaactttcc  | 480 |
| atcactgtag | ttgctgctgg  | tgcaactgga  | ggtgctactc  | ctgggtcgcg  | tgctacccca  | 540 |
| gcacctggat | caaccccaaag | tactggagga  | accactcctc  | ccactgcggg  | tgggaccaca  | 600 |
| acaccttcag | gctctagcgg  | aaccactact  | ccagctggaa  | atgcccgctc  | ctcattaggt  | 660 |
| ggtgtcaact | ttctgtgtcg  | ttttgtttct  | gctgtgtgtg  | ctctcttttg  | agtcacactc  | 720 |
| gaaacctagt | tatgtgtttg  | ttttaccta   | ctctccttat  | ttaaatagtc  | atgtatttga  | 780 |
| ttatttgtga | gaataaggac  | ttgttttcaa  | gtcattataa  | acgtcttata  | cttgtgatta  | 840 |
| gtattgagtt | tcaatatatg  | attattcggt  | tgc         |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1841:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..196

(D) OTHER INFORMATION: / Ceres Seq. ID 1571139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1841:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Gly | Val | Phe | Lys | Thr | Val | Thr | Phe | Leu | Val | Leu | Val | Phe | Ala |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Ala | Val | Val | Val | Phe | Ala | Glu | Asp | Tyr | Asp | Val | Gly | Asp | Asp | Thr | Glu |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Trp | Thr | Arg | Pro | Met | Asp | Pro | Glu | Phe | Tyr | Thr | Thr | Trp | Ala | Thr | Gly |  |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |  |
| Lys | Thr | Phe | Arg | Val | Gly | Asp | Glu | Leu | Glu | Phe | Asp | Phe | Ala | Ala | Gly |  |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |  |
| Arg | His | Asp | Val | Ala | Val | Val | Ser | Glu | Ala | Ala | Phe | Glu | Asn | Cys | Gly |  |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |  |
| Lys | Glu | Lys | Pro | Ile | Ser | His | Met | Thr | Val | Pro | Pro | Val | Lys | Ile | Met |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Leu | Asn | Thr | Thr | Gly | Pro | Gln | Tyr | Phe | Ile | Cys | Thr | Val | Gly | Asp | His |  |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |  |
| Cys | Arg | Gly | Gly | Gln | Lys | Leu | Ser | Ile | Thr | Val | Val | Ala | Ala | Gly | Ala |  |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |  |
| Thr | Gly | Gly | Ala | Thr | Pro | Gly | Ala | Gly | Ala | Thr | Pro | Ala | Pro | Gly | Ser |  |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |  |
| Thr | Pro | Ser | Thr | Gly | Gly | Thr | Thr | Pro | Pro | Thr | Ala | Gly | Gly | Thr | Thr |  |
|     |     |     |     | 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |  |
| Thr | Pro | Ser | Gly | Ser | Ser | Gly | Thr | Thr | Thr | Pro | Ala | Gly | Asn | Ala | Ala |  |

|     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|
|     | 165 |     | 170 |     | 175 |
| Ser | Ser | Leu | Gly | Ala | Thr |
|     | 160 |     |     |     |     |
| Val | Ala | Leu | Phe |     |     |
|     | 195 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1842:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Pro | Glu | Phe | Tyr | Thr | Thr | Trp | Ala | Thr | Gly | Lys | Thr | Phe | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Gly | Asp | Glu | Leu | Glu | Phe | Asp | Phe | Ala | Ala | Gly | Arg | His | Asp | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Val | Val | Ser | Glu | Ala | Ala | Phe | Glu | Asn | Cys | Glu | Lys | Glu | Lys | Pro |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Ile | Ser | His | Met | Thr | Val | Pro | Pro | Val | Lys | Ile | Met | Leu | Asn | Thr | Thr |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Gly | Pro | Gln | Tyr | Phe | Ile | Cys | Thr | Val | Gly | Asp | His | Cys | Arg | Phe | Gly |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     | 80  |
| Gln | Lys | Leu | Ser | Ile | Thr | Val | Val | Ala | Ala | Gly | Ala | Thr | Gly | Gly | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Thr | Pro | Gly | Ala | Gly | Ala | Thr | Pro | Ala | Pro | Gly | Ser | Thr | Pro | Ser | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Gly | Thr | Pro | Pro | Thr | Ala | Gly | Gly | Thr | Thr | Thr | Pro | Ser | Gly |     |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Ser | Ser | Gly | Thr | Thr | Thr | Pro | Ala | Gly | Asn | Ala | Ala | Ser | Ser | Leu | Gly |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |
| Gly | Ala | Thr | Phe | Leu | Val | Ala | Phe | Val | Ser | Ala | Val | Val | Ala | Leu | Phe |
|     |     |     | 145 |     |     |     |     | 150 |     |     |     | 155 |     |     | 160 |

(2) INFORMATION FOR SEQ ID NO:1843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1843:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Val | Pro | Pro | Val | Lys | Ile | Met | Leu | Asn | Thr | Thr | Gly | Pro | Gln |
| 1   |     |     |     |     |     | 5   |     |     |     |     | 10  |     |     | 15  |     |
| Tyr | Phe | Ile | Cys | Thr | Val | Gly | Asp | His | Cys | Arg | Phe | Gly | Gln | Lys | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ile | Thr | Val | Val | Ala | Ala | Gly | Ala | Thr | Gly | Gly | Ala | Thr | Pro | Gly |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Ala | Gly | Ala | Thr | Pro | Ala | Pro | Gly | Ser | Thr | Pro | Ser | Thr | Gly | Gly | Thr |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Thr | Pro | Pro | Thr | Ala | Gly | Gly | Thr | Thr | Thr | Pro | Ser | Gly | Ser | Ser | Gly |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     | 80  |

Thr Thr Thr Pro Ala Gly Asn Ala Ala Ser Ser Leu Gly Gly Ala Thr  
85 90 95  
Phe Leu Val Ala Phe Val Ser Ala Val Val Ala Leu Phe  
100 105

(2) INFORMATION FOR SEQ ID NO:1844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..620
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1844:

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| ctcgtagca  | atctgGatct | aatccaccac | tctctccaat | tgctcattcac | tcgggtttttg | 60  |
| ctatttccaa | ggagagaaag | atgatagctg | tgatcggatt | gcttctgggt  | tttctagtat  | 120 |
| cagcattgtt | cttaatccaa | ggaaagcgaa | gaagaacaaa | cgacaatcaa  | gagaagaaga  | 180 |
| gatctagcag | tgagccctga | gaagatgtgg | taagaccaaa | aagtaccagc  | aagagtgaag  | 240 |
| tcgcagtaca | taacaaaagg | aacgattgtt | ggatcataat | caaagataaa  | gtctatgata  | 300 |
| ttactttcta | ttgtgaagaa | catctcgttg | gtgacgctat | tcttgatcat  | gctgggtgat  | 360 |
| atttcaactg | tggctttctc | ggacctcaac | acgccactcg | tgttttcgac  | atgattgaag  | 420 |
| attttacat  | cggggaact  | cattagtaaa | agcttaaaga | tttgagattt  | gattgaagat  | 480 |
| ttgagatttc | ttcttaagta | agcttaaa   | tggtttttt  | aattctcttc  | tcattgaaga  | 540 |
| tttgagattg | cattaccttt | ttgtcttget | agtgtaAcac | ttctctcttc  | attgtattgc  | 600 |
| caaagtttcc | tcattttctc |            |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1845:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Gln | Gln | Ser | Gly | Ser | Asn | Pro | Pro | Leu | Ser | Pro | Ile | Val | Ile | His |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Gly | Phe | Ala | Ile | Ser | Lys | Glu | Arg | Lys | Met | Ile | Ala | Val | Ile | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Leu | Leu | Gly | Phe | Leu | Val | Ser | Ala | Leu | Phe | Leu | Ile | Gln | Gly | Lys |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Arg | Arg | Arg | Thr | Asn | Asp | Asn | Gln | Glu | Lys | Lys | Arg | Ser | Ser | Ser | Glu |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Pro | Val | Glu | Asp | Val | Val | Arg | Pro | Lys | Ser | Tyr | Ser | Lys | Ser | Glu | Val |
|     |     |     |     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |
| Ala | Val | His | Asn | Lys | Arg | Asn | Asp | Cys | Trp | Ile | Ile | Ile | Lys | Asp | Lys |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Val | Tyr | Asp | Ile | Thr | Ser | Tyr | Val | Glu | Glu | His | Pro | Gly | Gly | Asp | Ala |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ile | Leu | Asp | His | Ala | Gly | Asp | Asp | Ser | Thr | Asp | Gly | Phe | Phe | Gly | Pro |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Gln | His | Ala | Thr | Arg | Val | Phe | Asp | Met | Ile | Glu | Asp | Phe | Tyr | Ile | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Glu | Leu | His |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

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(2) INFORMATION FOR SEQ ID NO:1846:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..121  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571155  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1846:  
Met Ile Ala Val Ile Gly Leu Leu Leu Gly Phe Leu Val Ser Ala Leu  
1 5 10 15  
Phe Leu Ile Gln Gly Lys Arg Arg Arg Thr Asn Asp Asn Gln Glu Lys  
20 25 30  
Lys Arg Ser Ser Ser Glu Pro Val Glu Asp Val Val Arg Pro Lys Ser  
35 40 45  
Tyr Ser Lys Ser Glu Val Ala Val His Asn Lys Arg Asn Asp Cys Trp  
50 55 60  
Ile Ile Ile Lys Asp Lys Val Tyr Asp Ile Thr Ser Tyr Val Glu Glu  
65 70 75 80  
His Pro Gly Gly Asp Ala Ile Leu Asp His Ala Gly Asp Asp Ser Thr  
85 90 95  
Asp Gly Phe Phe Gly Pro Gln His Ala Thr Arg Val Phe Asp Met Ile  
100 105 110  
Glu Asp Phe Tyr Ile Gly Glu Leu His  
115 120

(2) INFORMATION FOR SEQ ID NO:1847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..290  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1847:

aaaaWaWaga aatgatgact tcgcataacc ggaagttagc tcaacccccg gaaggtaacg 60  
aggaagctag ggcagatcca aaaggaccag ctaaattgtg tgtgatgtga agagaggttg 120  
gtgggaatca gctatttgta ttaatagaag gaacagtgtata taaaaaacat catttgaagc 180  
tttgaatttc cctacaacct cctaattgta tagtcttggt tgagaatata tatatgtccc 240  
ccaaaaacag ttgatgatta ttttaataaa cctcatctct accttctctt

(2) INFORMATION FOR SEQ ID NO:1848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..35  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1848:

Xaa Xaa Glu Met Met Thr Ser His Asn Arg Lys Leu Ala Gln Pro Pro  
1 5 10 15  
Glu Gly Asn Glu Glu Ala Arg Ala Asp Pro Lys Gly Pro Ala Lys Cys  
20 25 30  
Cys Val Met  
35

(2) INFORMATION FOR SEQ ID NO:1849:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..32  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1849:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Thr | Ser | His | Asn | Arg | Lys | Leu | Ala | Gln | Pro | Pro | Glu | Gly | Asn |
| 1   |     |     | 5   |     |     |     | 10  |     |     | 15  |     |     |     |     |     |
| Glu | Glu | Ala | Arg | Ala | Asp | Pro | Lys | Gly | Pro | Ala | Lys | Cys | Cys | Val | Met |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1850:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..36  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1850:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Cys | Asp | Val | Lys | Arg | Gly | Trp | Trp | Glu | Ser | Ala | Ile | Cys | Ile |
| 1   |     |     | 5   |     |     |     | 10  |     |     | 15  |     |     |     |     |     |
| Asn | Arg | Arg | Asn | Ser | Val | Tyr | Lys | Thr | Ser | Phe | Glu | Ala | Leu | Lys | Phe |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Pro | Thr | Thr | Ser |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 35  |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1851:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 560 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..560  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1851:

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| atcaaaaaaa  | gtaataaagt | aaagtatttc  | gccgtgagag | aaagaacaat | caccatcgtc | 60  |
| taggggtttca | attcattggt | ccagtaacctc | atcgtagcgc | cgctcctctc | ttgtccagac | 120 |
| tccagaagat  | tcaatggcac | ccaagaaaga  | caaagtctct | cctccgtcct | ctaaaccgcc | 180 |
| caaatccggt  | ggcggaagc  | aaaagaaaaa  | gaagtggagc | aaaggaagac | aaaaggagaa | 240 |
| agtgaacaa   | atggttttgt | ttgaccaagc  | aacttacgac | aagcttctct | ctgaggctcc | 300 |
| caagttcaaa  | cttatcactc | cttctatcct  | ctctgaccgt | ttgaggatca | atggatcgct | 360 |
| tgctagaagg  | gcgatcaag  | aattgatggc  | taagggaaca | atcaggatgg | tctctgctca | 420 |
| ctcaagccag  | catagctaca | ctagggcaac  | ccacggctaa | cttcctctga | atgttttagt | 480 |
| tgtttctctg  | tattttactc | aattgcttta  | tgaaccatta | tctttctaga | atgcaccttt | 540 |
| acttgcaaac  | attggtctac |             |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1852:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 108 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..108  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1571164  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1852:  
Met Ala Pro Lys Lys Asp Lys Val Pro Pro Pro Ser Ser Lys Pro Ala  
1                  5                  10                  15  
Lys Ser Gly Gly Gly Lys Gln Lys Lys Lys Trp Ser Lys Gly Lys  
                  20                  25                  30  
Gln Lys Glu Lys Val Asn Asn Met Val Leu Phe Asp Gln Ala Thr Tyr  
                  35                  40                  45  
Asp Lys Leu Leu Ser Glu Ala Pro Lys Phe Lys Leu Ile Thr Pro Ser  
                  50                  55                  60  
Ile Leu Ser Asp Arg Leu Arg Ile Asn Gly Ser Leu Ala Arg Arg Ala  
65                  70                  75                  80  
Ile Arg Glu Leu Met Ala Lys Gly Thr Ile Arg Met Val Ser Ala His  
                  85                  90                  95  
Ser Ser Gln Gln Ile Tyr Thr Arg Ala Thr His Gly  
                  100                 105

(2) INFORMATION FOR SEQ ID NO:1853:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 69 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..69  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1571165  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1853:  
Met Val Leu Phe Asp Gln Ala Thr Tyr Asp Lys Leu Leu Ser Glu Ala  
1                  5                  10                  15  
Pro Lys Phe Lys Leu Ile Thr Pro Ser Ile Leu Ser Asp Arg Leu Arg  
                  20                  25                  30  
Ile Asn Gly Ser Leu Ala Arg Arg Ala Ile Arg Glu Leu Met Ala Lys  
                  35                  40                  45  
Gly Thr Ile Arg Met Val Ser Ala His Ser Ser Gln Gln Ile Tyr Thr  
50                  55                  60  
Arg Ala Thr His Gly  
65

(2) INFORMATION FOR SEQ ID NO:1854:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 748 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..748  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1571166  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1854:  
aaccaaaaaca aaacaaaaca aaaaaaacac gagtggaagc ttttaaacaa aattagaaaa    60  
agagagagag aaatggcgac gtcgggaaca tacgtgacgg aggtgccgct aaaaggaagc    120  
gtggagaaac acttcaagag gtacaggaac gagaactatc tcttcctga cactatcgcc    180  
caccacatcc aaagtgttac tgttcacgat ggcgaatggg acactcaagg aggcacaaag    240



|            |            |             |            |             |            |     |
|------------|------------|-------------|------------|-------------|------------|-----|
| atttggaaat | acacactcgg | agatggaaa   | gaggaggat  | tcaaggagag  | gagagagata | 300 |
| gacgatgaca | ataagatagt | aaaggttgt   | ggattggaag | gtcacgtgat  | ggagcagttc | 360 |
| aaggtgtatg | agattgactt | ccaattttat  | cccaagctcg | aagaagattg  | cgtctgcaaa | 420 |
| atcactatga | tatgggagaa | gcgcaacgat  | gatttcccg  | aaccaagcag  | ctacatgcaa | 480 |
| ctcctcaaga | gtatggttat | tgatattggag | gaccacgtcc | ttaaagctta  | ataaatatca | 540 |
| caaccaccac | catoatcaca | accaccatca  | tcatactcct | atatgtttat  | taaattgttt | 600 |
| tcatttatat | ataatagact | agataagaac  | ctgtataatg | tgccgggataa | aatgattgaa | 660 |
| ataaattatt | atgcgtaaac | ttattgtatg  | agatatcata | tatgtttgta  | tacaagaaaa | 720 |
| tatgtaatta | aagtBttttg | ttttattt    |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:1855:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1571167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1855:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Gln | Asn | Lys | Thr | Lys | Gln | Lys | Lys | His | Glu | Trp | Lys | Leu | Leu | Asn |  |
| 1   |     | 5   |     |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys | Ile | Arg | Lys | Arg | Glu | Arg | Glu | Met | Ala | Thr | Ser | Gly | Thr | Tyr | Val |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Thr | Glu | Val | Pro | Leu | Lys | Gly | Thr | Val | Glu | Lys | His | Phe | Lys | Arg | Tyr |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Asn | Glu | Asn | Tyr | Leu | Phe | Pro | Asp | Thr | Ile | Gly | His | His | Ile | Gln |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ser | Val | Thr | Val | His | Asp | Gly | Glu | Trp | Asp | Thr | Gln | Gly | Gly | Ile | Lys |  |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Ile | Trp | Asn | Tyr | Thr | Leu | Gly | Asp | Gly | Lys | Glu | Glu | Val | Phe | Lys | Glu |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Arg | Arg | Glu | Ile | Asp | Asp | Asp | Asn | Lys | Ile | Val | Lys | Val | Val | Gly | Leu |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |
| Glu | Gly | His | Val | Met | Glu | Gln | Phe | Lys | Val | Tyr | Glu | Ile | Asp | Phe | Gln |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Phe | Ile | Pro | Lys | Ser | Glu | Glu | Asp | Cys | Val | Cys | Lys | Ile | Thr | Met | Ile |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Trp | Glu | Lys | Arg | Asn | Asp | Asp | Phe | Pro | Glu | Pro | Ser | Ser | Tyr | Met | Gln |  |
|     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |  |
| Leu | Leu | Lys | Ser | Met | Val | Ile | Asp | Met | Glu | Asp | His | Val | Leu | Lys | Ala |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |

(2) INFORMATION FOR SEQ ID NO:1856:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1571168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1856:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Thr | Ser | Gly | Thr | Tyr | Val | Thr | Glu | Val | Pro | Leu | Lys | Gly | Thr |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |  |
| Val | Glu | Lys | His | Phe | Lys | Arg | Tyr | Arg | Asn | Glu | Asn | Tyr | Leu | Phe | Pro |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1857:

(A) LENGTH: 1066 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(A) NAME/KEY: -

(B) LOCATION: 1..1066

(D) OTHER INFORMATION: / Ceres Seq. ID 1571206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1857:

|             |             |             |             |            |            |      |
|-------------|-------------|-------------|-------------|------------|------------|------|
| aagactctgt  | tttttccaa   | gatgtctggt  | tctctcttt   | gtttctgcc  | aatctctact | 60   |
| tttttaggga  | ctgtctcttc  | tctttttctg  | tgattaaaac  | ctctgaattc | gtctccaatt | 120  |
| gacgcgaaaa  | agggcattga  | ggaggtgaac  | gagagaatcat | caactagtac | gtcttaactc | 180  |
| gataataaca  | atgcacaaaa  | tgtatcaagg  | ggagactctg  | aattgaatac | ttgtttgcga | 240  |
| ctagctcaag  | atccgattgt  | caactctctg  | ggcactcttc  | ttgtgtggcc | ttgtctatac | 300  |
| cgtttgtaac  | accacaaatc  | acatctctca  | gaatgtccgg  | tttgtaaagc | cggtggtcaa | 360  |
| gacgataagc  | ttgttcctct  | tacgtgttga  | ggcagaagac  | actgacgcc  | gactgacaaa | 420  |
| cgttatccgg  | gtttcaagat  | tgactaacga  | ccaacaggct  | aaagacgtca | gactgtgcct | 480  |
| ctctctcttc  | gcttcgaagc  | tgcgataaag  | tttttcaact  | acagctattg | ttgtatgggt | 540  |
| ggaaatctgc  | cgatgatggc  | gactacaggg  | tttgggaatt  | ctcagatgtg | gtttgtgtgt | 600  |
| ttgtttacct  | ctttgtttaa  | ctttccagtt  | caatggattc  | atgatgTcac | gctttatggc | 660  |
| tcaaacaccgg | gttatctctta | cggtggttat  | cataacggtt  | tctgtgtgag | tcctctctgt | 720  |
| ggcaacaagac | gtctcatggc  | tcgtggagga  | aaccaaaagt  | atgcattctc | gaagaatact | 780  |
| ctctcttttt  | ttggaaatgc  | tgttgtgata  | ttctctactc  | ggtgaaaacg | aatcacattt | 840  |
| gggtgatctc  | caggttatgat | caaaacttact | tacttgtgtgc | aagtgtgtta | tgtaaatagt | 900  |
| gtaatagctg  | tgctgaactg  | tcgtctattt  | cgaactgtgt  | attgtatttt | ttgtttgaag | 960  |
| atgaacatgt  | agttcacaag  | cttttttaca  | caactctctt  | gttgcctttg | tgttttgtct | 1020 |
| aagcatctta  | ttaaaactaq  | tgttqaaaata | gaagctgcgt  | gtatgag    |            |      |

(2) INFORMATION FOR SEQ ID NO:1858:

(A) LENGTH: 227 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..227

(D) OTHER INFORMATION: / Ceres Seq.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1858:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Asn | Gly | Glu | Ser | Ser | Thr | Ser | Thr | Ser | Tyr | Ser | Asp | Asn | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Asp | Thr | Asn | Asp | Gln | Gly | Gly | Asp | Phe | Glu | Cys | Asn | Ile | Cys | Phe |

|                         |                         |                             |
|-------------------------|-------------------------|-----------------------------|
| 20                      | 25                      | 30                          |
| Glu Leu Ala Gln Asp Pro | Ile Val Thr Leu Cys Gly | His Leu Phe Cys             |
| 35                      | 40                      | 45                          |
| Trp Pro Cys Leu Tyr Arg | Trp Leu His His His     | Ser His Gln Glu             |
| 50                      | 55                      | 60                          |
| Cys Pro Val Cys Lys Ala | Val Val Gln Asp Asp     | Lys Leu Val Pro Leu         |
| 65                      | 70                      | 75                          |
| Tyr Gly Arg Gly Lys     | Asn Gln Thr Asp         | Pro Arg Ser Lys Arg Tyr Pro |
| 85                      | 90                      | 95                          |
| Gly Leu Arg Ile Pro     | Asn Arg Pro Thr         | Gly Gln Arg Pro Glu Thr Ala |
| 100                     | 105                     | 110                         |
| Ala Pro Pro Gln Pro     | Glu Ala Ser Asn Phe     | Phe Asn Tyr Gly             |
| 115                     | 120                     | 125                         |
| Ile Gly Leu Met Gly     | Gly Ile Met Pro Met     | Met Ala Thr Thr Arg Phe     |
| 130                     | 135                     | 140                         |
| Gly Asn Phe Ser Met     | Gly Phe Gly Gly Leu     | Leu Pro Ser Leu Phe Asn     |
| 145                     | 150                     | 155                         |
| Phe Gln Phe His Gly     | Phe His Asp Ala Thr     | Leu Tyr Gly Ser Thr Pro     |
| 165                     | 170                     | 175                         |
| Gly Tyr Pro Tyr Gly     | Gly Tyr His Asn Gly     | Phe Arg Gly Val Pro Pro     |
| 180                     | 185                     | 190                         |
| Arg Gly Gln Glu Arg     | Pro Met Ala Arg         | Gly Gly Asn Gln Ser Asp Ala |
| 195                     | 200                     | 205                         |
| Phe Leu Lys Asn Ile     | Leu Phe Phe Val Gly     | Ile Cys Val Val Ile Phe     |
| 210                     | 215                     | 220                         |
| Leu Ile Trp             |                         |                             |
| 225                     |                         |                             |

(2) INFORMATION FOR SEQ ID NO:1859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..520
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1859:

|             |            |             |            |             |             |     |
|-------------|------------|-------------|------------|-------------|-------------|-----|
| aagttctaaaa | gtcctcaaat | cccgcaaaagc | tttttcagct | tctttgttga  | attgcgagca  | 60  |
| gaggtagaaaa | tcagcaggaa | acaaaaatgt  | tgttcttttc | ttacttcaag  | gatttggttg  | 120 |
| gacaagaagt  | gacggttgag | ctgaagaatg  | atttagccat | aagaggaaact | cttcaactaag | 180 |
| ttgatcagta  | tctgaatatc | aagctcgaga  | acactagggt | tggtgaccag  | gaagtaccct  | 240 |
| cacatgcttt  | cagtgagaaa | ctgtttcatt  | agaggatctg | tgttaaggta  | cgtgcagtta  | 300 |
| cctaaagatg  | gagtcgatgt | tgatttgcct  | ccagcgccag | Ctagaagaga  | agctagggggt | 360 |
| ggctgattct  | gaatatcttt | tgatctcca   | aaacttgat  | acttttcatt  | cggcgtaagt  | 420 |
| gctttataat  | gaattattcc | ctgatgtaga  | gccaatggta | tgcccatgaa  | tcttgtttcca | 480 |
| ttttattaac  | aatggataat | ttaatttctt  | ttctcgctcc |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1860:

Met Leu Phe Phe Ser Tyr Phe Lys Asp Leu Val Gly Gln Glu Val Thr

1 5 10 15  
Val Glu Leu Lys Asn Asp Leu Ala Ile Arg Gly Thr Leu His Ser Val  
20 25 30  
Asp Gln Tyr Leu Asn Ile Lys Leu Glu Asn Thr Arg Val Val Asp Gln  
35 40 45  
Glu Val Pro Ser His Ala Phe Ser Glu Lys Leu Phe His Gln Arg Ile  
50 55 60  
Cys Gly Lys Val Arg Ala Val Thr  
65 70

(2) INFORMATION FOR SEQ ID NO:1861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571222
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1861:

Met Leu Ser Val Arg Asn Cys Phe Ile Arg Gly Ser Val Val Arg Tyr  
1 5 10 15  
Val Gln Leu Pro Lys Asp Gly Val Asp Val Asp Leu Leu His Gly Ala  
20 25 30  
Ala Arg Arg Glu Ala Arg Gly Gly  
35 40

(2) INFORMATION FOR SEQ ID NO:1862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571223
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1862:

Met Glu Ser Met Leu Ile Cys Phe Thr Ala Gln Leu Glu Glu Lys Leu  
1 5 10 15  
Gly Val Ala Asp Ser Glu Ile Ser Leu Tyr Leu Gln Asn Leu Asn Thr  
20 25 30  
Phe His Ser Ala  
35

(2) INFORMATION FOR SEQ ID NO:1863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2401
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571228
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1863:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| acaaatcttt | ctctttctct | ttctctctct | aacacaattt | agaacaaaaa | tttcttcttt | 60  |
| ctctctcccc | gagaggccct | tcgctgttca | ttgaagttct | cttagaattt | tcatacaact | 120 |
| tggttctgta | atttgcaaaa | cagacaacaa | tggttgagcg | tggaagagg  | actcaacaat | 180 |
| gtttcagaga | caacaacaat | gacaacaacc | ggaatcaagg | gagaagactt | tcttacgaat | 240 |

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| cogaagaaaa  | aaagatcgat  | aacaaagacg | atctcgttgt  | tgtttacaga  | atcttatgcc  | 300  |
| caagtgggtg  | catgggaagt  | gttatagcca | aaagtggcaa  | agttattaac  | ttgattaggc  | 360  |
| aagaaactag  | agctaggagt  | aaagtgtgtg | atcctttttc  | aggttgtagc  | gaaagagctc  | 420  |
| taacgatctt  | ttgctcgggt  | tcggagaaga | aaagacattg  | tgacatttag  | tatagtgaat  | 480  |
| tggaattact  | tggtctcttg  | tggtctgctc | aaagctgctc  | tcttaaaagt  | catgatgcta  | 540  |
| ttgtgggttc  | tttagctact  | gctgctgaga | acactaaagt  | tgatagagat  | gacttttaga  | 600  |
| aatgtcgtct  | tttagtcccg  | tctagtcagt | gttctattgt  | catttggtaaa | tctgggtcga  | 660  |
| ttattaagaa  | cattagaggt  | agaactagag | ctaacggttaa | gggtgtctct  | aaagatgctt  | 720  |
| ctgatccttc  | tcacacttgt  | gccatggatt | ttgacaacat  | tggttatgata | tctgggtgaga | 780  |
| McTtgaatcc  | gtgaagaagg  | cactttttcg | tgttttcgca  | atcatgtaca  | aagtcaagtcc | 840  |
| tcgagaacag  | attcctctcg  | atacaactgt | ccaagaagtt  | cccgctagta  | ttataattcc  | 900  |
| gtctgatctg  | tctatctatg  | cacaagccgg | tttataccoc  | agtcaggatt  | ctattttcca  | 960  |
| acatgggggc  | aatgttttcat | cgttttatcg | tacactacct  | cagggtcatg  | gagaaaatgc  | 1020 |
| tgcaaatcca  | ctgcgggttt  | tttctgcttc | tgctcttctc  | gtggttcaatg | gtttttggtg  | 1080 |
| gtcttcaga   | tcagaaaaagt | tggtctataa | agttatttgc  | gctttctcca  | aaattggtcg  | 1140 |
| tggtatcggt  | aaaggaggat  | taaccattaa | gggaataaga  | caagcaagcg  | ggctctcatat | 1200 |
| cgaaagttaat | gactcgagag  | caaatcatga | tgatgactgt  | gttatcactg  | tcactgctac  | 1260 |
| agagtctctc  | gatgatttga  | agtcctatgc | gggtgaagct  | gttctctctac | ttcaagagaa  | 1320 |
| aattaatgat  | gaagcagagg  | acaaagttaa | aatgcaactc  | cttgatctctt | ctaaggtaat  | 1380 |
| agggatgcatt | atagggaaaa  | gtggctcaat | cataagtga   | atcagagaaa  | ggacaagaagc | 1440 |
| tgatattctat | attctcgaaag | gaaataatac | gcttaagagc  | tgatcccaat  | gatgactctg  | 1500 |
| ttcgagatgc  | tggtgaagta  | agcaatgtga | gagatgctct  | tattcagata  | gttctgagggc | 1560 |
| ttcgagatga  | tggttttaag  | gatagagaga | ctgggttccag | gaatcaacct  | ctcgcaagat  | 1620 |
| ctgagataaa  | caattttctc  | tttccaagta | tgatgaatac  | tggtcttgca  | cttctctcaat | 1680 |
| ctttctatgc  | ttctgttccg  | caagttgctt | ctgtagattt  | cgataggaga  | ccagaaaacc  | 1740 |
| ggagcagcat  | gaagcatgct  | ctctcgagt  | gtggaatact  | tggttatgga  | agttttccgg  | 1800 |
| tgggcaaatc  | aaagtattgga | tccaactctc | cttaactcat  | caatctatat  | ggaggattgc  | 1860 |
| ctcagctctac | tactatggag  | gttcgaatcc | cagcaaatgc  | agtggtgtaa  | gttatgggca  | 1920 |
| gaggagagag  | caactgtggc  | aacataagaa | ggatatacag  | agccatgata  | gaaatttctc  | 1980 |
| attccaaaaa  | ttcccatggc  | ggtgcgcttg | ctctcatctc  | cgggacattc  | gaacagaaGc  | 2040 |
| gtaccgcaga  | gaactgtgtc  | caagctttta | tcatgtccac  | ttgaataatt  | tgctctgccc  | 2100 |
| cttaatacct  | ttccatggaa  | gtgtgttcca | tcaatctacc  | tctcaagtgt  | ttcttttgat  | 2160 |
| cggtgtttct  | aggttttctc  | ctctccatca | agctcatgtt  | tagatatggt  | tgcatctctc  | 2220 |
| atcaaacatt  | tcggtatctc  | atctcgactc | agttactttt  | gggttctcgt  | gctagacatt  | 2280 |
| tttagtgtct  | tcaggaccat  | tcttttcccc | tttctctgog  | agctgttctg  | actataacta  | 2340 |
| cttatctccg  | tcgagtaaaa  | caaaatcggt | cttatatcaa  | tcaaaacttg  | cttattctSc  | 2400 |

(2) INFORMATION FOR SEQ ID NO:1864:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1571229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1864:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Glu | Arg | Gly | Lys | Arg | Thr | His | Asn | Arg | Phe | Arg | Asp | Asn | Asn |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Asn | Asp | Asn | Asn | Arg | Asn | Gln | Arg | Arg | Arg | Leu | Ser | Tyr | Glu | Ser | Glu |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Lys | Lys | Ile | Asp | Asn | Lys | Asp | Asp | Leu | Val | Val | Val | Tyr | Arg | Ile |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Leu | Cys | Pro | Ser | Gly | Val | Met | Gly | Ser | Val | Ile | Gly | Lys | Ser | Gly | Lys |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Val | Ile | Asn | Leu | Ile | Arg | Gln | Glu | Thr | Arg | Ala | Arg | Ile | Lys | Val | Val |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |
| Asp | Pro | Phe | Pro | Gly | Cys | Ser | Glu | Arg | Val | Ile | Thr | Ile | Phe | Cys | Ser |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |

Val Ser Glu Lys Lys Asp Ile Val Asp Ile Glu Tyr Ser Glu Leu Asp  
100 105 110  
Tyr Ser Val Pro Leu Cys Ser Ala Gln Ala Ala Leu Lys Val His  
115 120 125  
Asp Ala Ile Val Ala Ser Leu Ala Thr Ala Ala Glu Asn Thr Lys Ile  
130 135 140  
Asp Arg Asp Asp Phe Arg Glu Cys Arg Leu Leu Val Pro Ser Ser Gln  
145 150 155 160  
Cys Ser Ile Val Ile Gly Lys Ser Gly Ser Ile Ile Lys Asn Ile Arg  
165 170 175  
Gly Arg Thr Arg Ala Asn Val Lys Val Val Ser Lys Asp Ala Ser Asp  
180 185 190  
Pro Ser His Thr Cys Ala Met Asp Phe Asp Asn Ile Val Met Ile Ser  
195 200 205  
Gly Glu Xaa Leu Asn Pro  
210

(2) INFORMATION FOR SEQ ID NO:1865:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1571230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1865:

Met Gly Ser Val Ile Gly Lys Ser Gly Lys Val Ile Asn Leu Ile Arg  
1 5 10 15  
Gln Glu Thr Arg Ala Arg Ile Lys Val Val Asp Pro Phe Pro Gly Cys  
20 25 30  
Ser Glu Arg Val Ile Thr Ile Phe Cys Ser Val Ser Glu Lys Lys Asp  
35 40 45  
Ile Val Asp Ile Glu Tyr Ser Glu Leu Asp Tyr Ser Val Pro Leu Cys  
50 55 60  
Ser Ala Gln Ala Ala Leu Leu Lys Val His Asp Ala Ile Val Ala Ser  
65 70 75 80  
Leu Ala Thr Ala Ala Glu Asn Thr Lys Ile Asp Arg Asp Asp Phe Arg  
85 90 95  
Glu Cys Arg Leu Leu Val Pro Ser Ser Gln Cys Ser Ile Val Ile Gly  
100 105 110  
Lys Ser Gly Ser Ile Ile Lys Asn Ile Arg Gly Arg Thr Arg Ala Asn  
115 120 125  
Val Lys Val Val Ser Lys Asp Ala Ser Asp Pro Ser His Thr Cys Ala  
130 135 140  
Met Asp Phe Asp Asn Ile Val Met Ile Ser Gly Glu Xaa Leu Asn Pro  
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:1866:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1571231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1866:

Met Tyr Lys Val Ser Pro Arg Glu Gln Ile Pro Leu Asp Thr Thr Val  
1 5 10 15  
Gln Glu Val Pro Ala Ser Ile Ile Ile Pro Ser Asp Leu Ser Ile Tyr  
20 25 30  
Pro Gln Ala Gly Leu Tyr Pro Ser Gln Asp Ser Ile Phe Gln His Gly  
35 40 45  
Ala Asn Val Ser Ser Phe Ile Gly Thr Leu Pro Gln Gly Tyr Gly Glu  
50 55 60  
Asn Ala Ala Asn Pro Leu Pro Val Phe Ser Ala Ser Ala Leu Pro Val  
65 70 75 80  
Val His Gly Phe Gly Gly Ser Ser Arg Ser Glu Lys Leu Ala Ile Lys  
85 90 95  
Val Ile Cys Ala Ser Ser Lys Ile Gly Arg Val Ile Gly Lys Gly Gly  
100 105 110  
Leu Thr Ile Lys Gly Ile Arg Gln Ala Ser Gly Ser His Ile Glu Val  
115 120 125  
Asn Asp Ser Arg Thr Asn His Asp Asp Asp Cys Val Ile Thr Val Thr  
130 135 140  
Ala Thr Glu Ser Pro Asp Asp Leu Lys Ser Met Ala Val Glu Ala Val  
145 150 155 160  
Leu Leu Leu Gln Glu Lys Ile Asn Asp Glu Asp Glu Asp Lys Val Lys  
165 170 175  
Met Gln Leu Leu Val Ser Ser Lys Val Ile Gly Cys Ile Ile Gly Lys  
180 185 190  
Ser Gly Ser Ile Ile Ser Glu Ile Arg Lys Arg Thr Lys Ala Asp Ile  
195 200 205  
His Ile Ser Lys Gly Asn Asn Thr Pro Lys Ser  
210 215

(2) INFORMATION FOR SEQ ID NO:1867:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..731
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1867:

aaaaacacaa actctctata ctcaacaat tgtttaactc atctttctaa gttggtttcg 60  
attcaagaat atcacaatga ctaagtgtcg ccttctatt ctgctctct cggtctgttt 120  
cctgtctctt atttcatcgt ccctctgttt ccctacacct agttttgtcg ctagagtaa 180  
ctattctctg gtgcaagaag aggtcaaaaa ggttcacaga tacacagaac ctgaggagcc 240  
ggaagttcca gaagagccgg agctgccttc accggaggag cctgagattc cagaagagcc 300  
tgagattcca gaagagcctg aggttctctg agaaccggaa gttcctgaag agcccgaaga 360  
accagaagag ccagcagggt caacatttga atttccatca tggtttcoga gcttccctat 420  
tcccgtgttt aatggcgggt tgccaaagac tgaaaagaca aaacctacat caacagttga 480  
agaggttaac gtttctaaca agaagccata gatcaatggg taaagaacgt caaatgatta 540  
tataaactat atatgcaatt atagtttttg ttgtttttg gttaaagatg agagattaca 600  
tatgtattac agtattagag tcttcacctat gtcattgatt gttctctaaa cgctcctgat 660  
ataactctgt actaattctc tcttgtaaca tgtatatctc ttgtggtaca aaaaatatat 720  
ataaactct t

(2) INFORMATION FOR SEQ ID NO:1868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1571236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1868:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Asn | Val | Arg | Leu | Pro | Ile | Leu | Val | Ser | Ser | Val | Leu | Phe | Leu |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Phe | Ile | Ser | Ser | Ser | Leu | Leu | Phe | Pro | Thr | Pro | Ser | Phe | Ala | Ala |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Arg | Val | Ser | His | Ser | Ser | Leu | Val | Gln | Glu | Glu | Val | Lys | Lys | Val | Pro | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |     |
| Tyr | Thr | Glu | Pro | Glu | Glu | Pro | Pro | Glu | Glu | Pro | Glu | Pro | Glu | Leu | Pro |     |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |     |
| Ser | Pro | Glu | Glu | Pro | Glu | Ile | Pro | Glu | Glu | Pro | Glu | Ile | Pro | Glu | Glu |     |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |     |
| Pro | Glu | Val | Pro | Gly | Glu | Pro | Glu | Val | Pro | Glu | Glu | Pro | Glu | Glu | Pro |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Glu | Glu | Pro | Ala | Gly | Ser | Thr | Phe | Glu | Phe | Pro | Ser | Trp | Phe | Pro | Ser |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Phe | Pro | Ile | Pro | Gly | Val | Asn | Gly | Gly | Leu | Pro | Lys | Thr | Glu | Lys | Thr |     |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |     |
| Lys | Pro | Thr | Ser | Thr | Val | Glu | Glu | Val | Asn | Val | Ser | Asn | Lys | Lys | Pro |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1869:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 941 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..941

(D) OTHER INFORMATION: / Ceres Seq. ID 1571241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1869:

|             |             |             |            |            |             |     |
|-------------|-------------|-------------|------------|------------|-------------|-----|
| atagaatata  | aaagttgcta  | aatttgatta  | aagatatgga | caaagttcca | agattttttg  | 60  |
| tttgtaaact  | ttaaaatggt  | ttatgttatt  | acttggtttt | ggtttttgta | ggagttctcg  | 120 |
| gtgatggatt  | tatggctcgt  | gatttaacta  | tagagaacac | ggcaggagca | gatgcgcacc  | 180 |
| aagcggttgc  | gttttagatca | gacagtgatt  | tttcggtact | tgaaaactgc | gagtttcttg  | 240 |
| ggaaccaaga  | cactctttat  | gctcactctc  | tcgcgtcagt | ctacaaacaa | tgtcgaaatcc | 300 |
| aaggcaacct  | agacttcact  | tttggttaact | cagctgcctg | attccaaagt | tgtgatatcc  | 360 |
| taatcgctgc  | aaaacactcc  | aaactcgagc  | aaggcggctg | aaacaaacgc | atcacagcac  | 420 |
| acgggaggat  | tgatcgcctg  | cagtcocacg  | gattttgtgt | tttgaactgt | tcgatttaacg | 480 |
| gaacagaggga | atacatgaag  | gagtttcaag  | ctaaccctga | aaggcataag | aactctcttg  | 540 |
| gaagaccgtg  | gaaggagttt  | tcgaggacgc  | ttttttgtaa | ctgtaactct | gagttcttga  | 600 |
| ttagtctctga | tggatggatg  | ccttggaaag  | gggatttcgc | attgaagact | ttgtattacg  | 660 |
| gtgatataaa  | gaatacgggt  | ccgggatcgc  | ttagatcgag | tagggttcca | tggagtagtg  | 720 |
| agataccaga  | gaagcatggt  | gatgtttact  | ctgttgccaa | ttttattcag | gctgatgagt  | 780 |
| gggcttccac  | gactgcttga  | ttttttTtaa  | aggaaacatg | aggtttttag | attttgaaaa  | 840 |
| gaagagaaga  | gaagtctgtca | ttgtaacttt  | attgtagtgt | caaatattag | tgtggtttct  | 900 |
| ttatcgctca  | ttgggggattc | ataatagatt  | aataattgaa | g          |             |     |

(2) INFORMATION FOR SEQ ID NO:1870:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:



- (A) NAME/KEY: peptide  
(B) LOCATION: 1..222  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1870:

```
Met Ala Arg Asp Leu Thr Ile Glu Asn Thr Ala Gly Ala Asp Ala His
1 5 10 15
Gln Ala Val Ala Phe Arg Ser Asp Ser Asp Phe Ser Val Leu Glu Asn
20 25 30
Cys Glu Phe Leu Gly Asn Gln Asp Thr Leu Tyr Ala His Ser Leu Arg
35 40 45
Gln Phe Tyr Lys Gln Cys Arg Ile Gln Gly Asn Val Asp Phe Ile Phe
50 55 60
Gly Asn Ser Ala Ala Val Phe Gln Asp Cys Asp Ile Leu Ile Ala Ser
65 70 75 80
Lys His Ser Lys Leu Glu Gln Gly Gly Ala Asn Asn Ala Ile Thr Ala
85 90 95
His Gly Arg Ile Asp Ala Ser Gln Ser Thr Gly Phe Val Phe Leu Asn
100 105 110
Cys Ser Ile Asn Gly Thr Glu Glu Tyr Met Lys Glu Phe Gln Ala Asn
115 120 125
Pro Glu Arg His Lys Asn Phe Leu Gly Arg Pro Trp Lys Glu Phe Ser
130 135 140
Arg Thr Val Phe Val Asn Cys Asn Leu Glu Ser Leu Ile Ser Pro Asp
145 150 155 160
Gly Trp Met Pro Trp Asn Gly Asp Phe Ala Leu Lys Thr Leu Tyr Tyr
165 170 175
Gly Glu Tyr Lys Asn Thr Gly Pro Gly Ser Val Arg Ser Ser Arg Val
180 185 190
Pro Trp Ser Ser Glu Ile Pro Glu Lys His Val Asp Val Tyr Ser Val
195 200 205
Ala Asn Phe Ile Gln Ala Asp Glu Trp Ala Ser Thr Thr Ala
210 215 220
```

(2) INFORMATION FOR SEQ ID NO:1871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..543  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1871:

```
ctcagaacat ctcaaatctca attgaaatct taaaatccaa aattttcccg agaaaaatta 60
aagtttccgt agaaaatgtc aggtcgtggg aaggagagca aaggattggg caaaggagga 120
gctaaacgtc acaggaagggt tctgagagac aacatccaag gaatcactaa gccgcgcgatt 180
cggagattgg ctgctagagg tggagtcaag cgtattagtg gtttdRatct acgaggagac 240
acgtggcggt ctcaagatct ttttgagaa tggtatccgt gacgccgtta cttacactga 300
gcaagctcgg aggaagaagg tgactgctat ggatgttgtt tatgctotta agagacaagg 360
aagaactctc tacggattcg gcggctaggg tttttgattg ttgttttttg tgttttctacg 420
ttttattaga ttgtaatatt cagaatttgg tgttaacttc gaaaaaatta aagaattgaa 480
ggttgttgtt gcaatttcgt gattgttgaa ggtgttgttg caaacttyya gtaatttcag 540
ttt
```

(2) INFORMATION FOR SEQ ID NO:1872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1571244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1872:

Met Ser Gly Arg Gly Lys Gly Gly Lys Gly Leu Gly Lys Gly Gly Ala  
1 5 10 15  
Lys Arg His Arg Lys Val Leu Arg Asp Asn Ile Gln Gly Ile Thr Lys  
20 25 30  
Pro Ala Ile Arg Arg Leu Ala Arg Arg Gly Gly Val Lys Arg Ile Ser  
35 40 45  
Gly Xaa Xaa Leu Arg Gly Asp Thr Trp Arg Ser Gln Asp Leu Phe Gly  
50 55 60  
Glu Cys Tyr Pro  
65

(2) INFORMATION FOR SEQ ID NO:1873:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2135 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2135

(D) OTHER INFORMATION: / Ceres Seq. ID 1571245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1873:

|            |             |             |            |             |             |      |
|------------|-------------|-------------|------------|-------------|-------------|------|
| atcacctctc | tcttctctcg  | aaatcacccat | gagtatggaa | gcaacggagc  | tacaagatct  | 60   |
| ctctgacgac | gcgcattacg  | ccgcttctca  | acaacaagga | tcggctagta  | tgatgcgtaS  | 120  |
| cgatagcgga | aagagaagtt  | tacaaaagtg  | acacgaagac | gctgtattga  | tttatttgaa  | 180  |
| agataacgtt | gcaattcatc  | ctacacagtt  | cgcatctgag | aggattagtg  | gtagattgaa  | 240  |
| gttgactaag | caagattctg  | tctcttctct  | gtcgtggatt | ccgtacaagg  | gacaaacatc  | 300  |
| aaatgcaaa  | ctatcagaga  | aagacaggag  | tctttatacc | atcaccgcgg  | ttccgtttac  | 360  |
| tgaagtgagg | tccattagga  | gacacactcc  | tgctctcgga | tgccagtatg  | taattgttgt  | 420  |
| ccgtgtctct | ggacttgcat  | tccacctctc  | gtacttctac | aatggaggag  | tcaggggagt  | 480  |
| tctggccatg | gtgaagcagc  | atgtttttct  | tgcaaggtcg | tcagaagatc  | aaaatgtgtt  | 540  |
| cattgtgaat | gatttttcaga | gtcccttgca  | gagaactttg | tcttcattgg  | agtgccaa    | 600  |
| ttcaactgct | gtagcaagtg  | gacaatccgt  | ataccattat | gacggagggt  | ctcttagtga  | 660  |
| aaatcaaa   | agaaacagtt  | cagatgttgg  | taataagata | tctagtgttt  | ccagctctgg  | 720  |
| cttcagaaa  | caaaagagtc  | atgatccaac  | tcgggatctt | tcaatccatc  | tactagagaa  | 780  |
| gtttctctcg | gtttaccaat  | ttgctcgaga  | tacaactact | cagctgtttt  | cggaacaaa   | 840  |
| tggtcttggt | tccattgaca  | agagatggaa  | taacaaaccc | gtacatagtt  | atcctgaaaa  | 900  |
| gttgctgaac | atcgttgagg  | aaaaagcatc  | tgaactccgt | catagttatt  | ctgaaaatga  | 960  |
| ccctctcaag | gatgacgaaa  | tttcttatat  | tgatgtccct | gctgatccct  | tagagtttga  | 1020 |
| taaatataat | ttgatgtggg  | gaaaaccaa   | gcaaccacca | atggggcgata | aagagtctaac | 1080 |
| agcatgtttg | gattctgaag  | ggcaggttgt  | ggaatcaaaa | gctcttcagg  | agagagtgtt  | 1140 |
| ctatggaggc | attgagcacc  | agttgcgtag  | agaggatagg | cccttctctc  | tgggatatta  | 1200 |
| tgcatatgat | tcgacatatg  | cagagagaga  | atattcttga | tctgtcaaac  | ggatggaaata | 1260 |
| tgaacattg  | aaacagcaat  | ggcagagcat  | ttcccttgaa | caagcaaaaa  | gggttcacaaa | 1320 |
| atatacgtag | agaaaaggat  | tgatagataa  | agatgtggta | agaactgata  | gggcatttga  | 1380 |
| atactatgaa | ggggatgaca  | atctacatgt  | caatagcatg | cgatgatatt  | tggtgaccta  | 1440 |
| ctctctctac | aaattttgac  | tggtgttactg | ccagggaatg | agtgattatc  | tgctctctaat | 1500 |
| cttgtctcgt | atggaggatg  | aatcagaatc  | tttttggtgW | ttcRtgccac  | tgatggaaacg | 1560 |
| acttgaccac | aaactttaac  | gtgaccagaa  | tggaatgcac | actcagctct  | ctgcactctc  | 1620 |
| aaagctggta | gagttgctcg  | atagcccgcct | acataattac | tttaaggaga  | atgactgctt  | 1680 |
| gaattacttc | ttctgttttc  | gctggtattct | gattcagttt | aaaagggaat  | ttgagtatga  | 1740 |
| gaagacaatg | cagctgtggg  | aggtgatgtg  | gacccactac | ctctcagaac  | attttcacct  | 1800 |
| atatgtttgt | gtggcggtct  | tgaagcgatg  | ccgcagcaag | ataatgggag  | aacagatgga  | 1860 |
| ttttgtactc | ctcttaaatg  | tctcaatgta  | gtctctggg  | catattgac   | tcgattcaac  | 1920 |
| agtcagagat | gcgcagaacac | tttccataga  | agctggtgaa | aatggtgctg  | ctagcattcc  | 1980 |
| tccaggaaac | ctcctctctc  | tacccttga   | tgacggtacc | ttatatctc   | aggaagatga  | 2040 |

tgttttgtaa gtaatacgac ttttcttttt tcttctggac atgttaccaa aatttggatt 2100  
gcttttacta gaaatcccat acaatgatta agggc

(2) INFORMATION FOR SEQ ID NO:1874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 682 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..682
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1874:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Pro | Leu | Ser | Ser | Pro | Glu | Ile | Thr | Met | Ser | Met | Glu | Ala | Thr | Glu |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu | Gln | Asp | Leu | Ser | Asp | Asp | Ala | Asp | Tyr | Ala | Ala | Ser | Gln | Gln | Gln |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gly | Ser | Ala | Ser | Met | Met | Arg | Xaa | Asp | Ser | Gly | Lys | Arg | Ser | Leu | Gln |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Glu | His | Glu | Asp | Ala | Val | Leu | Ile | Tyr | Leu | Lys | Asp | Asn | Val | Ala |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ile | His | Pro | Thr | Gln | Phe | Ala | Ser | Glu | Arg | Ile | Ser | Gly | Arg | Leu | Lys |  |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Leu | Thr | Lys | Gln | Asp | Ser | Val | Leu | Phe | Leu | Ser | Trp | Ile | Pro | Tyr | Lys |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Gly | Gln | Thr | Ser | Asn | Ala | Lys | Leu | Ser | Glu | Lys | Asp | Arg | Ser | Leu | Tyr |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |
| Thr | Ile | Thr | Ala | Val | Pro | Phe | Thr | Glu | Val | Arg | Ser | Ile | Arg | Arg | His |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Thr | Pro | Ala | Leu | Gly | Trp | Gln | Tyr | Val | Ile | Val | Val | Leu | Ser | Ser | Gly |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Leu | Ala | Phe | Pro | Pro | Leu | Tyr | Phe | Tyr | Asn | Gly | Gly | Val | Arg | Glu | Phe |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Leu | Ala | Met | Val | Lys | Gln | His | Val | Phe | Leu | Ala | Arg | Ser | Ser | Glu | Asp |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Gln | Asn | Val | Phe | Ile | Val | Asn | Asp | Phe | Gln | Ser | Pro | Leu | Gln | Arg | Thr |  |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |
| Leu | Ser | Ser | Leu | Glu | Leu | Pro | Ser | Ser | Leu | Pro | Val | Ala | Ser | Gly | Gln |  |
|     |     |     | 195 |     |     | 200 |     |     |     |     | 205 |     |     |     |     |  |
| Ser | Val | Tyr | Pro | Leu | Asp | Gly | Gly | Ser | Ser | Ser | Glu | Asn | Gln | Arg | Arg |  |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Thr | Ser | Ser | Asp | Val | Gly | Asn | Arg | Val | Ser | Ser | Val | Ser | Gln | Ser | Gly |  |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |  |
| Phe | Arg | Lys | Gln | Lys | Ser | His | Asp | Pro | Thr | Arg | Asp | Leu | Ser | Ile | His |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Leu | Leu | Glu | Lys | Phe | Ser | Leu | Val | Thr | Lys | Phe | Ala | Arg | Asp | Thr | Thr |  |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |  |
| Thr | Gln | Leu | Phe | Ser | Glu | Asn | Asn | Gly | Phe | Gly | Ser | Ile | Asp | Lys | Arg |  |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Trp | Asn | Asn | Gln | Pro | Val | His | Ser | Tyr | Pro | Glu | Lys | Leu | Ser | Asn | Ile |  |
|     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Ala | Glu | Glu | Lys | His | His | Glu | Ile | Arg | His | Ser | Tyr | Ser | Glu | Asn | Asp |  |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     | 320 |     |  |
| Leu | Leu | Lys | Asp | Asp | Glu | Ile | Ser | Tyr | Ile | Asp | Val | Pro | Ala | Asp | Pro |  |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Leu | Glu | Phe | Asp | Lys | Leu | Ser | Leu | Met | Trp | Gly | Lys | Pro | Arg | Gln | Pro |  |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     | 350 |     |     |     |  |
| Pro | Met | Gly | His | Lys | Glu | Phe | Thr | Ala | Leu | Leu | Asp | Ser | Glu | Gly | Arg |  |
|     |     |     | 355 |     |     | 360 |     |     |     |     | 365 |     |     |     |     |  |
| Val | Val | Glu | Ser | Lys | Ala | Leu | Arg | Glu | Arg | Val | Phe | Tyr | Gly | Gly | Ile |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Met | Glu | Ala | Thr | Glu | Leu | Gln | Asp | Leu | Ser | Asp | Asp | Ala | Asp |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Ala | Ala | Ser | Gln | Gln | Gln | Gly | Ser | Ala | Ser | Met | Met | Arg | Xaa | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Gly | Lys | Arg | Ser | Leu | Gln | Ser | Glu | His | Glu | Asp | Ala | Val | Leu | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Tyr | Leu | Lys | Asp | Asn | Val | Ala | Ile | His | Pro | Thr | Gln | Phe | Ala | Ser | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Ile | Ser | Gly | Arg | Leu | Lys | Leu | Thr | Lys | Gln | Asp | Ser | Val | Leu | Phe |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |

Leu Ser Trp Ile Pro Tyr Lys Gly Gln Thr Ser Asn Ala Lys Leu Ser  
85 90 95  
Glu Lys Asp Arg Ser Leu Tyr Thr Ile Thr Ala Val Pro Phe Thr Glu  
100 105 110  
Val Arg Ser Ile Arg Arg His Thr Pro Ala Leu Gly Trp Gln Tyr Val  
115 120 125  
Ile Val Val Leu Ser Ser Gly Leu Ala Phe Pro Pro Leu Tyr Phe Tyr  
130 135 140  
Asn Gly Gly Val Arg Glu Phe Leu Ala Met Val Lys Gln His Val Phe  
145 150 155 160  
Leu Ala Arg Ser Ser Glu Asp Gln Asn Val Phe Ile Val Asn Asp Phe  
165 170 175  
Gln Ser Pro Leu Gln Arg Thr Leu Ser Ser Leu Glu Leu Pro Ser Ser  
180 185 190  
Leu Pro Val Ala Ser Gly Gln Ser Val Tyr Pro Leu Asp Gly Gly Ser  
195 200 205  
Ser Ser Glu Asn Gln Arg Arg Thr Ser Ser Asp Val Gly Asn Arg Val  
210 215 220  
Ser Ser Val Ser Gln Ser Gly Phe Arg Lys Gln Lys Ser His Asp Pro  
225 230 235 240  
Thr Arg Asp Leu Ser Ile His Leu Leu Glu Lys Phe Ser Leu Val Thr  
245 250 255  
Lys Phe Ala Arg Asp Thr Thr Thr Gln Leu Phe Ser Glu Asn Asn Gly  
260 265 270  
Phe Gly Ser Ile Asp Lys Arg Trp Asn Asn Gln Pro Val His Ser Tyr  
275 280 285  
Pro Glu Lys Leu Ser Asn Ile Ala Glu Glu Lys His His Glu Ile Arg  
290 295 300  
His Ser Tyr Ser Glu Asn Asp Leu Leu Lys Asp Asp Glu Ile Ser Tyr  
305 310 315 320  
Ile Asp Val Pro Ala Asp Pro Leu Glu Phe Asp Lys Leu Ser Leu Met  
325 330 335  
Trp Gly Lys Pro Arg Gln Pro Pro Met Gly His Lys Glu Phe Thr Ala  
340 345 350  
Leu Leu Asp Ser Glu Gly Arg Val Val Glu Ser Lys Ala Leu Arg Glu  
355 360 365  
Arg Val Phe Tyr Gly Gly Ile Glu His Gln Leu Arg Arg Glu Val Trp  
370 375 380  
Pro Phe Leu Leu Gly Tyr Tyr Ala Tyr Asp Ser Thr Tyr Ala Glu Arg  
385 390 395 400  
Glu Tyr Leu Arg Ser Val Lys Arg Met Glu Tyr Tyr Ala Thr Leu Lys Gln  
405 410 415  
Gln Trp Gln Ser Ile Ser Pro Glu Gln Ala Lys Arg Phe Thr Lys Tyr  
420 425 430  
Arg Glu Arg Lys Gly Leu Ile Asp Lys Asp Val Val Arg Thr Asp Arg  
435 440 445  
Ala Phe Glu Tyr Tyr Glu Gly Asp Asp Asn Leu His Val Asn Ser Met  
450 455 460  
Arg Asp Ile Leu Leu Thr Tyr Ser Phe Tyr Asn Phe Asp Leu Gly Tyr  
465 470 475 480  
Cys Gln Gly Met Ser Asp Tyr Leu Ser Pro Ile Leu Phe Val Met Glu  
485 490 495  
Asp Glu Ser Glu Ser Phe Trp Xaa Phe Xaa Ala Leu Met Glu Arg Leu  
500 505 510  
Gly Pro Asn Phe Asn Arg Asp Gln Asn Gly Met His Thr Gln Leu Phe  
515 520 525  
Ala Leu Ser Lys Leu Val Glu Leu Leu Asp Ser Pro Leu His Asn Tyr  
530 535 540  
Phe Lys Glu Asn Asp Cys Leu Asn Tyr Phe Phe Cys Phe Arg Trp Ile  
545 550 555 560  
Leu Ile Gln Phe Lys Arg Glu Phe Glu Tyr Glu Lys Thr Met Gln Leu

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|-----|--|--|--|--|--|--|--|--|--|--|-----|--|--|
|     |     |     |     |     |     |     |     |     |     | 565 |     |     |     |     |     |  |  |  |  |  | 570 |  |  |  |  |  |  |  |  |  |  | 575 |  |  |
| Trp | Glu | Val | Met | Trp | Thr | His | Tyr | Leu | Ser | Glu | His | Phe | His | Leu | Tyr |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 580 |     |     |     |     |     |  |  |  |  |  | 585 |  |  |  |  |  |  |  |  |  |  | 590 |  |  |
| Val | Cys | Val | Ala | Val | Leu | Lys | Arg | Cys | Arg | Ser | Lys | Ile | Met | Gly | Glu |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 595 |     |     |     |     |     |  |  |  |  |  | 600 |  |  |  |  |  |  |  |  |  |  | 605 |  |  |
| Gln | Met | Asp | Phe | Asp | Thr | Leu | Leu | Lys | Phe | Ile | Asn | Glu | Leu | Ser | Gly |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 610 |     |     |     |     |     |  |  |  |  |  | 615 |  |  |  |  |  |  |  |  |  |  | 620 |  |  |
| His | Ile | Asp | Leu | Asp | Ser | Thr | Val | Arg | Asp | Ala | Glu | Ala | Leu | Cys | Ile |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 625 |     |     |     |     |     |  |  |  |  |  | 630 |  |  |  |  |  |  |  |  |  |  | 635 |  |  |
| Glu | Ala | Gly | Glu | Asn | Gly | Ala | Ala | Ser | Ile | Pro | Pro | Gly | Thr | Pro | Pro |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 645 |     |     |     |     |     |  |  |  |  |  | 650 |  |  |  |  |  |  |  |  |  |  | 655 |  |  |
| Ser | Leu | Pro | Leu | Asp | Asp | Gly | Thr | Leu | Tyr | Pro | Gln | Glu | Asp | Val |     |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 660 |     |     |     |     |     |  |  |  |  |  | 665 |  |  |  |  |  |  |  |  |  |  | 670 |  |  |
| Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |

(2) INFORMATION FOR SEQ ID NO:1876:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 671 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..671

(D) OTHER INFORMATION: / Ceres Seq. ID 1571248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1876:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|-----|--|--|--|--|--|--|--|--|--|--|-----|--|--|
| Met | Glu | Ala | Thr | Glu | Leu | Gln | Asp | Leu | Ser | Asp | Asp | Ala | Asp | Tyr | Ala |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
| 1   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 5   |     |     |     |     |     |  |  |  |  |  | 10  |  |  |  |  |  |  |  |  |  |  | 15  |  |  |
| Ala | Ser | Gln | Gln | Gln | Gly | Ser | Ala | Ser | Met | Met | Arg | Xaa | Asp | Ser | Gly |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 20  |     |     |     |     |     |  |  |  |  |  | 25  |  |  |  |  |  |  |  |  |  |  | 30  |  |  |
| Lys | Arg | Ser | Leu | Gln | Ser | Glu | His | Glu | Asp | Ala | Val | Leu | Ile | Tyr | Leu |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 35  |     |     |     |     |     |  |  |  |  |  | 40  |  |  |  |  |  |  |  |  |  |  | 45  |  |  |
| Lys | Asp | Asn | Val | Ala | Ile | His | Pro | Thr | Gln | Phe | Ala | Ser | Glu | Arg | Ile |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 50  |     |     |     |     |     |  |  |  |  |  | 55  |  |  |  |  |  |  |  |  |  |  | 60  |  |  |
| Ser | Gly | Arg | Leu | Lys | Leu | Thr | Lys | Gln | Asp | Ser | Val | Leu | Phe | Leu | Ser |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 65  |     |     |     |     |     |  |  |  |  |  | 70  |  |  |  |  |  |  |  |  |  |  | 75  |  |  |
| Trp | Ile | Pro | Tyr | Lys | Gly | Gln | Thr | Ser | Asn | Ala | Lys | Leu | Ser | Glu | Lys |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 85  |     |     |     |     |     |  |  |  |  |  | 90  |  |  |  |  |  |  |  |  |  |  | 95  |  |  |
| Asp | Arg | Ser | Leu | Tyr | Thr | Ile | Thr | Ala | Val | Pro | Phe | Thr | Glu | Val | Arg |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 100 |     |     |     |     |     |  |  |  |  |  | 105 |  |  |  |  |  |  |  |  |  |  | 110 |  |  |
| Ser | Ile | Arg | Arg | His | Thr | Pro | Ala | Leu | Gly | Trp | Gln | Tyr | Val | Ile | Val |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 115 |     |     |     |     |     |  |  |  |  |  | 120 |  |  |  |  |  |  |  |  |  |  | 125 |  |  |
| Val | Leu | Ser | Ser | Gly | Leu | Ala | Phe | Pro | Pro | Leu | Tyr | Phe | Tyr | Asn | Gly |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 130 |     |     |     |     |     |  |  |  |  |  | 135 |  |  |  |  |  |  |  |  |  |  | 140 |  |  |
| Gly | Val | Arg | Glu | Phe | Leu | Ala | Met | Val | Lys | Gln | His | Val | Phe | Leu | Ala |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 145 |     |     |     |     |     |  |  |  |  |  | 150 |  |  |  |  |  |  |  |  |  |  | 155 |  |  |
| Arg | Ser | Ser | Glu | Asp | Gln | Asn | Val | Phe | Ile | Val | Asn | Asp | Phe | Gln | Ser |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 165 |     |     |     |     |     |  |  |  |  |  | 170 |  |  |  |  |  |  |  |  |  |  | 175 |  |  |
| Pro | Leu | Gln | Arg | Thr | Leu | Ser | Ser | Leu | Glu | Leu | Pro | Ser | Ser | Leu | Pro |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 180 |     |     |     |     |     |  |  |  |  |  | 185 |  |  |  |  |  |  |  |  |  |  | 190 |  |  |
| Val | Ala | Ser | Gly | Gln | Ser | Val | Tyr | Pro | Leu | Asp | Gly | Gly | Ser | Ser | Ser |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 195 |     |     |     |     |     |  |  |  |  |  | 200 |  |  |  |  |  |  |  |  |  |  | 205 |  |  |
| Glu | Asn | Gln | Arg | Arg | Thr | Ser | Ser | Asp | Val | Gly | Asn | Arg | Val | Ser | Ser |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 210 |     |     |     |     |     |  |  |  |  |  | 215 |  |  |  |  |  |  |  |  |  |  | 220 |  |  |
| Val | Ser | Gln | Ser | Gly | Phe | Arg | Lys | Gln | Lys | Ser | His | Asp | Pro | Thr | Arg |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 225 |     |     |     |     |     |  |  |  |  |  | 230 |  |  |  |  |  |  |  |  |  |  | 235 |  |  |
| Asp | Leu | Ser | Ile | His | Leu | Leu | Glu | Lys | Phe | Ser | Leu | Val | Thr | Lys | Phe |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 245 |     |     |     |     |     |  |  |  |  |  | 250 |  |  |  |  |  |  |  |  |  |  | 255 |  |  |
| Ala | Arg | Asp | Thr | Thr | Gln | Leu | Phe | Ser | Glu | Asn | Asn | Gly | Phe | Gly |     |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |     |  |  |
|     |     |     |     |     |     |     |     |     |     | 260 |     |     |     |     |     |  |  |  |  |  | 265 |  |  |  |  |  |  |  |  |  |  | 270 |  |  |

Ser Ile Asp Lys Arg Trp Asn Asn Gln Pro Val His Ser Tyr Pro Glu  
275 280 285  
Lys Leu Ser Asn Ile Ala Glu Glu Lys His His Glu Ile Arg His Ser  
290 295 300  
Tyr Ser Glu Asn Asp Leu Leu Lys Asp Asp Glu Ile Ser Tyr Ile Asp  
305 310 315 320  
Val Pro Ala Asp Pro Leu Glu Phe Asp Lys Leu Ser Leu Met Trp Gly  
325 330 335  
Lys Pro Arg Gln Pro Pro Met Gly His Lys Glu Phe Thr Ala Leu Leu  
340 345 350  
Asp Ser Glu Gly Arg Val Val Glu Ser Lys Ala Leu Arg Glu Arg Val  
355 360 365  
Phe Tyr Gly Gly Ile Glu His Gln Leu Arg Arg Glu Val Trp Pro Phe  
370 375 380  
Leu Leu Gly Tyr Tyr Ala Tyr Asp Ser Thr Tyr Ala Glu Arg Glu Tyr  
385 390 395 400  
Leu Arg Ser Val Lys Arg Met Glu Tyr Ala Thr Leu Lys Gln Gln Trp  
405 410 415  
Gln Ser Ile Ser Pro Glu Gln Ala Lys Arg Phe Thr Lys Tyr Arg Glu  
420 425 430  
Arg Lys Gly Leu Ile Asp Lys Asp Val Val Arg Thr Asp Arg Ala Phe  
435 440 445  
Glu Tyr Tyr Glu Gly Asp Asp Asn Leu His Val Asn Ser Met Arg Asp  
450 455 460  
Ile Leu Leu Thr Tyr Ser Phe Tyr Asn Phe Asp Leu Gly Tyr Cys Gln  
465 470 475 480  
Gly Met Ser Asp Tyr Leu Ser Pro Ile Leu Phe Val Met Glu Asp Glu  
485 490 495  
Ser Glu Ser Phe Trp Xaa Phe Xaa Ala Leu Met Glu Arg Leu Gly Pro  
500 505 510  
Asn Phe Asn Arg Asp Gln Asn Gly Met His Thr Gln Leu Phe Ala Leu  
515 520 525  
Ser Lys Leu Val Glu Leu Leu Asp Ser Pro Leu His Asn Tyr Phe Lys  
530 535 540  
Glu Asn Asp Cys Leu Asn Tyr Phe Phe Cys Phe Arg Trp Ile Leu Ile  
545 550 555 560  
Gln Phe Lys Arg Glu Phe Glu Tyr Glu Lys Thr Met Gln Leu Trp Glu  
565 570 575  
Val Met Trp Thr His Tyr Leu Ser Glu His Phe His Leu Tyr Val Cys  
580 585 590  
Val Ala Val Leu Lys Arg Cys Arg Ser Lys Ile Met Gly Glu Gln Met  
595 600 605  
Asp Phe Asp Thr Leu Leu Lys Phe Ile Asn Glu Leu Ser Gly His Ile  
610 615 620  
Asp Leu Asp Ser Thr Val Arg Asp Ala Glu Ala Leu Cys Ile Glu Ala  
625 630 635 640  
Gly Glu Asn Gly Ala Ala Ser Ile Pro Pro Gly Thr Pro Pro Ser Leu  
645 650 655  
Pro Leu Asp Asp Gly Thr Leu Tyr Pro Gln Glu Asp Asp Val Leu  
660 665 670

(2) INFORMATION FOR SEQ ID NO:1877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..726
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1877:

|             |             |             |            |             |             |     |
|-------------|-------------|-------------|------------|-------------|-------------|-----|
| aagagatcac  | ttctccgacg  | cagaaatgac  | gaagtTcagg | aagcttggtc  | ggccggcggg  | 60  |
| tcaccgtatg  | ttccatgctta | ggactatggt  | ttctcagttg | gtgaagcacg  | agcgatttga  | 120 |
| gaccactgtc  | actaaggcta  | aagagggttcg | tcgtcttgct | gataaatatga | ttcaactcgg  | 180 |
| caaagagggg  | tcactctctg  | ctgcaaggcg  | agcagctggt | tttgtgagag  | gagatgatgt  | 240 |
| ctttacaag   | attttcacag  | aactggcaca  | tagatacaaa | gataagagctg | gtggatacac  | 300 |
| aagatgctta  | cgtactcgca  | tacgagttgg  | tgatgctgct | cctatggcct  | atatcgagtt  | 360 |
| tattgcacaga | gagaaacgagc | ttaggcaatc  | aaaaccagca | acacotcaac  | caccgcaacg  | 420 |
| agtgcattg   | gacccatggg  | aaagatctctg | gctcaccagg | cagttcgCtc  | cgccataagga | 480 |
| ggagaaaatc  | cctgattctg  | agctgtaatg  | tggcataagc | aatttccctc  | tggtcaccaa  | 540 |
| atatcttctg  | tctgtctcaa  | aaatgtattt  | tcgtgatcat | ttatcatatg  | ccacaatatg  | 600 |
| ttttcacaga  | aggaacacaa  | taagttagct  | ttttcattg  | tttgaacatt  | gaaagtgtac  | 660 |
| tcttgaatac  | attaacagcg  | ttagagagac  | tctttctttg | cctatctacc  | tatgaactaa  | 720 |

(2) INFORMATION FOR SEQ ID NO:1878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..168
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1878:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Asp | His | Phe | Ser | Asp | Ala | Glu | Met | Thr | Lys | Phe | Arg | Lys | Leu | Gly |
| 1   |     | 5   |     |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Arg | Pro | Ala | Gly | His | Arg | Met | Ser | Met | Leu | Arg | Thr | Met | Val | Ser | Gln |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Val | Lys | His | Glu | Arg | Ile | Glu | Thr | Thr | Val | Thr | Lys | Ala | Lys | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Arg | Arg | Leu | Ala | Asp | Asn | Met | Ile | Gln | Leu | Gly | Lys | Glu | Gly | Ser |
|     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |
| Leu | Ser | Ala | Ala | Arg | Arg | Ala | Ala | Gly | Phe | Val | Arg | Gly | Asp | Asp | Val |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| Leu | His | Lys | Ile | Phe | Thr | Glu | Leu | Ala | His | Arg | Tyr | Lys | Asp | Arg | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Gly | Gly | Tyr | Thr | Arg | Leu | Leu | Arg | Thr | Arg | Ile | Arg | Val | Gly | Asp | Ala |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ala | Pro | Met | Ala | Tyr | Ile | Glu | Phe | Ile | Asp | Arg | Glu | Asn | Glu | Leu | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Ser | Lys | Pro | Ala | Thr | Pro | Gln | Pro | Pro | Gln | Arg | Val | Pro | Leu | Asp |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Trp | Glu | Arg | Ser | Arg | Leu | Thr | Arg | Gln | Phe | Ala | Pro | Pro | Lys | Glu |
|     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Glu | Lys | Ile | Pro | Asp | Ser | Glu | Leu |     |     |     |     |     |     |     |     |
|     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1879:

Met Thr Lys Phe Arg Lys Leu Gly Arg Pro Ala Gly His Arg Met Ser



(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 576 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..576  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1881:

|            |            |             |             |             |            |     |
|------------|------------|-------------|-------------|-------------|------------|-----|
| atgaatgtaa | tgccgtatag | tcagcctatg  | tccgctgggc  | aattggctac  | ttcccttgct | 60  |
| aatgctacac | ctgctcaaca | gagaaacatt  | cttgggtgaga | gtctatatcc  | attagtggac | 120 |
| cagatagaga | gtgagcacgc | tgcgaaagtg  | actgggatgc  | ttctggaaat  | ggatcagacc | 180 |
| gaggttttgc | atctgctoga | gtcaccagag  | gtctctaaatg | ccaaagtttc  | agaggcatta | 240 |
| gatgtgtttg | gaaacgtgaa | tcagccatct  | tcacagggaa  | gtgaaggcaa  | caaaagtggg | 300 |
| agtccaagtg | atctctttgc | ttcaactttc  | atcaatgatc  | acttatgaga  | agcttttgg  | 360 |
| cgagtttttt | tttttacttt | tgactctctt  | ctctctctatc | ctctctctctg | attgacaaat | 420 |
| tttgcgggga | atctatttgc | tgtttttagac | tttttttgct  | cgatatgatt  | gtttctgttt | 480 |
| tgGacttctt | acttttttgg | gttgacttaa  | aaaaggatgg  | ttttatttta  | ttttgttggg | 540 |

tttatatttta ctgttgcaaa attttgcgct cagttt

(2) INFORMATION FOR SEQ ID NO:1882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..115  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1882:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asn | Val | Met | Pro | Tyr | Ser | Gln | Pro | Met | Ser | Ala | Gly | Gln | Leu | Ala |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Thr | Ser | Leu | Ala | Asn | Ala | Thr | Pro | Ala | Gln | Gln | Arg | Thr | Leu | Leu | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | Ser | Leu | Tyr | Pro | Leu | Val | Asp | Gln | Ile | Glu | Ser | Glu | His | Ala | Ala |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Lys | Val | Thr | Gly | Met | Leu | Leu | Glu | Met | Asp | Gln | Thr | Glu | Val | Leu | His |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |  |
| Leu | Leu | Glu | Ser | Pro | Glu | Ala | Leu | Asn | Ala | Lys | Val | Ser | Glu | Ala | Leu |  |
|     |     |     |     |     |     |     | 70  |     |     |     |     | 75  |     |     | 80  |  |
| Asp | Val | Leu | Arg | Asn | Val | Asn | Gln | Pro | Ser | Ser | Gln | Gly | Ser | Glu | Gly |  |
|     |     |     |     |     |     |     | 85  |     |     |     | 90  |     |     | 95  |     |  |
| Asn | Lys | Ser | Gly | Ser | Pro | Ser | Asp | Leu | Leu | Ala | Ser | Leu | Ser | Ile | Asn |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 110 |     |  |
| Asp | His | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..112  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1883:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Pro | Tyr | Ser | Gln | Pro | Met | Ser | Ala | Gly | Gln | Leu | Ala | Thr | Ser | Leu |  |
| 1   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Ala | Asn | Ala | Thr | Pro | Ala | Gln | Gln | Arg | Thr | Leu | Leu | Gly | Glu | Ser | Leu |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Tyr | Pro | Leu | Val | Asp | Gln | Ile | Glu | Ser | Glu | His | Ala | Ala | Lys | Val | Thr |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Gly | Met | Leu | Leu | Glu | Met | Asp | Gln | Thr | Glu | Val | Leu | His | Leu | Leu | Glu |  |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 50                                                              | 55  | 60  |
| Ser Pro Glu Ala Leu Asn Ala Lys Val Ser Glu Ala Leu Asp Val Leu |     |     |
| 65                                                              | 70  | 75  |
| Arg Asn Val Asn Gln Pro Ser Ser Gln Gly Ser Glu Gly Asn Lys Ser |     | 80  |
| 85                                                              | 90  | 95  |
| Gly Ser Pro Ser Asp Leu Leu Ala Ser Leu Ser Ile Asn Asp His Leu |     |     |
| 100                                                             | 105 | 110 |

(2) INFORMATION FOR SEQ ID NO:1884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 632 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..632
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1884:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| attccccatc  | gcacagacc  | gcctaagaat | ccgagagaga | agaagagata | atgcagatct | 60  |
| togtcaaaac  | cctcaccggc | aaaactataa | ccctagaggt | tgagagcagc | gacaccatcg | 120 |
| acaatgttaa  | agccaaaatc | caggacaaat | agggcatacc | acctgatcaa | cagaggctga | 180 |
| tttttgctgg  | taagcaattg | gaagatggcc | ggaccttagc | tgactacaac | atccagaaga | 240 |
| agtcactctc  | tcactctgtc | ctcagggtca | gaggtggaac | catgatcaag | gtgaagacac | 300 |
| tcactgtaaa  | agaaatcgag | attgatatcg | aaccaaccca | cactattgat | cggatcaaa  | 360 |
| aacgtgttga  | agagaaagaa | ggcatccctc | ctgttcaaca | aaggctcctc | tatgccggaa | 420 |
| aacagcttgc  | tgatgacaaa | acggccaaag | attatgcgat | agagggaggc | tctgttcttc | 480 |
| atttggttct  | tgctcttagg | ggtggtcttc | tctgatctga | ataaataagc | ttttcaacaa | 540 |
| acatctttcc  | cctcactatt | gtcctccttt | tgtggaAttc | atgacacaca | aaaattgcta | 600 |
| tgggaaaattg | gaatattatg | atgttttttc | tc         |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1885:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Lys | Val | Lys | Thr | Leu | Thr | Gly | Lys | Glu | Ile | Glu | Ile | Asp | Ile |
| 1   |     | 5   |     |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Glu | Pro | Thr | Asp | Thr | Ile | Asp | Arg | Ile | Lys | Glu | Arg | Val | Glu | Glu | Lys |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     | 30  |     |
| Glu | Gly | Ile | Pro | Pro | Val | Gln | Gln | Arg | Leu | Ile | Tyr | Ala | Gly | Lys | Gln |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Leu | Ala | Asp | Asp | Lys | Thr | Ala | Lys | Asp | Tyr | Ala | Ile | Glu | Gly | Gly | Ser |
|     |     | 50  |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Val | Leu | His | Leu | Val | Leu | Ala | Leu | Arg | Gly | Gly | Leu | Leu |     |     |     |
| 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1120

(D) OTHER INFORMATION: / Ceres Seq. ID 1571271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1886:

|             |             |             |             |             |            |      |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| aaaactcaag  | gggttgatt   | ttctttctca  | actacggttaa | gattttctct  | acacttttct | 60   |
| ttttcccggt  | attctctttt  | agtcctcgat  | tctctacgcg  | tttcagcgctc | aagctctcta | 120  |
| gatctctaaa  | gccttcgtgc  | tcgccaatat  | aaatctctga  | gatcggtccc  | gtaaaaatcg | 180  |
| attcgcgctg  | tttttgagta  | aaaaaaatgg  | cgcaacaatc  | gttgatctac  | agtttcgtcg | 240  |
| ctcggtgtac  | cggtatcttc  | gttgagttca  | cagattttcaa | aggcaatttc  | acatcaaatg | 300  |
| ctgctcagtg  | ccttcagaag  | cttccttctt  | ctaacacaac  | gtttacctac  | aactgcgcat | 360  |
| gtcacacgtt  | caattacctc  | gtcgaaaatg  | gattcaccta  | ttgtgttgtt  | gcagttgatt | 420  |
| ctgctgggag  | gcagattcct  | atggctttct  | tggaacgagt  | taaggaggat  | ttcaacaaga | 480  |
| gatatggttg  | tggaagggtc  | gcaactgctc  | aagcaaacag  | cttgaataaa  | gaatttgggt | 540  |
| cgaaactgaa  | agagcatatg  | cagtattgca  | tgatcatccc  | tgatgagatt  | agcaagcttg | 600  |
| ctaagggttaa | agctcaagtg  | tctgaagtta  | aaggtgttat  | gatggaaaaa  | attgagaagg | 660  |
| ttcttgaccg  | tggtgagaag  | attgagcttt  | tggttgacaa  | aacagaaaaa  | cttcgctcac | 720  |
| agggcgcaaga | ttttagaaca  | caaggaaactc | aaatgagaag  | aaagatgtgg  | tttcagaaca | 780  |
| tgaagataaa  | gctcaattgtc | cttgcaatta  | tcattgcctt  | gattctcatc  | atcatcctct | 840  |
| caatttgtgg  | gggattcaac  | tcgcgttaaat | aagtcgtgaa  | catttcttcc  | cgcggttatc | 900  |
| gactgcgctc  | tgtgcttccc  | aagatctctg  | agaatatctt  | cattcagttc  | gttgcgtcac | 960  |
| cttttttttt  | ttWttgtttt  | tgwgatttct  | atattctcat  | actatatgtt  | ttctctttag | 1020 |
| ttgtactttt  | tgaattttgt  | ttgtatagg   | ctatatatat  | tatatatata  | tgtatgcatt | 1080 |
| ttcgacaatc  | tgcaattgtg  | ctattgctgg  | tactgacact  |             |            |      |

(2) INFORMATION FOR SEQ ID NO:1887:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..221

(D) OTHER INFORMATION: / Ceres Seq. ID 1571272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1887:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gln | Gln | Ser | Leu | Ile | Tyr | Ser | Phe | Val | Ala | Arg | Gly | Thr | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Leu | Val | Glu | Phe | Thr | Asp | Phe | Lys | Gly | Asn | Phe | Thr | Ser | Ile | Ala |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Ala | Gln | Cys | Leu | Gln | Lys | Leu | Pro | Ser | Ser | Asn | Asn | Lys | Phe | Thr | Tyr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Cys | Asp | Gly | His | Thr | Phe | Asn | Tyr | Leu | Val | Glu | Asn | Gly | Phe | Thr |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Tyr | Cys | Val | Val | Ala | Val | Asp | Ser | Ala | Gly | Arg | Gln | Ile | Pro | Met | Ala |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Phe | Leu | Glu | Arg | Val | Lys | Glu | Asp | Phe | Asn | Lys | Arg | Tyr | Gly | Gly | Gly |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Ala | Ala | Thr | Ala | Gln | Ala | Asn | Ser | Leu | Asn | Lys | Glu | Phe | Gly | Ser |
|     |     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |
| Lys | Leu | Lys | Glu | His | Met | Gln | Tyr | Cys | Met | Asp | His | Pro | Asp | Glu | Ile |
|     |     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |
| Ser | Lys | Leu | Ala | Lys | Val | Lys | Ala | Gln | Val | Ser | Glu | Val | Lys | Gly | Val |
|     |     |     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |
| Met | Met | Glu | Asn | Ile | Glu | Lys | Val | Leu | Asp | Gly | Glu | Lys | Ile | Glu |     |
|     |     |     |     |     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |
| Leu | Leu | Val | Asp | Lys | Thr | Glu | Asn | Leu | Arg | Ser | Gln | Ala | Gln | Asp | Phe |
|     |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |     |
| Arg | Thr | Gln | Gly | Thr | Gln | Met | Arg | Arg | Lys | Met | Trp | Phe | Gln | Asn | Met |
|     |     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |
| Lys | Ile | Lys | Leu | Ile | Val | Leu | Ala | Ile | Ile | Ile | Ala | Leu | Ile | Leu | Ile |

195 200 205  
Ile Ile Leu Ser Ile Cys Gly Gly Phe Asn Cys Gly Lys  
210 215 220

(2) INFORMATION FOR SEQ ID NO:1888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571273
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1888:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Phe | Leu | Glu | Arg | Val | Lys | Glu | Asp | Phe | Asn | Lys | Arg | Tyr | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |     |
| Gly | Gly | Lys | Ala | Ala | Thr | Ala | Gln | Ala | Asn | Ser | Leu | Asn | Lys | Glu | Phe |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gly | Ser | Lys | Leu | Lys | Glu | His | Met | Gln | Tyr | Cys | Met | Asp | His | Pro | Asp |
|     |     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Glu | Ile | Ser | Lys | Leu | Ala | Lys | Val | Lys | Ala | Gln | Val | Ser | Glu | Val | Lys |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly | Val | Met | Met | Glu | Asn | Ile | Glu | Lys | Val | Leu | Asp | Arg | Gly | Glu | Lys |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Glu | Leu | Leu | Val | Asp | Lys | Thr | Glu | Asn | Leu | Arg | Ser | Gln | Ala | Gln |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asp | Phe | Arg | Thr | Gln | Gly | Thr | Gln | Met | Arg | Arg | Lys | Met | Trp | Phe | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Met | Lys | Ile | Lys | Leu | Ile | Val | Leu | Ala | Ile | Ile | Ile | Ala | Leu | Ile |
|     |     |     | 115 |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Leu | Ile | Ile | Leu | Ser | Ile | Cys | Gly | Gly | Phe | Asn | Cys | Gly | Lys |     |     |
|     |     |     | 130 |     |     | 135 |     |     |     | 140 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1348
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571291
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1889:

|             |            |             |            |             |             |     |
|-------------|------------|-------------|------------|-------------|-------------|-----|
| aaacacGcaa  | caacaacaat | gtctctctct  | ctccgatcta | ccaccgcgcg  | ttctcttctc  | 60  |
| ctccgcctcct | cctcctcctc | ctccagatcc  | actctcaact | tctccgcttc  | ctctctcttc  | 120 |
| tccttcgtca  | gatctctcgt | ctctctctcc  | cgctctctct | ctctctcaac  | ctctctcagc  | 180 |
| aaatgctgaa  | ttgcgtcggt | gaatcggagt  | ttcaactcca | ccaccgcgcg  | tactaaatct  | 240 |
| tcattctcag  | atcctgatca | gttgaagaac  | gctagagaag | atatcaaaga  | gctctctcagc | 300 |
| accaaattct  | gccatccgat | tttgtgttag  | ttaggttgcc | atgatgtcgg  | tacgtataac  | 360 |
| aagaaacatta | aggaatggcc | acaaagaggt  | ggagctaagt | gaagtttgag  | attcgatatt  | 420 |
| gagcttaaac  | atactgctaa | tgctggtctt  | gtgaatgctt | taaaactgtat | taaggatatt  | 480 |
| aaagagaaat  | actctgggat | cagttatgct  | gatttgttcc | agttagctag  | tgctactgtc  | 540 |
| atagagggaag | ctggaggacc | agaaataccg  | atgaaatgat | gtagagttag  | tgctctgtgt  | 600 |
| ctctgaggatt | gtccagaaga | aggaaggtct  | ccagatgctg | gtcctctctc  | gctctgctat  | 660 |
| catctcagag  | aagtgttttt | cagaatggga  | ttagatgaca | aggacatagt  | tgcatattct  | 720 |
| ggtgctcaca  | cggttagaag | attctaggcca | gaacgtagt  | gttgggggaa  | gcctgagacg  | 780 |
| aagtacacga  | aagaaggacc | tggagccaca  | ggaggacagt | catggacacc  | agagtggcgt  | 840 |
| aagtttgata  | attcgtactt | caaggagatc  | aaggaaaaga | gagatgaaga  | tctctcttgc  | 900 |
| ctaccacagt  | atgctgccat | ctctgaagat  | tcttctttca | aggtctatgc  | tgaaaagtat  | 960 |

gctgcagatc aggatgcatt tttcaaggat tacgctgtag cgcctgcgaa actcagcaat 1020  
cttggcgcag aatttaaccc tcggaggagt atcattatct aatggggcac ctaatttact 1080  
caaccagact tatgatttta gagaacgta gtccaataat gaaagagaag aaaaagttaga 1140  
cggaagaact ttcacgcgac tacttttcga gatacctttt ggacaaaatgt tcttgctgt 1200  
tcaaaggatt ttgttagacc gaaagtattt gatcgttttc atggttttgt gctttcatgt 1260  
tttttcttg taataaattg cggaagtgat tatccaaaat ctatacaaat ttgtctgga 1320  
attgaattat tttatcgatg ttataact

(2) INFORMATION FOR SEQ ID NO:1890:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..353

(D) OTHER INFORMATION: / Ceres Seq. ID 1571292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1890:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Xaa | Ala | Thr | Thr | Thr | Met | Ser | Ser | Ser | Ser | Leu | Arg | Ser | Thr | Thr | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Ser | Leu | Xaa | Leu | Arg | Ser | Ser | Ser | Ser | Ser | Ser | Arg | Ser | Thr | Leu |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Thr | Leu | Ser | Ala | Ser | Ser | Ser | Leu | Ser | Phe | Val | Arg | Ser | Leu | Val | Ser |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ser | Pro | Arg | Leu | Ser | Ser | Ser | Ser | Pro | Leu | Ser | Gln | Lys | Cys | Arg | Ile |     |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala | Ser | Val | Asn | Arg | Ser | Phe | Asn | Ser | Thr | Thr | Ala | Ala | Thr | Lys | Ser |     |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |     |
| Ser | Ser | Ser | Asp | Pro | Asp | Gln | Leu | Lys | Asn | Ala | Arg | Glu | Asp | Ile | Lys |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |
| Glu | Leu | Leu | Ser | Thr | Lys | Phe | Cys | His | Pro | Ile | Leu | Val | Arg | Leu | Gly |     |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |     |
| Trp | His | Asp | Ala | Gly | Thr | Tyr | Asn | Lys | Asn | Ile | Lys | Glu | Trp | Pro | Gln |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Arg | Gly | Gly | Ala | Asn | Gly | Ser | Leu | Arg | Phe | Asp | Ile | Glu | Leu | Lys | His |     |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Thr | Ala | Asn | Ala | Gly | Leu | Val | Asn | Ala | Leu | Asn | Leu | Ile | Lys | Asp | Ile |     |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |     |
| Lys | Glu | Lys | Tyr | Ser | Gly | Ile | Ser | Tyr | Ala | Asp | Leu | Phe | Gln | Leu | Ala |     |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ser | Ala | Thr | Ala | Ile | Glu | Glu | Ala | Gly | Gly | Pro | Lys | Ile | Pro | Met | Lys |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |     |     |
| Tyr | Gly | Arg | Val | Asp | Ala | Ser | Gly | Pro | Glu | Asp | Cys | Pro | Glu | Glu | Gly |     |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Arg | Leu | Pro | Asp | Ala | Gly | Pro | Pro | Ser | Pro | Ala | Thr | His | Leu | Arg | Glu |     |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Val | Phe | Tyr | Arg | Met | Gly | Leu | Asp | Asp | Lys | Asp | Ile | Val | Ala | Leu | Ser |     |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |     |
| Gly | Ala | His | Thr | Leu | Gly | Arg | Ser | Arg | Pro | Glu | Arg | Ser | Gly | Trp | Gly |     |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     | 255 |     |     |     |     |
| Lys | Pro | Glu | Thr | Lys | Tyr | Thr | Lys | Glu | Gly | Pro | Gly | Ala | Pro | Gly | Gly |     |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |     |
| Gln | Ser | Trp | Thr | Pro | Glu | Trp | Leu | Lys | Phe | Asp | Asn | Ser | Tyr | Phe | Lys |     |
|     |     |     | 275 |     |     |     | 280 |     |     |     | 285 |     |     |     |     |     |
| Glu | Ile | Lys | Glu | Lys | Arg | Asp | Glu | Asp | Leu | Leu | Val | Leu | Pro | Thr | Asp |     |
|     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| Ala | Ala | Ile | Phe | Glu | Asp | Ser | Ser | Phe | Lys | Val | Tyr | Ala | Glu | Lys | Tyr |     |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |     |
| Ala | Ala | Asp | Gln | Asp | Ala | Phe | Phe | Lys | Asp | Tyr | Ala | Val | Ala | His | Ala |     |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |     |

Lys Leu Ser Asn Leu Gly Ala Glu Phe Asn Pro Pro Glu Gly Ile Ile  
340 345 350  
Ile

(2) INFORMATION FOR SEQ ID NO:1891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..347
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1891:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ser | Ser | Leu | Arg | Ser | Thr | Thr | Ala | Ala | Ser | Leu | Xaa | Leu | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ser | Ser | Ser | Ser | Ser | Arg | Ser | Thr | Leu | Thr | Leu | Ser | Ala | Ser | Ser |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Leu | Ser | Phe | Val | Arg | Ser | Leu | Val | Ser | Ser | Pro | Arg | Leu | Ser | Ser |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Ser | Ser | Pro | Leu | Ser | Gln | Lys | Cys | Arg | Ile | Ala | Ser | Val | Asn | Arg | Ser |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Phe | Asn | Ser | Thr | Thr | Ala | Ala | Thr | Lys | Ser | Ser | Ser | Asp | Pro | Asp |     |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |     |
| Gln | Leu | Lys | Asn | Ala | Arg | Glu | Asp | Ile | Lys | Glu | Leu | Leu | Ser | Thr | Lys |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     | 95  |     |     |     |
| Phe | Cys | His | Pro | Ile | Leu | Val | Arg | Leu | Gly | Trp | His | Asp | Ala | Gly | Thr |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Tyr | Asn | Lys | Asn | Ile | Lys | Glu | Trp | Pro | Gln | Arg | Gly | Gly | Ala | Asn | Gly |
|     |     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Leu | Arg | Phe | Asp | Ile | Glu | Leu | Lys | His | Thr | Ala | Asn | Ala | Gly | Leu |
|     |     |     |     | 130 |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Val | Asn | Ala | Leu | Asn | Leu | Ile | Lys | Asp | Ile | Lys | Glu | Lys | Tyr | Ser | Gly |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     |     | 160 |
| Ile | Ser | Tyr | Ala | Asp | Leu | Phe | Gln | Leu | Ala | Ser | Ala | Thr | Ala | Ile | Glu |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     | 175 |     |     |     |
| Glu | Ala | Gly | Gly | Pro | Lys | Ile | Pro | Met | Lys | Tyr | Gly | Arg | Val | Asp | Ala |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Ser | Gly | Pro | Glu | Asp | Cys | Pro | Glu | Glu | Gly | Arg | Leu | Pro | Asp | Ala | Gly |
|     |     |     |     | 195 |     |     | 200 |     |     |     | 205 |     |     |     |     |
| Pro | Pro | Ser | Pro | Ala | Thr | His | Leu | Arg | Glu | Val | Phe | Tyr | Arg | Met | Gly |
|     |     |     |     | 210 |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Leu | Asp | Asp | Lys | Asp | Ile | Val | Ala | Leu | Ser | Gly | Ala | His | Thr | Leu | Gly |
| 225 |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     |     | 240 |
| Arg | Ser | Arg | Pro | Glu | Arg | Ser | Gly | Trp | Gly | Lys | Pro | Glu | Thr | Lys | Tyr |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     | 255 |     |     |     |
| Thr | Lys | Glu | Gly | Pro | Gly | Ala | Pro | Gly | Gly | Gln | Ser | Trp | Thr | Pro | Glu |
|     |     |     |     | 260 |     |     |     | 265 |     |     |     | 270 |     |     |     |
| Trp | Leu | Lys | Phe | Asp | Asn | Ser | Tyr | Phe | Lys | Glu | Ile | Lys | Glu | Lys | Arg |
|     |     |     |     | 275 |     |     | 280 |     |     |     | 285 |     |     |     |     |
| Asp | Glu | Asp | Leu | Leu | Val | Leu | Pro | Thr | Asp | Ala | Ala | Ile | Phe | Glu | Asp |
|     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |     |     |
| Ser | Ser | Phe | Lys | Val | Tyr | Ala | Glu | Lys | Tyr | Ala | Ala | Asp | Gln | Asp | Ala |
| 305 |     |     |     | 310 |     |     |     | 315 |     |     |     |     |     |     | 320 |
| Phe | Phe | Lys | Asp | Tyr | Ala | Val | Ala | His | Ala | Lys | Leu | Ser | Asn | Leu | Gly |
|     |     |     |     | 325 |     |     |     | 330 |     |     |     | 335 |     |     |     |
| Ala | Glu | Phe | Asn | Pro | Pro | Glu | Gly | Ile | Ile | Ile |     |     |     |     |     |
|     |     |     |     | 340 |     |     | 345 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1892:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1532 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1532

(D) OTHER INFORMATION: / Ceres Seq. ID 1571304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1892:

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| atatataagc  | tcacaggtctt | gtacatcttc | atcatctgat  | ctcggggaag  | ctccgatctg  | 60   |
| agtttttttt  | agcaatggcg  | aaaatgattc | ctagcctcgt  | ctctctaatt  | cttatcggct  | 120  |
| ttgttgogat  | cgctccgcgc  | gcagttattt | tcgaggagcg  | ctttgatgat  | ggctggggaga | 180  |
| acagatgggt  | taaatctggag | tggagaagg  | atgataacac  | tgctggggag  | tggaaagcaca | 240  |
| ctgcgggaaa  | ttggctcgtg  | gacgctaaag | ataaaggat   | ccagaccagt  | gaagactaca  | 300  |
| gattctacgc  | catttcagct  | gagttccctg | aattcagtaa  | caaggacaag  | accttagtgt  | 360  |
| ttcaattctc  | agtcacaagc  | gagcaaaaag | ttgactgcgg  | tggtgggtac  | atgaagctac  | 420  |
| taagtgggtg  | tggtgaccaa  | aagaattttg | gtggagacac  | accatacagt  | atcatgtttg  | 480  |
| gtcctgatat  | ctgtggctac  | agcacaaaag | aagtgcattg  | tatccttacc  | tataatgaag  | 540  |
| ccaaccacct  | gatcaagaaa  | gatgttccat | gtgAaactga  | ccagctcacc  | catgtgtaca  | 600  |
| catatttact  | cgccccaagt  | gctacttaca | gcattctcat  | cgacaatgtt  | gagaaacaaa  | 660  |
| ctggtagcct  | ttactctgac  | tgggatcttc | tcccacccaa  | gaagatcaag  | gaccccaagc  | 720  |
| ccaagaagcc  | tgaggactgg  | gacgaacaag | aatacatctt  | tgaccttgaa  | gacaaagaa   | 780  |
| ctgacgggta  | cgatgatatt  | cctaaggaga | tcccagacac  | cgactcaag   | aagcctgagg  | 840  |
| actgggagta  | tgaagaagat  | gtgagtgga  | ctgccccaac  | aatccccaac  | ccctgagtaca | 900  |
| tggttggaatg | gaagcctaag  | caaatacaag | acccccaaact | caaggggcaag | tgaggagctc  | 960  |
| catgtattga  | caaccctgac  | ttcaaggatg | acccaagagct | ctacgtcttc  | cccaagctga  | 1020 |
| aatatgttgg  | actcgaattg  | tgccaggtga | aatcaggatc  | atgtgtcag   | aatgtcttga  | 1080 |
| tctgcgatga  | cccagactat  | gccaaagaat | tgccagatga  | aacatgggga  | aagctcaagg  | 1140 |
| atcgcgagaa  | agcagctctt  | gatgaggctg | agaagaagaa  | tgaggaaag   | gaatccaagg  | 1200 |
| acgcaCctgc  | ggaattctgat | gctgaagacg | aaccagagga  | tgatgaagga  | ggagatgatt  | 1260 |
| ccgattctga  | atctaaggcc  | gaggagacca | aatcagaaga  | tagcgaggaa  | acctctgaga  | 1320 |
| aagacgcac   | cgctcatgat  | gagctatagg | tgaagggttg  | aagatttgaa  | gaccaaaagt  | 1380 |
| ttcagtcctc  | ttattgtttt  | atcgtttttt | tttgaagtat  | tttagcatct  | agtttgtcgg  | 1440 |
| agatagaaac  | aagttttatg  | aaaactaaaa | gggggatata  | atgtctgtca  | gatgtcatt   | 1500 |
| ttagacttta  | aaaaacatg   | aagaagtttt | gc          |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1893:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 424 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..424

(D) OTHER INFORMATION: / Ceres Seq. ID 1571305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1893:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Met | Ile | Pro | Ser | Leu | Val | Ser | Leu | Ile | Leu | Ile | Gly | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     | 15  |     |     |     |     |
| Val | Ala | Ile | Ala | Ser | Ala | Ala | Val | Ile | Phe | Glu | Glu | Arg | Phe | Asp | Asp |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Gly | Trp | Glu | Asn | Arg | Trp | Val | Lys | Ser | Glu | Trp | Lys | Lys | Asp | Asp | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Thr | Ala | Gly | Glu | Trp | Lys | His | Thr | Ala | Gly | Asn | Trp | Ser | Gly | Asp | Ala |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Asn | Asp | Lys | Gly | Ile | Gln | Thr | Ser | Glu | Asp | Trp | Arg | Phe | Tyr | Ala | Ile |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     |     | 80  |     |
| Ser | Ala | Glu | Phe | Pro | Glu | Phe | Ser | Asn | Lys | Lys | Thr | Leu | Val | Phe |     |
|     |     |     | 85  |     |     |     | 90  |     |     |     | 95  |     |     |     |     |



Gln Phe Ser Val Lys His Glu Gln Lys Leu Asp Cys Gly Gly Gly Tyr  
100 105 110  
Met Lys Leu Leu Ser Gly Asp Val Asp Gln Lys Lys Phe Gly Gly Asp  
115 120 125  
Thr Pro Tyr Ser Ile Met Phe Gly Pro Asp Ile Cys Gly Tyr Ser Thr  
130 135 140  
Lys Lys Val His Ala Ile Leu Thr Tyr Asn Glu Ala Asn His Leu Ile  
145 150 155 160  
Lys Lys Asp Val Pro Cys Glu Thr Asp Gln Leu Thr His Val Tyr Thr  
165 170 175  
Phe Ile Leu Arg Pro Asp Ala Thr Tyr Ser Ile Leu Ile Asp Asn Val  
180 185 190  
Glu Lys Gln Thr Gly Ser Leu Tyr Ser Asp Trp Asp Leu Leu Pro Pro  
195 200 205  
Lys Lys Ile Lys Asp Pro Ser Ala Lys Lys Pro Glu Asp Trp Asp Glu  
210 215 220  
Gln Glu Tyr Ile Ser Asp Pro Glu Asp Lys Lys Pro Asp Gly Tyr Asp  
225 230 235 240  
Asp Ile Pro Lys Glu Ile Pro Asp Thr Asp Ser Lys Lys Pro Glu Asp  
245 250 255  
Trp Asp Asp Glu Glu Asp Gly Glu Trp Thr Ala Pro Thr Ile Pro Asn  
260 265 270  
Pro Glu Tyr Met Gly Glu Trp Lys Pro Lys Gln Ile Lys Asn Pro Asn  
275 280 285  
Tyr Lys Gly Lys Trp Glu Ala Pro Leu Ile Asp Asn Pro Asp Phe Lys  
290 295 300  
Asp Asp Pro Glu Leu Tyr Val Phe Pro Lys Leu Lys Tyr Val Gly Leu  
305 310 315 320  
Glu Leu Trp Gln Val Lys Ser Gly Ser Leu Phe Asp Asn Val Leu Ile  
325 330 335  
Cys Asp Asp Pro Asp Tyr Ala Lys Lys Leu Ala Asp Glu Thr Trp Gly  
340 345 350  
Lys Leu Lys Asp Ala Glu Lys Ala Ala Phe Asp Glu Ala Glu Lys Lys  
355 360 365  
Asn Glu Glu Glu Glu Ser Lys Asp Ala Pro Ala Glu Ser Asp Ala Glu  
370 375 380  
Asp Glu Pro Glu Asp Asp Glu Gly Gly Asp Asp Ser Asp Ser Glu Ser  
385 390 395 400  
Lys Ala Glu Glu Thr Lys Ser Glu Asp Ser Glu Glu Thr Ser Glu Lys  
405 410 415  
Asp Ala Thr Ala His Asp Glu Leu  
420

(2) INFORMATION FOR SEQ ID NO:1894:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 421 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..421

(D) OTHER INFORMATION: / Ceres Seq. ID 1571306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1894:

Met Ile Pro Ser Leu Val Ser Leu Ile Leu Ile Gly Leu Val Ala Ile  
1 5 10 15  
Ala Ser Ala Ala Val Ile Phe Glu Glu Arg Phe Asp Asp Gly Trp Glu  
20 25 30  
Asn Arg Trp Val Lys Ser Glu Trp Lys Lys Asp Asp Asn Thr Ala Gly  
35 40 45  
Glu Trp Lys His Thr Ala Gly Asn Trp Ser Gly Asp Ala Asn Asp Lys

Met Lys Leu Leu Ser Gly Asp Val Asp Gln Lys Lys Phe Gly Gly Asp  
1 5 10 15

Thr Pro Tyr Ser Ile Met Phe Gly Pro Asp Ile Cys Gly Tyr Ser Thr  
20 25 30  
Lys Lys Val His Ala Ile Leu Thr Tyr Asn Glu Ala Asn His Leu Ile  
35 40 45  
Lys Lys Asp Val Pro Cys Glu Thr Asp Gln Leu Thr His Val Tyr Thr  
50 55 60  
Phe Ile Leu Arg Pro Asp Ala Thr Tyr Ser Ile Leu Ile Asp Asn Val  
65 70 75 80  
Glu Lys Gln Thr Gly Ser Leu Tyr Ser Asp Trp Asp Leu Leu Pro Pro  
85 90 95  
Lys Lys Ile Lys Asp Pro Ser Ala Lys Lys Pro Glu Asp Trp Asp Glu  
100 105 110  
Gln Glu Tyr Ile Ser Asp Pro Glu Asp Lys Lys Pro Asp Gly Tyr Asp  
115 120 125  
Asp Ile Pro Lys Glu Ile Pro Asp Thr Asp Ser Lys Lys Pro Glu Asp  
130 135 140  
Trp Asp Asp Glu Glu Asp Gly Glu Trp Thr Ala Pro Thr Ile Pro Asn  
145 150 155 160  
Pro Glu Tyr Met Gly Glu Trp Lys Pro Lys Gln Ile Lys Asn Pro Asn  
165 170 175  
Tyr Lys Gly Lys Trp Glu Ala Pro Leu Ile Asp Asn Pro Asp Phe Lys  
180 185 190  
Asp Asp Pro Glu Leu Tyr Val Phe Pro Lys Leu Lys Tyr Val Gly Leu  
195 200 205  
Glu Leu Trp Gln Val Lys Ser Gly Ser Leu Phe Asp Asn Val Leu Ile  
210 215 220  
Cys Asp Asp Pro Asp Tyr Ala Lys Lys Leu Ala Asp Glu Thr Trp Gly  
225 230 235 240  
Lys Leu Lys Asp Ala Glu Lys Ala Ala Phe Asp Glu Ala Glu Lys Lys  
245 250 255  
Asn Glu Glu Glu Glu Ser Lys Asp Ala Pro Ala Glu Ser Asp Ala Glu  
260 265 270  
Asp Glu Pro Glu Asp Asp Glu Gly Gly Asp Asp Ser Asp Ser Glu Ser  
275 280 285  
Lys Ala Glu Glu Thr Lys Ser Glu Asp Ser Glu Glu Thr Ser Glu Lys  
290 295 300  
Asp Ala Thr Ala His Asp Glu Leu  
305 310

(2) INFORMATION FOR SEQ ID NO:1896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1257
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1896:

|            |             |            |             |             |            |     |
|------------|-------------|------------|-------------|-------------|------------|-----|
| acactcgtct | taccaaaactc | tctctacac  | aaccaaiaacc | atctcttttcg | aacaaaactt | 60  |
| gttgtaactc | atcttcttct  | tcttcttctc | catcacagac  | tcataacaaa  | tgggagaagt | 120 |
| ttcagtggtg | gagaacaaga  | aagtgatact | aaagaattat  | gtagatggta  | ttcttacaga | 180 |
| aacagacatg | gaagtgaaac  | tcggagaaac | aattgagcta  | aaagcaccaa  | aaggatcttc | 240 |
| ttgtttcttc | gtcaaaaaatc | tatacttgtc | ttgtgatcct  | tacatgagag  | gtcgtatcgc | 300 |
| tgattttcac | gggttctatc  | tcccgccctt | tggttctggc  | caacgtatcg  | aaggggttgc | 360 |
| tttagcaaga | gtgatagatt  | ctgatgatac | taattataag  | cccgggcgata | tagctctcgg | 420 |
| tatcatctgt | tggaagaagt  | acagtttgct | acgtatgttc  | gataacctac  | agttgagaaa | 480 |
| tattcaatta | gacgacgaca  | tcccgctttc | ttatcatctc  | ggacttctcg  | ggatggctcg | 540 |
| atttacagca | tatgcagggt  | ttaatgagat | atgttgtctc  | aagaaagggg  | acagtggttt | 600 |
| tgtctctgca | gcagtgtggg  | cagtttgaca | acttggttgt  | cagctagcta  | agttgcacgc | 660 |

|            |             |            |            |            |            |      |
|------------|-------------|------------|------------|------------|------------|------|
| ctgctatgtt | gttggttagcg | ccggtagtaa | gcaaaaggtt | gagatcctta | aaaacgagct | 720  |
| tggatatgat | gaagccttta  | actacaagga | agaggctgat | cttgatactg | ctttgaagag | 780  |
| gtacttccca | gaggggatcg  | atatctactt | cgataacgtg | ggtggatcca | tgcttgatgc | 840  |
| agcactctc  | aacatgaagg  | ttcgtggaag | aatcgcgctc | tgtggaatgg | tgctttatac | 900  |
| aagcctctca | acttcacac   | aaggaatcaa | gaacctatac | agcgctatct | acaaacgctt | 960  |
| aaggctagaa | gggttcttgc  | agagtgatta | ccttcatac  | ttcccacagt | ttcttgaaaa | 1020 |
| tgtaagagaa | tattacaaga  | aaggcaagat | tgctacatc  | gaagatatat | ctgaagcctc | 1080 |
| cgaccAtcgc | tcNccgcgtc  | actgtttggg | ctgttttccg | ggaaaaatat | cggtaaaacg | 1140 |
| gtgtgtcggg | ttgctaaga   | gtgattgttt | ctaaaaagta | tattgtaagt | gacttaaaac | 1200 |
| agacattata | tgaataaaag  | ccgccataag | ttcttatagg | aaaaacgtta | gttaatc    |      |

(2) INFORMATION FOR SEQ ID NO:1897:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..354

(D) OTHER INFORMATION: / Ceres Seq. ID 1571313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1897:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Glu | Val | Ser | Val | Val | Glu | Asn | Lys | Lys | Val | Ile | Leu | Lys | Asn |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Tyr | Val | Asp | Gly | Ile | Pro | Thr | Glu | Thr | Asp | Met | Glu | Val | Lys | Leu | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Thr | Ile | Glu | Leu | Lys | Ala | Pro | Lys | Gly | Ser | Ser | Cys | Phe | Leu | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Asn | Leu | Tyr | Leu | Ser | Cys | Asp | Pro | Tyr | Met | Arg | Gly | Arg | Met | Arg |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Phe | His | Gly | Ser | Tyr | Leu | Pro | Pro | Phe | Val | Pro | Gly | Gln | Arg | Ile |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Gly | Phe | Gly | Leu | Ala | Arg | Val | Ile | Asp | Ser | Asp | Asp | Thr | Asn | Tyr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Lys | Pro | Gly | Asp | Ile | Val | Ser | Gly | Ile | Ile | Gly | Trp | Glu | Glu | Tyr | Ser |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Leu | Leu | Arg | Ser | Ser | Asp | Asn | Leu | Gln | Leu | Arg | Asn | Ile | Gly | Leu | Asp |
|     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Asp | Asp | Ile | Pro | Leu | Ser | Tyr | His | Leu | Gly | Leu | Leu | Gly | Met | Ala | Gly |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Thr | Ala | Tyr | Ala | Gly | Phe | Asn | Glu | Ile | Cys | Cys | Pro | Lys | Lys | Gly |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Asp | Ser | Val | Phe | Val | Ser | Ala | Ala | Cys | Gly | Ala | Val | Gly | Gln | Leu | Val |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Gly | Gln | Leu | Ala | Lys | Leu | His | Gly | Cys | Tyr | Val | Val | Gly | Ser | Ala | Gly |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ser | Lys | Gln | Lys | Val | Glu | Ile | Leu | Lys | Asn | Glu | Leu | Gly | Tyr | Asp | Glu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Phe | Asn | Tyr | Lys | Glu | Glu | Ala | Asp | Leu | Asp | Thr | Ala | Leu | Lys | Arg |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Tyr | Phe | Pro | Glu | Gly | Ile | Asp | Ile | Tyr | Phe | Asp | Asn | Val | Gly | Gly | Ser |
|     |     |     | 225 |     |     | 230 |     |     |     | 235 |     |     |     | 240 |     |
| Met | Leu | Asp | Ala | Ala | Leu | Leu | Asn | Met | Lys | Val | Arg | Gly | Arg | Ile | Ala |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Cys | Gly | Met | Val | Ser | Leu | Gln | Ser | Leu | Ser | Thr | Ser | Ser | Gln | Gly |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Ile | Lys | Asn | Leu | Tyr | Ser | Ala | Ile | Tyr | Lys | Arg | Leu | Arg | Leu | Glu | Gly |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Phe | Leu | Gln | Ser | Asp | Tyr | Leu | His | Ile | Phe | Pro | Gln | Phe | Leu | Glu | Asn |
|     |     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Val | Lys | Arg | Tyr | Tyr | Lys | Glu | Gly | Lys | Ile | Val | Tyr | Ile | Glu | Asp | Ile |

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(2) INFORMATION FOR SEQ ID NO:1898:

(A) LENGTH: 328 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY:  $\lim$

MOLECULE TYPE: pentide

(ix) FEATURE:  
(B) NEM

```
(A) NAME/KEY: peptide
(B) LOCATION: 1 328
```

(B) LOCATION: 1..328

(D) OTHER INFORMATION: / Ceres Seq. ID 1571314  
SEQUENCE DESCRIPTION: SEQ ID NO:1898:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1898:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..296

(D) OTHER INFORMATION: / Ceres Seq. ID 1571315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1899:

Met Arg Gly Arg Met Arg Asp Phe His Gly Ser Tyr Leu Pro Pro Phe  
1 5 10 15  
Val Pro Gly Gln Arg Ile Glu Gly Phe Gly Leu Ala Arg Val Ile Asp  
20 25 30  
Ser Asp Asp Thr Asn Tyr Lys Pro Gly Asp Ile Val Ser Gly Ile Ile  
35 40 45  
Gly Trp Gly Glu Tyr Ser Leu Leu Arg Ser Ser Asp Asn Leu Gln Leu  
50 55 60  
Arg Asn Ile Gln Leu Asp Asp Asp Ile Pro Leu Ser Tyr His Leu Gly  
65 70 75 80  
Leu Leu Gly Met Ala Gly Phe Thr Ala Tyr Ala Gly Phe Asn Glu Ile  
85 90 95  
Cys Cys Pro Lys Lys Gly Asp Ser Val Phe Val Ser Ala Ala Cys Gly  
100 105 110  
Ala Val Gly Gln Leu Val Gly Gln Leu Ala Lys Leu His Gly Cys Tyr  
115 120 125  
Val Val Gly Ser Ala Gly Ser Lys Gln Lys Val Glu Ile Leu Lys Asn  
130 135 140  
Glu Leu Gly Tyr Asp Glu Ala Phe Asn Tyr Lys Glu Glu Ala Asp Leu  
145 150 155 160  
Asp Thr Ala Leu Lys Arg Tyr Phe Pro Glu Gly Ile Asp Ile Tyr Phe  
165 170 175  
Asp Asn Val Gly Gly Ser Met Leu Asp Ala Ala Leu Leu Asn Met Lys  
180 185 190  
Val Arg Gly Arg Ile Ala Leu Cys Gly Met Val Ser Leu Gln Ser Leu  
195 200 205  
Ser Thr Ser Ser Gln Gly Ile Lys Asn Leu Tyr Ser Ala Ile Tyr Lys  
210 215 220  
Arg Leu Arg Leu Glu Gly Phe Leu Gln Ser Asp Tyr Leu His Ile Phe  
225 230 235 240  
Pro Gln Phe Leu Glu Asn Val Lys Arg Tyr Tyr Lys Glu Gly Lys Ile  
245 250 255  
Val Tyr Ile Glu Asp Ile Ser Glu Gly Leu Asp His Arg Xaa Pro Leu  
260 265 270  
His Leu Leu Gly Cys Phe Pro Gly Lys Ile Ser Val Asn Arg Leu Phe  
275 280 285  
Gly Leu Leu Lys Ser Asp Cys Phe  
290 295

(2) INFORMATION FOR SEQ ID NO:1900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1766

(D) OTHER INFORMATION: / Ceres Seq. ID 1571333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1900:

|             |             |             |             |             |            |      |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| ctaaccattgg | attcagagctc | tctagtgaag  | aatccgccat  | ggctgtttcca | tttctaagct | 60   |
| cttctcttaca | actcacaccc  | actctccga   | ttctcttcac  | taaagtaaca  | ccaacaccaa | 120  |
| taatccacaa  | ccacagatca  | acatgcacta  | taccacacaa  | gcctcgtcta  | cgtctccctc | 180  |
| gccgcctccg  | cgtcgttgga  | acgcgcgtat  | ctgatcaaac  | agaagagggt  | ggagatgttc | 240  |
| ttttaaacc   | tgaagaagag  | aaacgtgttg  | agggtgggga  | ttatgattgg  | acagaggaat | 300  |
| ggatccatt   | gtacttaact  | aaaaacgtcc  | ctgaagatgc  | gcctcttgcc  | ctcaccgtct | 360  |
| acgatcgta   | aattgttttg  | tataaagacg  | gYgaaggaac  | acttcgttgt  | tacgaagatc | 420  |
| gggtctctca  | tcgggtggct  | aagtgtgtctg | aaggacaatt  | gattgatggg  | agattggaat | 480  |
| gtttgtatca  | ttgtttggca  | tttgaaggag  | aggcgaaatg  | tgtcaagatt  | cctcagcttc | 540  |
| ctgcaagtcg  | taagatttcca | aaggctgtctt | gtgtgaagac  | gtatgaggtg  | aaggattcac | 600  |
| aaggagttgt  | gtgggtgtgt  | atgtcaacaa  | agacacctcc  | aaacctctgag | agacttccct | 660  |
| gggttgagaa  | tttcgctaga  | cccggttttt  | tcgacatttc  | gactactcoat | gagcttccct | 720  |
| atgaccattc  | cattctttta  | gagaatctga  | tgatcctctg  | tcattgtcct  | atctctcatg | 780  |
| atagaacgga  | tttcaactgc  | aaaaaagaaa  | atgctcagcc  | tttggttttc  | gaggtcacag | 840  |
| agcgaagtaa  | tcggggtttc  | gcaggagactt | ggggccgaga  | gagagaaggt  | gggaaagga  | 900  |
| gtataattact | tcgggttgat  | gtcctctgtg  | ttctgcagaa  | caatcgagag  | ttcgaggga  | 960  |
| aggatggagt  | gaagaactat  | ttttcagggc  | tgtttctttg  | tagacctaca  | gggcaagga  | 1020 |
| agtcctatgc  | tattgttagg  | tttggggtca  | caaaaagatc  | gcctttgggt  | tcggtgttac | 1080 |
| ctcaatgggt  | ctggcatcag  | aatgcctgca  | agggttttga  | acaagacatg  | gggtttctat | 1140 |
| cgctctcaaaa | acgaggtttc  | gatgaaggag  | aaagtaccaa  | ctaagctatt  | gtatttgaat | 1200 |
| ctaaagtcac  | cggacacatg  | ggctcgctgaa | tagaaagtgg  | atggacaaag  | ttgtgctatg | 1260 |
| gatgccttac  | catttcgggc  | ataggacctat | atctctcccc  | aaagtcctgc  | ctgtcgtgga | 1320 |
| acatgcgccg  | gcaggcctca  | ttgcagctct  | ctctgcttct  | taccctgcaa  | aaggcggaat | 1380 |
| tgggactatg  | catgctccca  | atttggctaa  | ccggtacttc  | agacatatat  | ttcattgtag | 1440 |
| aaagtcgagc  | aatgtgatca  | aatcttttga  | gcctcgaaa   | aatatcctct  | ctgcaccggc | 1500 |
| agtggtcttg  | acggcttttg  | ccattcttgt  | gggttagtaga | catgtggaag  | ctgtccttgt | 1560 |
| agtggtcaga  | gcatttgtct  | cagccgcgac  | ttatacctgc  | ttaaagagcta | taaatctaaa | 1620 |
| caccaataaac | ttcattagaa  | cacacagaag  | acatgaaaaa  | tgtatagtgt  | catgttctct | 1680 |
| ctctttccaa  | caaatgtgat  | ttcatgaaat  | aaatttttgc  | ttgtaaacgc  | aatatatata | 1740 |
| ttcagaaggt  | ttcaatgttt  | gccagc      |             |             |            |      |

(2) INFORMATION FOR SEQ ID NO:1901:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..393

(D) OTHER INFORMATION: / Ceres Seq. ID 1571334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1901:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ile | Gly | Phe | Glu | Leu | Ser | Ser | Glu | Glu | Ser | Ala | Met | Ala | Val | Pro |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Phe | Leu | Ser | Ser | Ser | Leu | Gln | Leu | Thr | Pro | Thr | Ser | Pro | Ile | Leu | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Lys | Val | Thr | Pro | Thr | Pro | Ile | Ile | His | Asn | His | Arg | Ser | Thr | Cys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Ile | Pro | Thr | Lys | Pro | Arg | Leu | Arg | Leu | Arg | Arg | Ser | Ala | Val |     |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ala | Gly | Thr | Ala | Val | Ser | Asp | Gln | Thr | Glu | Gly | Gly | Gly | Asp | Val | Leu |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     |     | 80  |     |
| Leu | Asn | Pro | Glu | Glu | Lys | Arg | Val | Glu | Val | Ala | Asp | Tyr | Asp | Trp |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |     |
| Thr | Glu | Glu | Trp | Tyr | Pro | Leu | Tyr | Leu | Thr | Lys | Asn | Val | Pro | Glu | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Ala | Pro | Leu | Gly | Leu | Thr | Val | Tyr | Asp | Arg | Gln | Ile | Val | Leu | Tyr | Lys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Xaa | Glu | Gly | Thr | Leu | Arg | Cys | Tyr | Glu | Asp | Arg | Cys | Pro | His | Arg |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |

Leu Ala Lys Leu Ser Glu Gly Gln Leu Ile Asp Gly Arg Leu Glu Cys  
145 150 155 160  
Leu Tyr His Gly Trp Gln Phe Glu Gly Glu Gly Lys Cys Val Lys Ile  
165 170 175  
Pro Gln Leu Pro Ala Ser Ala Lys Ile Pro Lys Ala Ala Cys Val Lys  
180 185 190  
Thr Tyr Glu Val Lys Asp Ser Gln Gly Val Val Trp Val Trp Met Ser  
195 200 205  
Thr Lys Thr Pro Pro Asn Pro Glu Lys Leu Pro Trp Phe Glu Asn Phe  
210 215 220  
Ala Arg Pro Gly Phe Phe Asp Ile Ser Thr Thr His Glu Leu Pro Tyr  
225 230 235 240  
Asp His Ser Ile Leu Leu Glu Asn Leu Met Asp Pro Ala His Val Pro  
245 250 255  
Ile Ser His Asp Arg Thr Asp Phe Thr Ala Lys Arg Lys Asp Ala Gln  
260 265 270  
Pro Leu Val Phe Glu Val Thr Glu Arg Ser Asn Arg Gly Phe Ala Gly  
275 280 285  
Thr Trp Gly Arg Glu Arg Glu Gly Gly Lys Gly Ser Asn Leu Leu Arg  
290 295 300  
Phe Asp Ala Pro Cys Val Leu Gln Asn Asn Arg Glu Phe Glu Gly Lys  
305 310 315 320  
Asp Gly Val Lys Asn Tyr Phe Ser Gly Leu Phe Leu Cys Arg Pro Thr  
325 330 335  
Gly Gln Gly Lys Ser Met Leu Ile Val Arg Phe Gly Val Thr Lys Arg  
340 345 350  
Ser Pro Leu Val Ser Val Leu Pro Gln Trp Phe Trp His Gln Asn Ala  
355 360 365  
Cys Lys Val Phe Glu Gln Asp Met Gly Phe Leu Ser Ser Gln Lys Arg  
370 375 380  
Gly Ser Asp Glu Gly Glu Ser Thr Asn  
385 390

(2) INFORMATION FOR SEQ ID NO:1902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..381
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1902:

Met Ala Val Pro Phe Leu Ser Ser Ser Leu Gln Leu Thr Pro Thr Ser  
1 5 10 15  
Pro Ile Leu Phe Thr Lys Val Thr Pro Thr Pro Ile Ile His Asn His  
20 25 30  
Arg Ser Thr Cys Thr Ile Pro Thr Lys Pro Arg Leu Arg Leu Leu Arg  
35 40 45  
Arg Ser Ala Val Ala Gly Thr Ala Val Ser Asp Gln Thr Glu Gly Gly  
50 55 60  
Gly Asp Val Leu Leu Asn Pro Glu Glu Glu Lys Arg Val Glu Val Ala  
65 70 75 80  
Asp Tyr Asp Trp Thr Glu Glu Trp Tyr Pro Leu Tyr Leu Thr Lys Asn  
85 90 95  
Val Pro Glu Asp Ala Pro Leu Gly Leu Thr Val Tyr Asp Arg Gln Ile  
100 105 110  
Val Leu Tyr Lys Asp Xaa Glu Gly Thr Leu Arg Cys Tyr Glu Asp Arg  
115 120 125  
Cys Pro His Arg Leu Ala Lys Leu Ser Glu Gly Gln Leu Ile Asp Gly



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 130                                                             | 135 | 140 |
| Arg Leu Glu Cys Leu Tyr His Gly Trp Gln Phe Glu Gly Glu Gly Lys |     |     |
| 145                                                             | 150 | 155 |
| Cys Val Lys Ile Pro Gln Leu Pro Ala Ser Ala Lys Ile Pro Lys Ala |     |     |
|                                                                 | 165 | 170 |
| Ala Cys Val Lys Thr Tyr Glu Val Lys Asp Ser Gln Gly Val Val Trp |     |     |
|                                                                 | 180 | 185 |
| Val Trp Met Ser Thr Lys Thr Pro Pro Asn Pro Glu Lys Leu Pro Trp |     |     |
|                                                                 | 195 | 200 |
| Phe Glu Asn Phe Ala Arg Pro Gly Phe Phe Asp Ile Ser Thr Thr His |     |     |
|                                                                 | 210 | 215 |
| Glu Leu Pro Tyr Asp His Ser Ile Leu Leu Glu Asn Leu Met Asp Pro |     |     |
| 225                                                             | 230 | 235 |
| Ala His Val Pro Ile Ser His Asp Arg Thr Asp Phe Thr Ala Lys Arg |     |     |
|                                                                 | 245 | 250 |
| Lys Asp Ala Gln Pro Leu Val Phe Glu Val Thr Glu Arg Ser Asn Arg |     |     |
|                                                                 | 260 | 265 |
| Gly Phe Ala Gly Thr Trp Gly Arg Glu Arg Glu Gly Gly Lys Gly Ser |     |     |
|                                                                 | 275 | 280 |
| Asn Leu Leu Arg Phe Asp Ala Pro Cys Val Leu Gln Asn Asn Arg Glu |     |     |
|                                                                 | 290 | 295 |
| Phe Glu Gly Lys Asp Gly Val Lys Asn Tyr Phe Ser Gly Leu Phe Leu |     |     |
| 305                                                             | 310 | 315 |
| Cys Arg Pro Thr Gly Gln Gly Lys Ser Met Leu Ile Val Arg Phe Gly |     |     |
|                                                                 | 325 | 330 |
| Val Thr Lys Arg Ser Pro Leu Val Ser Val Leu Pro Gln Trp Phe Trp |     |     |
|                                                                 | 340 | 345 |
| His Gln Asn Ala Cys Lys Val Phe Glu Gln Asp Met Gly Phe Leu Ser |     |     |
|                                                                 | 355 | 360 |
| Ser Gln Lys Arg Gly Ser Asp Glu Gly Glu Ser Thr Asn             |     |     |
|                                                                 | 370 | 375 |
|                                                                 |     | 380 |

(2) INFORMATION FOR SEQ ID NO:1903:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1486 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1486

(D) OTHER INFORMATION: / Ceres Seq. ID 1571340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1903:

|              |             |             |             |             |             |      |
|--------------|-------------|-------------|-------------|-------------|-------------|------|
| atcacaaattt  | ttctacggctc | agagattcaaa | aagagttcttt | tctctctatc  | ttattctccg  | 60   |
| atcatcatga   | tgcaagcagcc | accaccgcgga | ggtatccttc  | cacatcacgc  | tcctcctcct  | 120  |
| ttctgcgcgaac | aacagtagcgg | ttaccaacaaa | cottacggga  | ttgctggagc  | tgctccacca  | 180  |
| ccaccacagaa  | tgtaggaatcc | tcagacggcg  | gcgcgcgcCat | cagttcacgc  | tacgaccgct  | 240  |
| gcagagatcc   | ggactctttg  | tacagtgatt  | ggatgggatg  | gaatttcctc  |             | 300  |
| tacgggttgc   | ttgctcatatc | cggagagatg  | gtttctgcta  | aagtgtatcg  | taacaagcaa  | 360  |
| accggtcaa    | ttgaaggata  | cgttttcatt  | gaatttcgat  | ctcatgctgc  | tgctgaagaa  | 420  |
| gtcttcacaaa  | cattcaacaaa | cgctcctatc  | ccgagctttc  | ctgatcagct  | ctttagacgt  | 480  |
| mactggggat   | cattgagttc  | aggagataaaa | cgagacgatt  | caccggacta  | cacgatattt  | 540  |
| gtcgggtgatc  | tgagctgctga | tgttacggat  | tatatcttac  | ttgagacgtt  | cagagcctct  | 600  |
| tatccgtcag   | tgaagggtgc  | aaaggttggt  | attaacagag  | tcactggagc  | tacaaaaagg  | 660  |
| tatgggtttg   | ttagggtttc  | tgatgaaagt  | gaacagatcc  | gtgctatgac  | ggagatgaat  | 720  |
| ggcggtctct   | gtctctactag | acctatgaga  | attggtccc   | ctgctagcaa  | gaaaggtgta  | 780  |
| atcggtcaca   | gagattcata  | ccagagctct  | gctgcagggg  | taacaaactga | taatgatcca  | 840  |
| aataacacaaa  | ctgtttttgt  | tggtgggata  | gatgcattct  | tcacggatga  | tcactctgaag | 900  |
| aatgctcttta  | gcgaatatgg  | tgagattgtg  | catgtgaaaa  | taccocgctgg | aaagcgctgt  | 960  |
| ggattcgttc   | agttttccga  | gaagagctgt  | gcagagggaag | ctcttagaat  | gctgaatgga  | 1020 |
| gtgcaattag   | gcggaacaa   | cgctcagctc  | tcatggggcg  | gaagtccttc  | gaacaaacag  | 1080 |

```

tcgggggagc cgagccagtt ttactacggt gggataggac aaggacagga gcagtatggg 1140
tacacgatgc ctcaagaccc taatgcatat tacggaggct actctgggtg aggatacagc 1200
gggtggttacc agcagacacc acaggcagga cagcaaccac cacaacagcc accacagcag 1260
caacaagtgc ggttttagcta ctaaccccga gagtattgct tgagttaatg tcaactctgt 1320
tggttggtgc gtactttggt atgaacttgc ttctgcgtgc cttgttatga atattttccc 1380
aaacacaggt tatttgtctt tgcttttctc taggtgtgtg ttgagttttt aactcttaat 1440
aatgtttctg cgatgctctt gtttttaagt ttttcacac cttttg

```

(2) INFORMATION FOR SEQ ID NO:1904:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 427 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..427

(D) OTHER INFORMATION: / Ceres Seq. ID 1571341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1904:

```

Ile Thr Ile Phe Leu Arg Ser Glu Ile Gln Lys Ser Ser Phe Ser Leu
1 5 10
Ser Tyr Ser Pro Ile Ile Met Met Gln Gln Pro Pro Pro Gly Gly Ile
20 25 30
Leu Pro His His Ala Pro Pro Pro Ser Ala Gln Gln Gln Tyr Gly Tyr
35 40 45
Gln Gln Pro Tyr Gly Ile Ala Gly Ala Ala Pro Pro Pro Gln Met
50 55 60
Trp Asn Pro Gln Ala Ala Ala Pro Pro Ser Val Gln Pro Thr Thr Ala
65 70 75 80
Asp Glu Ile Arg Thr Leu Trp Ile Gly Asp Leu Gln Tyr Trp Met Asp
85 90 95
Glu Asn Phe Leu Tyr Gly Cys Phe Ala His Thr Gly Glu Met Val Ser
100 105 110
Ala Lys Val Ile Arg Asn Lys Gln Thr Gly Gln Val Glu Gly Tyr Gly
115 120 125
Phe Ile Glu Phe Ala Ser His Ala Ala Ala Glu Arg Val Leu Gln Thr
130 135 140
Phe Asn Asn Ala Pro Ile Pro Ser Phe Pro Asp Gln Leu Phe Arg Leu
145 150 155 160
Xaa Trp Ala Ser Leu Ser Ser Gly Asp Lys Arg Asp Asp Ser Pro Asp
165 170 175
Tyr Thr Ile Phe Val Gly Asp Leu Ala Ala Asp Val Thr Asp Tyr Ile
180 185 190
Leu Leu Glu Thr Phe Arg Ala Ser Tyr Pro Ser Val Lys Gly Ala Lys
195 200 205
Val Val Ile Asn Arg Val Thr Gly Arg Thr Lys Gly Tyr Gly Phe Val
210 215 220
Arg Phe Ser Asp Glu Ser Glu Gln Ile Arg Ala Met Thr Glu Met Asn
225 230 235 240
Gly Val Pro Cys Ser Thr Arg Pro Met Arg Ile Gly Pro Ala Ala Ser
245 250 255
Lys Lys Gly Val Thr Gly Gln Arg Asp Ser Tyr Gln Ser Ser Ala Ala
260 265 270
Gly Val Thr Thr Asp Asn Asp Pro Asn Asn Thr Thr Val Phe Val Gly
275 280 285
Gly Leu Asp Ala Ser Val Thr Asp Asp His Leu Lys Asn Val Phe Ser
290 295 300
Gln Tyr Gly Glu Ile Val His Val Lys Ile Pro Ala Gly Lys Arg Cys
305 310 315 320
Gly Phe Val Gln Phe Ser Glu Lys Ser Cys Ala Glu Glu Ala Leu Arg
325 330 335

```

Met Leu Asn Gly Val Gln Leu Gly Gly Thr Thr Val Arg Leu Ser Trp  
340 345 350  
Gly Arg Ser Pro Ser Asn Lys Gln Ser Gly Asp Pro Ser Gln Phe Tyr  
355 360 365  
Tyr Gly Gly Tyr Gly Gln Gly Gln Glu Gln Tyr Gly Tyr Thr Met Pro  
370 375 380  
Gln Asp Pro Asn Ala Tyr Tyr Gly Gly Tyr Ser Gly Gly Tyr Ser  
385 390 395 400  
Gly Gly Tyr Gln Gln Thr Pro Gln Ala Gly Gln Gln Pro Pro Gln Gln  
405 410 415  
Pro Pro Gln Gln Gln Gln Val Gly Phe Ser Tyr  
420 425

(2) INFORMATION FOR SEQ ID NO:1905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..405
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1905:

Met Met Gln Gln Pro Pro Pro Gly Gly Ile Leu Pro His His Ala Pro  
1 5 10 15  
Pro Pro Ser Ala Gln Gln Gln Tyr Gly Tyr Gln Gln Pro Tyr Gly Ile  
20 25 30  
Ala Gly Ala Ala Pro Pro Pro Pro Gln Met Trp Asn Pro Gln Ala Ala  
35 40 45  
Ala Pro Pro Ser Val Gln Pro Thr Thr Ala Asp Glu Ile Arg Thr Leu  
50 55 60  
Trp Ile Gly Asp Leu Gln Tyr Trp Met Asp Glu Asn Phe Leu Tyr Gly  
65 70 75 80  
Cys Phe Ala His Thr Gly Glu Met Val Ser Ala Lys Val Ile Arg Asn  
85 90 95  
Lys Gln Thr Gly Gln Val Glu Gly Tyr Gly Phe Ile Glu Phe Ala Ser  
100 105 110  
His Ala Ala Ala Glu Arg Val Leu Gln Thr Phe Asn Asn Ala Pro Ile  
115 120 125  
Pro Ser Phe Pro Asp Gln Leu Phe Arg Leu Xaa Trp Ala Ser Leu Ser  
130 135 140  
Ser Gly Asp Lys Arg Asp Ser Pro Asp Tyr Thr Ile Phe Val Gly  
145 150 155 160  
Asp Leu Ala Ala Asp Val Thr Asp Tyr Ile Leu Leu Glu Thr Phe Arg  
165 170 175  
Ala Ser Tyr Pro Ser Val Lys Gly Ala Lys Val Val Ile Asn Arg Val  
180 185 190  
Thr Gly Arg Thr Lys Gly Tyr Gly Phe Val Arg Phe Ser Asp Glu Ser  
195 200 205  
Glu Gln Ile Arg Ala Met Thr Glu Met Asn Gly Val Pro Cys Ser Thr  
210 215 220  
Arg Pro Met Arg Ile Gly Pro Ala Ala Ser Lys Lys Gly Val Thr Gly  
225 230 235 240  
Gln Arg Asp Ser Tyr Gln Ser Ser Ala Ala Gly Val Thr Thr Asp Asn  
245 250 255  
Asp Pro Asn Asn Thr Thr Val Phe Val Gly Gly Leu Asp Ala Ser Val  
260 265 270  
Thr Asp Asp His Leu Lys Asn Val Phe Ser Gln Tyr Gly Glu Ile Val  
275 280 285  
His Val Lys Ile Pro Ala Gly Lys Arg Cys Gly Phe Val Gln Phe Ser

|                     |                     |                             |
|---------------------|---------------------|-----------------------------|
| 290                 | 295                 | 300                         |
| Glu Lys Ser Cys Ala | Glu Glu Ala Leu Arg | Met Leu Asn Gly Val Gln     |
| 305                 | 310                 | 315                         |
| Leu Gly Gly Thr Thr | Val Arg Leu Ser Trp | Gly Arg Ser Pro Ser Asn     |
| 325                 | 330                 | 335                         |
| Lys Gln Ser Gly Asp | Pro Ser Gln Phe Tyr | Tyr Gly Gly Tyr Gly Gln     |
| 340                 | 345                 | 350                         |
| Gly Gln Glu Gln Tyr | Gly Tyr Thr Met     | Pro Gln Asp Pro Asn Ala Tyr |
| 355                 | 360                 | 365                         |
| Tyr Gly Gly Tyr Ser | Gly Gly Gly Tyr Ser | Gly Gly Tyr Gln Gln Thr     |
| 370                 | 375                 | 380                         |
| Pro Gln Ala Gly Gln | Gln Gln Gln Gln     | Pro Gln Gln Gln Gln         |
| 385                 | 390                 | 395                         |
| Val Gly Phe Ser Tyr |                     | 400                         |

(2) INFORMATION FOR SEQ ID NO:1906:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 404 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..404

(D) OTHER INFORMATION: / Ceres Seq. ID 1571343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1906:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Gln | Pro | Pro | Pro | Gly | Gly | Ile | Leu | Pro | His | Ala | Pro | Pro |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ser | Ala | Gln | Gln | Tyr | Gly | Tyr | Gln | Gln | Pro | Tyr | Gly | Ile | Ala |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ala | Ala | Pro | Pro | Pro | Gln | Met | Trp | Asn | Pro | Gln | Ala | Ala | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Pro | Pro | Ser | Val | Gln | Pro | Thr | Ala | Asp | Glu | Ile | Arg | Thr | Leu | Trp |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ile | Gly | Asp | Leu | Gln | Tyr | Trp | Met | Asp | Glu | Ala | Phe | Leu | Tyr | Gly |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Phe | Ala | His | Thr | Gly | Glu | Met | Val | Ser | Ala | Lys | Val | Ile | Arg | Asn |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Thr | Gly | Gln | Val | Glu | Gly | Tyr | Gly | Phe | Ile | Glu | Phe | Ala | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Ala | Ala | Ala | Glu | Arg | Val | Leu | Gln | Thr | Phe | Asn | Asn | Ala | Pro | Ile |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Ser | Phe | Pro | Asp | Gln | Leu | Phe | Arg | Leu | Xaa | Trp | Ala | Ser | Leu | Ser |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |
| Gly | Asp | Lys | Arg | Asp | Asp | Ser | Pro | Asp | Tyr | Thr | Ile | Phe | Val | Gly |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Ala | Ala | Asp | Val | Thr | Asp | Tyr | Ile | Leu | Leu | Glu | Thr | Phe | Arg |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Tyr | Pro | Ser | Val | Lys | Gly | Ala | Lys | Val | Val | Ile | Asn | Arg | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |
| Gly | Arg | Thr | Lys | Gly | Tyr | Gly | Phe | Val | Arg | Phe | Ser | Asp | Glu | Ser |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Gln | Ile | Arg | Ala | Met | Thr | Glu | Met | Asn | Gly | Val | Pro | Cys | Ser | Thr |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |
| Pro | Met | Arg | Ile | Gly | Pro | Ala | Ala | Ser | Lys | Lys | Gly | Val | Thr | Gly |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |
| Arg | Asp | Ser | Tyr | Gln | Ser | Ser | Ala | Ala | Gly | Val | Thr | Thr | Asp | Asn |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     | 255 |     |
| Pro | Asn | Asn | Thr | Thr | Val | Phe | Val | Gly | Gly | Leu | Asp | Ala | Ser | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |

Asp Asp His Leu Lys Asn Val Phe Ser Gln Tyr Gly Glu Ile Val His  
275 280 285  
Val Lys Ile Pro Ala Gly Lys Arg Cys Gly Phe Val Gln Phe Ser Glu  
290 295 300  
Lys Ser Cys Ala Glu Glu Ala Leu Arg Met Leu Asn Gly Val Gln Leu  
305 310 315 320  
Gly Gly Thr Thr Val Arg Leu Ser Trp Gly Arg Ser Pro Ser Asn Lys  
325 330 335  
Gln Ser Gly Asp Pro Ser Gln Phe Tyr Tyr Gly Gly Tyr Gly Gln Gly  
340 345 350  
Gln Glu Gln Tyr Gly Tyr Thr Met Pro Gln Asp Pro Asn Ala Tyr Tyr  
355 360 365  
Gly Gly Tyr Ser Gly Gly Gly Tyr Ser Gly Gly Tyr Gln Gln Thr Pro  
370 375 380  
Gln Ala Gly Gln Gln Pro Pro Gln Gln Pro Pro Gln Gln Gln Val  
385 390 395 400  
Gly Phe Ser Tyr

(2) INFORMATION FOR SEQ ID NO:1907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..481
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1907:

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| atcttctctt | cttttgcttc  | tcctttcttt | gagtgcttc  | acttctcttg | catccttcaa  | 60  |
| atctatccac | agcaaggaat  | ggcgacagCa | gcagcaccag | cagtgatttc | atggacaaga  | 120 |
| tcaggcatgt | tgcccaaat   | oggacaaacc | cagaagaaat | ctgagatgaa | agtttcttac  | 180 |
| ataactggac | ttaaactcata | tggttggttc | aaggcacaga | acaacaaggt | tgtctcaatg  | 240 |
| ggatcaccac | ctgcacacaga | acagtgtttt | gctaacgttg | tgatgtctct | caaagggaaga | 300 |
| agagttggat | tcgttcttct  | tcgaatcgaa | acttctgttg | aagaagctga | agcagagtaa  | 360 |
| atagagtaaa | ttgctgctct  | tataattata | tatttttggt | tattgttgtt | gtcaagcttt  | 420 |
| ggtaaaactt | gatggataca  | tgttacattt | gtttatgaag | aagctctttt | cttggttagat | 480 |

(2) INFORMATION FOR SEQ ID NO:1908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1908:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ile Phe Ser Ser Phe Ala Ser Pro Phe Phe Glu Ser Leu His Phe Ser |  |
| 1 5 10 15                                                       |  |
| Cys Ile Leu Gln Thr His Pro Gln Gln Gly Met Ala Thr Ala Ala Ala |  |
| 20 25 30                                                        |  |
| Pro Ala Val Ile Ser Trp Thr Arg Ser Gly Ile Val Ser Lys Ser Gly |  |
| 35 40 45                                                        |  |
| Gln Thr Gln Lys Lys Ser Glu Met Lys Val Ser Tyr Ile Thr Gly Leu |  |
| 50 55 60                                                        |  |
| Asn Ser Tyr Gly Gly Leu Lys Ala Gln Asn Asn Lys Val Val Ser Met |  |
| 65 70 75 80                                                     |  |

Gly Ser Pro Leu Cys Thr Glu Gln Cys Phe Ala Asn Val Val Met Ser  
85 90 95  
Leu Lys Gly Arg Arg Val Gly Phe Val Leu Leu Arg Ile Glu Thr Ser  
100 105 110  
Val Glu Glu Ala Glu Ala Glu  
115

(2) INFORMATION FOR SEQ ID NO:1909:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1571350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1909:

Met Ala Thr Ala Ala Pro Ala Val Ile Ser Trp Thr Arg Ser Gly  
1 5 10 15  
Ile Val Ser Lys Ser Gly Gln Thr Gln Lys Lys Ser Glu Met Lys Val  
20 25 30  
Ser Tyr Ile Thr Gly Leu Asn Ser Tyr Gly Gly Leu Lys Ala Gln Asn  
35 40 45  
Asn Lys Val Val Ser Met Gly Ser Pro Leu Cys Thr Glu Gln Cys Phe  
50 55 60  
Ala Asn Val Val Met Ser Leu Lys Gly Arg Arg Val Gly Phe Val Leu  
65 70 75 80  
Leu Arg Ile Glu Thr Ser Val Glu Glu Ala Glu Ala Glu  
85 90

(2) INFORMATION FOR SEQ ID NO:1910:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1571351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1910:

Met Lys Val Ser Tyr Ile Thr Gly Leu Asn Ser Tyr Gly Gly Leu Lys  
1 5 10 15  
Ala Gln Asn Asn Lys Val Val Ser Met Gly Ser Pro Leu Cys Thr Glu  
20 25 30  
Gln Cys Phe Ala Asn Val Val Met Ser Leu Lys Gly Arg Arg Val Gly  
35 40 45  
Phe Val Leu Leu Arg Ile Glu Thr Ser Val Glu Glu Ala Glu Ala Glu  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1911:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

{B} LOCATION: 1..426

{D} OTHER INFORMATION: / Ceres Seq. ID 1571360

{xi} SEQUENCE DESCRIPTION: SEQ ID NO:1911:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| aattctctac | tttcatataa | gcttagtaag | caaatgtgtt | atgtgtgagt  | gagatttgtt | 60  |
| gagagaaaag | aagaagataa | gtgagagaga | aagagagaaa | gagagaaaat  | gaagttcttg | 120 |
| ttccagtgtc | catgttgctc | ttgcttctgc | ttcatgaaac | caaaagccggg | caaaccataa | 180 |
| gctgttgagg | atacaaaacc | aaaggaggag | aagaagaaag | aggtgaagaa  | agaagagatc | 240 |
| aagaagaggg | agaagaaaga | agagaagaaa | gaagagaaga | aggaaccaca  | agcagagaag | 300 |
| gctgagttaa | aactctactt | tgagaaaatg | taattaatta | tccattatt   | tattattatt | 360 |
| tatctgctat | ttgatgatta | tgcaagtaat | aacatgttat | ttttatggtt  | ggtaaccttt | 420 |
| ttaggc     |            |            |            |             |            |     |

{2} INFORMATION FOR SEQ ID NO:1912:

{i} SEQUENCE CHARACTERISTICS:

{A} LENGTH: 66 amino acids

{B} TYPE: amino acid

{C} STRANDEDNESS:

{D} TOPOLOGY: linear

{ii} MOLECULE TYPE: peptide

{ix} FEATURE:

{A} NAME/KEY: peptide

{B} LOCATION: 1..66

{D} OTHER INFORMATION: / Ceres Seq. ID 1571361

{xi} SEQUENCE DESCRIPTION: SEQ ID NO:1912:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Lys | Phe | Leu | Phe | Gln | Cys | Pro | Cys | Cys | Ser | Cys | Phe | Cys | Phe | Met |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |  |
| Lys | Pro | Lys | Pro | Gly | Lys | Pro | Lys | Ala | Val | Gly | Asp | Thr | Lys | Pro | Lys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | Glu | Lys | Lys | Lys | Glu | Val | Lys | Lys | Glu | Glu | Ile | Lys | Lys | Glu | Glu |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Lys | Lys | Lys | Glu | Glu | Lys | Lys | Glu | Lys | Lys | Glu | Thr | Lys | Ala | Glu | Lys |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ala | Glu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

{2} INFORMATION FOR SEQ ID NO:1913:

{i} SEQUENCE CHARACTERISTICS:

{A} LENGTH: 57 amino acids

{B} TYPE: amino acid

{C} STRANDEDNESS:

{D} TOPOLOGY: linear

{ii} MOLECULE TYPE: peptide

{ix} FEATURE:

{A} NAME/KEY: peptide

{B} LOCATION: 1..57

{D} OTHER INFORMATION: / Ceres Seq. ID 1571362

{xi} SEQUENCE DESCRIPTION: SEQ ID NO:1913:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Leu | Leu | Leu | Leu | Leu | Leu | His | Glu | Thr | Lys | Ala | Gly | Gln | Thr | Lys |  |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |  |
| Ser | Cys | Trp | Arg | Tyr | Lys | Thr | Lys | Gly | Gly | Glu | Glu | Glu | Arg | Gly | Glu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | Arg | Arg | Asp | Gln | Glu | Arg | Gly | Glu | Glu | Arg | Arg | Glu | Glu | Arg | Arg |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Glu | Glu | Gly | Asn | Gln | Ser | Arg | Glu | Gly |     |     |     |     |     |     |     |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     |     |     |     |     |     |  |

{2} INFORMATION FOR SEQ ID NO:1914:

{i} SEQUENCE CHARACTERISTICS:

{A} LENGTH: 51 amino acids

{B} TYPE: amino acid

{C} STRANDEDNESS:

{D} TOPOLOGY: linear

{ii} MOLECULE TYPE: peptide

{ix} FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..51  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571363  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1914:  
Met Lys Pro Lys Pro Gly Lys Pro Lys Ala Val Gly Asp Thr Lys Pro  
1 5 10 15  
Lys Glu Glu Lys Lys Lys Glu Val Lys Lys Glu Glu Ile Lys Lys Glu  
20 25 30  
Glu Lys Lys Glu Glu Lys Lys Glu Glu Lys Lys Glu Thr Lys Ala Glu  
35 40 45  
Lys Ala Glu  
50

(2) INFORMATION FOR SEQ ID NO:1915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..754  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1915:

|            |             |             |             |             |             |     |
|------------|-------------|-------------|-------------|-------------|-------------|-----|
| aagtgactgc | gagcgccgaa  | aatcgcaatg  | ggtgcgtaca  | aatacgtgtc  | ggagctatgg  | 60  |
| aggaagaagc | agtcggatgt  | gatgagggtt  | cttcagaggg  | ttaggtgttg  | ggagtatcgc  | 120 |
| cagcagcctt | ccattgttgc  | tctgtgtcgt  | cccaactcgc  | ccgacaaggc  | tcgtcgtctc  | 180 |
| ggctacaagg | ccaagcaggg  | gtttgtgtgc  | taccgtgttc  | gagtcagacg  | tgggtggacgc | 240 |
| aaagagccag | tgcctaaggg  | tatcgtgtac  | ggtaaaaccca | ccaaccaggg  | agtgacacag  | 300 |
| ctcaaattcc | agcgtagtta  | gagatctgtt  | gctgaggaaac | gtgctggtcg  | caaacctggga | 360 |
| ggccttaggg | ttgttaactc  | ctactggctc  | aatgaggact  | ctacctacaa  | gtactacgag  | 420 |
| attatccctg | tagaccctgc  | acacaaatgcc | gtccgaaatg  | atccaaggat  | caactggatc  | 480 |
| tgcaaccctg | tgacacaagca | cagagaactc  | agaggctctca | ccctccgaaGg | aaagaagaat  | 540 |
| cggtgtcttc | gtggaaaagg  | tcacaacaac  | cacaagaaca  | gaccttcccc  | cagggaacacc | 600 |
| tggaagaaga | acaacagtat  | ctctctccgt  | cgttaccggt  | gatcagtttt  | atgtttttgt  | 660 |
| ttttctcgaa | ctggtatatt  | ttcagtgtgg  | attgtgtttc  | ggaattctgg  | aattacattg  | 720 |
| ggatggaaga | ctttcacatt  | caagagtttg  | tttc        |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..204  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1916:

|                                                                 |                                 |  |
|-----------------------------------------------------------------|---------------------------------|--|
| Met Gly Ala Tyr Lys Tyr Val Ser                                 | Glu Leu Trp Arg Lys Lys Gln Ser |  |
| 1 5 10 15                                                       |                                 |  |
| Asp Val Met Arg Phe Leu Gln Arg Val Arg Cys Trp Glu Tyr Arg Gln |                                 |  |
| 20 25 30                                                        |                                 |  |
| Gln Pro Ser Ile Val Arg Leu Val Arg Pro Thr Arg Pro Asp Lys Ala |                                 |  |
| 35 40 45                                                        |                                 |  |
| Arg Arg Leu Gly Tyr Lys Ala Lys Gln Gly Phe Val Val Tyr Arg Val |                                 |  |
| 50 55 60                                                        |                                 |  |
| Arg Val Arg Arg Gly Gly Arg Lys Arg Pro Val Pro Lys Gly Ile Val |                                 |  |
| 65 70 75 80                                                     |                                 |  |
| Tyr Gly Lys Pro Thr Asn Gln Gly Val Thr Gln Leu Lys Phe Gln Arg |                                 |  |
| 85 90 95                                                        |                                 |  |



Ser Lys Arg Ser Val Ala Glu Glu Arg Ala Gly Arg Lys Leu Gly Gly  
100 105 110  
Leu Arg Val Val Asn Ser Tyr Trp Leu Asn Glu Asp Ser Thr Tyr Lys  
115 120 125  
Tyr Tyr Glu Ile Ile Leu Val Asp Pro Ala His Asn Ala Val Arg Asn  
130 135 140  
Asp Pro Arg Ile Asn Trp Ile Cys Asn Pro Val His Lys His Arg Glu  
145 150 155 160  
Leu Arg Gly Leu Thr Ser Glu Gly Lys Lys Asn Arg Gly Leu Arg Gly  
165 170 175  
Lys Gly His Asn Asn His Lys Asn Arg Pro Ser Arg Arg Ala Thr Trp  
180 185 190  
Lys Lys Asn Asn Ser Ile Ser Leu Arg Arg Tyr Arg  
195 200

(2) INFORMATION FOR SEQ ID NO:1917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1917:

Met Arg Phe Leu Gln Arg Val Arg Cys Trp Glu Tyr Arg Gln Pro  
1 5 10 15  
Ser Ile Val Arg Leu Val Arg Pro Thr Arg Pro Asp Lys Ala Arg Arg  
20 25 30  
Leu Gly Tyr Lys Ala Lys Gln Gly Phe Val Val Tyr Arg Val Arg Val  
35 40 45  
Arg Arg Gly Gly Arg Lys Arg Pro Val Pro Lys Gly Ile Val Tyr Gly  
50 55 60  
Lys Pro Thr Asn Gln Gly Val Thr Gln Leu Lys Phe Gln Arg Ser Lys  
65 70 75 80  
Arg Ser Val Ala Glu Glu Arg Ala Gly Arg Lys Leu Gly Gly Leu Arg  
85 90 95  
Val Val Asn Ser Tyr Trp Leu Asn Glu Asp Ser Thr Tyr Lys Tyr Tyr  
100 105 110  
Glu Ile Ile Leu Val Asp Pro Ala His Asn Ala Val Arg Asn Asp Pro  
115 120 125  
Arg Ile Asn Trp Ile Cys Asn Pro Val His Lys His Arg Glu Leu Arg  
130 135 140  
Gly Leu Thr Ser Glu Gly Lys Lys Asn Arg Gly Leu Arg Gly Lys Gly  
145 150 155 160  
His Asn Asn His Lys Asn Arg Pro Ser Arg Arg Ala Thr Trp Lys Lys  
165 170 175  
Asn Asn Ser Ile Ser Leu Arg Arg Tyr Arg  
180 185

(2) INFORMATION FOR SEQ ID NO:1918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1918:

Met Pro Ser Glu Met Ile Gln Gly Ser Thr Gly Ser Ala Thr Leu Cys  
1 5 10 15  
Thr Ser Thr Glu Asn Ser Glu Val Ser Pro Pro Lys Glu Arg Arg Ile  
20 25 30  
Val Val Phe Val Glu Arg Val Thr Thr Thr Arg Thr Asp Leu Pro  
35 40 45  
Ala Gly Gln Pro Gly Arg Arg Thr Thr Val Ser Leu Ser Val Val Thr  
50 55 60  
Gly Asp Gln Phe Tyr Val Leu Phe Phe Leu Glu Leu Val Tyr Leu Gln  
65 70 75 80  
Cys Gly Leu Cys Phe Gly Ile Leu Glu Leu His Trp Asp Gly Arg Leu  
85 90 95  
Ser His Ser Arg Val Cys Phe  
100

(2) INFORMATION FOR SEQ ID NO:1919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..651
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1919:

|             |             |            |             |             |            |     |
|-------------|-------------|------------|-------------|-------------|------------|-----|
| aaaagttccc  | ttcgttggtc  | atcggaatcc | ctagaacact  | cgatttcagc  | aaaatcaaat | 60  |
| cggtattcag  | gatacaaaagt | caatttggtc | gagaagaagt  | tgagcgttga  | agatgacgga | 120 |
| ggcgtatgata | agaaataaagc | caggaatggc | gagtgtagag  | gatatgccgc  | tgcttcagga | 180 |
| tggtccgccca | ccgggtgggt  | tcgcacccgt | ccgatatgcc  | cgccggatat  | ccaataccgg | 240 |
| toctagtgc   | atggccaagt  | tccttgcgct | ttctgggtgcc | tttcttggg   | gaatgtacca | 300 |
| ggtcggccag  | ggaaacaaaa  | tcgcgaGggc | attgaaggaa  | gagaataatg  | ctgctcgtag | 360 |
| aacaatactt  | cccattcttc  | aagcagaaga | agatgaaagg  | tttgtgtctg  | agtggaaaaa | 420 |
| gtatctggaa  | tatgaggctg  | atgtaatgaa | agatgttccg  | ggatggaaaag | ttggcgagaa | 480 |
| tgtgtacaat  | tctggtcgct  | ggatGcctcc | ggctactggg  | gaactccgct  | ctgatgtgtg | 540 |
| gtgatcttcc  | agtttctctc  | aaatgcata  | gatgatgat   | aatgatgttt  | cgctgaggat | 600 |
| tgatattgtc  | ttgttatatc  | ttttttctt  | cggttaataa  | gagaatgatt  | c          |     |

(2) INFORMATION FOR SEQ ID NO:1920:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1920:

Met Thr Glu Ala Met Ile Arg Asn Lys Pro Gly Met Ala Ser Val Lys  
1 5 10 15  
Asp Met Pro Leu Leu Gln Asp Gly Pro Pro Pro Gly Gly Phe Ala Pro  
20 25 30  
Val Arg Tyr Ala Arg Arg Ile Ser Asn Thr Gly Pro Ser Ala Met Ala  
35 40 45  
Met Phe Leu Ala Val Ser Gly Ala Phe Ala Trp Gly Met Tyr Gln Val  
50 55 60  
Gly Gln Gly Asn Lys Ile Arg Arg Ala Leu Lys Glu Glu Lys Tyr Ala  
65 70 75 80  
Ala Arg Arg Thr Ile Leu Pro Ile Leu Gln Ala Glu Glu Asp Glu Arg

|                                                                 |                                 |  |    |  |     |
|-----------------------------------------------------------------|---------------------------------|--|----|--|-----|
|                                                                 | 85                              |  | 90 |  | 95  |
| Phe Val Ser Glu Trp Lys Lys Tyr                                 | Leu Glu Tyr Glu Ala Asp Val Met |  |    |  |     |
| 100                                                             | 105                             |  |    |  | 110 |
| Lys Asp Val Pro Gly Trp Lys Val Gly Glu Asn Val Tyr Asn Ser Gly |                                 |  |    |  |     |
| 115                                                             | 120                             |  |    |  | 125 |
| Arg Trp Met Pro Pro Ala Thr Gly Glu Leu Arg Pro Asp Val Trp     |                                 |  |    |  |     |
| 130                                                             | 135                             |  |    |  | 140 |

(2) INFORMATION FOR SEQ ID NO:1921:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1571374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1921:

|                                                                 |     |  |    |  |     |
|-----------------------------------------------------------------|-----|--|----|--|-----|
| Met Ile Arg Asn Lys Pro Gly Met Ala Ser Val Lys Asp Met Pro Leu |     |  |    |  |     |
| 1                                                               | 5   |  | 10 |  | 15  |
| Leu Gln Asp Gly Pro Pro Pro Gly Gly Phe Ala Pro Val Arg Tyr Ala |     |  |    |  |     |
| 20                                                              | 25  |  |    |  | 30  |
| Arg Arg Ile Ser Asn Thr Gly Pro Ser Ala Met Ala Met Phe Leu Ala |     |  |    |  |     |
| 35                                                              | 40  |  |    |  | 45  |
| Val Ser Gly Ala Phe Ala Trp Gly Met Tyr Gln Val Gly Gln Gly Asn |     |  |    |  |     |
| 50                                                              | 55  |  | 60 |  |     |
| Lys Ile Arg Arg Ala Leu Lys Glu Glu Lys Tyr Ala Ala Arg Arg Thr |     |  |    |  |     |
| 65                                                              | 70  |  | 75 |  | 80  |
| Ile Leu Pro Ile Leu Gln Ala Glu Glu Asp Gly Arg Phe Val Ser Gly |     |  |    |  |     |
| 85                                                              | 90  |  |    |  | 95  |
| Trp Lys Lys Tyr Leu Glu Tyr Glu Ala Asp Val Met Lys Asp Val Pro |     |  |    |  |     |
| 100                                                             | 105 |  |    |  | 110 |
| Gly Trp Lys Val Gly Glu Asn Val Tyr Asn Ser Gly Arg Trp Met Pro |     |  |    |  |     |
| 115                                                             | 120 |  |    |  | 125 |
| Pro Ala Thr Gly Glu Leu Arg Pro Asp Val Trp                     |     |  |    |  |     |
| 130                                                             | 135 |  |    |  |     |

(2) INFORMATION FOR SEQ ID NO:1922:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1571375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1922:

|                                                                 |    |  |    |  |    |
|-----------------------------------------------------------------|----|--|----|--|----|
| Met Ala Ser Val Lys Asp Met Pro Leu Leu Gln Asp Gly Pro Pro Pro |    |  |    |  |    |
| 1                                                               | 5  |  | 10 |  | 15 |
| Gly Gly Phe Ala Pro Val Arg Tyr Ala Arg Arg Ile Ser Asn Thr Gly |    |  |    |  |    |
| 20                                                              | 25 |  |    |  | 30 |
| Pro Ser Ala Met Ala Met Phe Leu Ala Val Ser Gly Ala Phe Ala Trp |    |  |    |  |    |
| 35                                                              | 40 |  |    |  | 45 |
| Gly Met Tyr Gln Val Gly Gln Gly Asn Lys Ile Arg Arg Ala Leu Lys |    |  |    |  |    |
| 50                                                              | 55 |  | 60 |  |    |
| Glu Glu Lys Tyr Ala Ala Arg Arg Thr Ile Leu Pro Ile Leu Gln Ala |    |  |    |  |    |
| 65                                                              | 70 |  | 75 |  | 80 |
| Glu Glu Asp Glu Arg Phe Val Ser Glu Trp Lys Lys Tyr Leu Glu Tyr |    |  |    |  |    |
| 85                                                              | 90 |  |    |  | 95 |

Glu Ala Asp Val Met Lys Asp Val Pro Gly Trp Lys Val Gly Glu Asn  
100 105 110  
Val Tyr Asn Ser Gly Arg Trp Met Pro Pro Ala Thr Gly Glu Leu Arg  
115 120 125  
Pro Asp Val Trp  
130

(2) INFORMATION FOR SEQ ID NO:1923:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1755 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1755

(D) OTHER INFORMATION: / Ceres Seq. ID 1571376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1923:

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| acatctatct  | ctttctctct  | ctttccttgc  | aaattttcag | ctctcaaaaga | gttaagaggtt | 60   |
| agagagagag  | aggatgtgcca | ttagggaaaat | caaagatgta | gagagggggtg | aaatagtgaa  | 120  |
| taaggtagaa  | gatcttggga  | aaccattttt  | gactcatgaa | gatgatgaaa  | aaagagagtga | 180  |
| gaataaagaa  | tcaatattga  | tggtttctct  | cagtactttt | gttgctgtct  | gtggctcctt  | 240  |
| tgagttggcg  | tctgtgtgtg  | gatactcagc  | gcctactcag | tcatctataa  | gacaagatct  | 300  |
| caatctctcc  | cttgcagagt  | tctccatggt  | ttgatccatc | ttaactatcg  | gtgcaatgct  | 360  |
| tggtgctgtt  | atgagtggga  | aaatttcaga  | tttctccggc | cgaaaaaggg  | caatgaggac  | 420  |
| gtcagcttgc  | ttctgcatta  | caggttggct  | cgctgtcttc | ttcaccaagg  | gggcatgttt  | 480  |
| acttgatgta  | ggagagttct  | ttacaggata  | tggaaattga | gttttttctt  | atgtgggtccc | 540  |
| tggtgacatt  | gctgagatat  | ctcccaagaa  | tctccagagt | ggactcacaa  | cactgaacca  | 600  |
| actcatgatt  | gtgatccgct  | catcggtttc  | tttcttgatc | ggactctcca  | tttcttgtaa  | 660  |
| aactctgtcc  | ctaacocgtac | tgtctccctg  | catgtgtttg | ctctttggct  | tggtcttcac  | 720  |
| acccgaatct  | cctcgatggc  | tggcaaaaag  | aggccatgag | aaagagtttc  | gcgtagccct  | 780  |
| gcaaaagctg  | cgaggaaaaag | atgcagatat  | cacaaatgaa | gcagacggta  | ttcaactctc  | 840  |
| gattcaagct  | ctagagattc  | ttccaaaagc  | agaattccaa | gcaccttgtt  | ccaagaaata  | 900  |
| tggtcgatct  | gtcatcattg  | gtgtttccct  | gatggtatcc | caacagtttg  | ttggaatcaa  | 960  |
| tgggatcgga  | ttctacgcaa  | gtgaaacggt  | tgtaaaagcc | ggatttacct  | ctgggaaact  | 1020 |
| aggaacaatc  | gctatcgctt  | gttcaggtgc  | caataactgt | tcttggaaca  | atcttgatag  | 1080 |
| ataaatctgg  | acgaaggcca  | ctaattatga  | tttcagctgg | tggtatcttc  | ttgggatgca  | 1140 |
| tactcacagg  | cacatctttc  | ttactcaagg  | gacagagctt | gttgcttgaa  | tggtgctcct  | 1200 |
| ccttagccgt  | tggaggtgta  | cttatctatg  | tagctgcttt | ctccatcgga  | atgggacctg  | 1260 |
| ttccttgggt  | gataatgtct  | gagatatctc  | cgataaaact | aaaggggaac  | gcagggaagct | 1320 |
| tagtggtaact | agtgaatttg  | tctggtgctt  | gggctgtttc | ttacactttc  | aaacttccca  | 1380 |
| tgagctggag  | ctctccaggt  | acattctatt  | tgtactcgcc | ttttgcagct  | gcgcagataa  | 1440 |
| tatttctggc  | gaagatgggt  | ccagagacga  | aaggggaagc | actggaagag  | atccaaagctt | 1500 |
| gtattcgaa   | agaaacataa  | gaagaaagat  | acaatcaatg | ttatgggaat  | gttatcaaat  | 1560 |
| gaaaagactc  | gaactattcc  | cgttgggtgag | ctcaaatggt | agtagagtaa  | aaattatcgc  | 1620 |
| cgggagataa  | cgttgaaagt  | ccgatgatga  | ggcataaagg | ttttgcatga  | atgttatgag  | 1680 |
| aataggttta  | cttttatgta  | ttgttctcag  | ttttTaagtt | ttcatcaaat  | aggtttttga  | 1740 |
| wtggtaaaaa  | aaacc       |             |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1924:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..336

(D) OTHER INFORMATION: / Ceres Seq. ID 1571377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1924:

Met Ala Ile Arg Glu Ile Lys Asp Val Glu Arg Gly Glu Ile Val Asn

|                 |                 |                 |                 |
|-----------------|-----------------|-----------------|-----------------|
| 1               | 5               | 10              | 15              |
| Lys Val Glu Asp | Leu Gly Lys Pro | Phe Leu Thr His | Glu Asp Asp Glu |
| 20              | 25              | 30              | 35              |
| Lys Glu Ser Glu | Asn Asn Glu Ser | Tyr Leu Met Val | Leu Phe Ser Thr |
| 40              | 45              | 50              | 55              |
| Phe Val Ala Val | Cys Gly Ser Phe | Glu Phe Gly Ser | Cys Val Gly Tyr |
| 60              | 65              | 70              | 75              |
| Ser Ala Pro Thr | Gln Ser Ser Ile | Arg Gln Asp Leu | Asn Leu Ser Leu |
| 80              | 85              | 90              | 95              |
| Ala Glu Phe Ser | Met Phe Gly Ser | Ile Leu Thr Ile | Gly Ala Met Leu |
| 100             | 105             | 110             | 115             |
| Gly Ala Val Met | Ser Gly Lys Ile | Ser Asp Phe Ser | Gly Arg Lys Gly |
| 120             | 125             | 130             | 135             |
| Ala Met Arg Thr | Ser Ala Cys Phe | Cys Ile Thr Gly | Trp Leu Ala Val |
| 140             | 145             | 150             | 155             |
| Phe Phe Thr Lys | Gly Ala Leu Leu | Asp Val Gly Arg | Phe Phe Thr     |
| 160             | 165             | 170             | 175             |
| Gly Tyr Gly Ile | Gly Val Phe Ser | Tyr Val Val Pro | Val Tyr Ile Ala |
| 180             | 185             | 190             | 195             |
| Glu Ile Ser Pro | Lys Asn Leu Arg | Gly Gly Leu Thr | Thr Leu Asn Gln |
| 200             | 205             | 210             | 215             |
| Leu Met Ile Val | Ile Gly Ser Ser | Val Ser Phe Leu | Ile Gly Ser Leu |
| 220             | 225             | 230             | 235             |
| Ile Ser Trp Lys | Thr Leu Ala Leu | Thr Val Leu Ala | Pro Cys Ile Val |
| 240             | 245             | 250             | 255             |
| Leu Leu Phe Gly | Leu Cys Phe Ile | Pro Glu Ser Pro | Arg Trp Leu Ala |
| 260             | 265             | 270             | 275             |
| Lys Ala Gly His | Glu Lys Glu Phe | Arg Val Ala Leu | Gln Lys Leu Arg |
| 280             | 285             | 290             | 295             |
| Gly Lys Asp Ala | Asp Ile Thr Asn | Glu Ala Asp Gly | Ile Gln Val Ser |
| 300             | 305             | 310             | 315             |
| Ile Gln Ala Leu | Glu Ile Leu Pro | Lys Ala Arg Ile | Gln Asp Leu Val |
| 320             | 325             | 330             | 335             |
| Ser Lys Lys Tyr | Gly Arg Ser Val | Ile Ile Gly Val | Ser Leu Met Val |
| 340             | 345             | 350             | 355             |
| Phe Gln Gln Phe | Val Gly Ile Asn | Gly Ile Gly Phe | Tyr Ala Ser Glu |
| 360             | 365             | 370             | 375             |
| Thr Phe Val Lys | Ala Gly Phe Thr | Ser Gly Lys Leu | Gly Thr Ile Ala |
| 380             | 385             | 390             | 395             |
| Ile Ala Cys Ser | Gly Ala Asn Asn | Cys Ser Trp Asn | Asn Leu Asp Arg |

(2) INFORMATION FOR SEQ ID NO:1925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..294

(D) OTHER INFORMATION: / Ceres Seq. ID 1571378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1925:

|                 |                 |                 |                     |
|-----------------|-----------------|-----------------|---------------------|
| Met Val Leu Phe | Ser Thr Phe Val | Ala Val Cys     | Gly Ser Phe Glu Phe |
| 1               | 5               | 10              | 15                  |
| Gly Ser Cys Val | Gly Tyr Ser Ala | Pro Thr Gln Ser | Ser Ile Arg Gln     |
| 20              | 25              | 30              | 35                  |
| Asp Leu Asn Leu | Ser Leu Ala Glu | Phe Ser Met Phe | Gly Ser Ile Leu     |
| 35              | 40              | 45              |                     |

Thr Ile Gly Ala Met Leu Gly Ala Val Met Ser Gly Lys Ile Ser Asp  
50 55 60  
Phe Ser Gly Arg Lys Gly Ala Met Arg Thr Ser Ala Cys Phe Cys Ile  
65 70 75 80  
Thr Gly Trp Leu Ala Val Phe Phe Thr Lys Gly Ala Leu Leu Asp  
85 90 95  
Val Gly Arg Phe Phe Thr Gly Tyr Gly Ile Gly Val Phe Ser Tyr Val  
100 105 110  
Val Pro Val Tyr Ile Ala Glu Ile Ser Pro Lys Asn Leu Arg Gly Gly  
115 120 125  
Leu Thr Thr Leu Asn Gln Leu Met Ile Val Ile Gly Ser Ser Val Ser  
130 135 140  
Phe Leu Ile Gly Ser Leu Ile Ser Trp Lys Thr Leu Ala Leu Thr Val  
145 150 155 160  
Leu Ala Pro Cys Ile Val Leu Leu Phe Gly Leu Cys Phe Ile Pro Glu  
165 170 175  
Ser Pro Arg Trp Trp Leu Ala Lys Ala Gly His Glu Lys Glu Phe Arg Val  
180 185 190  
Ala Leu Gln Lys Leu Arg Gly Lys Asp Ala Asp Ile Thr Asn Glu Ala  
195 200 205  
Asp Gly Ile Gln Val Ser Ile Gln Ala Leu Glu Ile Leu Pro Lys Ala  
210 215 220  
Arg Ile Gln Asp Leu Val Ser Lys Lys Tyr Gly Arg Ser Val Ile Ile  
225 230 235 240  
Gly Val Ser Leu Met Val Phe Gln Gln Phe Val Gly Ile Asn Gly Ile  
245 250 255  
Gly Phe Tyr Ala Ser Glu Thr Phe Val Lys Ala Gly Phe Thr Ser Gly  
260 265 270  
Lys Leu Gly Thr Ile Ala Ile Ala Cys Ser Gly Ala Asn Asn Cys Ser  
275 280 285  
Trp Asn Asn Leu Asp Arg  
290

(2) INFORMATION FOR SEQ ID NO:1926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..252

(D) OTHER INFORMATION: / Ceres Seq. ID 1571379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1926:

Met Phe Gly Ser Ile Leu Thr Ile Gly Ala Met Leu Gly Ala Val Met  
1 5 10 15  
Ser Gly Lys Ile Ser Asp Phe Ser Gly Arg Lys Gly Ala Met Arg Thr  
20 25 30  
Ser Ala Cys Phe Cys Ile Thr Gly Trp Leu Ala Val Phe Phe Thr Lys  
35 40 45  
Gly Ala Leu Leu Leu Asp Val Gly Arg Phe Phe Thr Gly Tyr Gly Ile  
50 55 60  
Gly Val Phe Ser Tyr Val Val Pro Val Tyr Ile Ala Glu Ile Ser Pro  
65 70 75 80  
Lys Asn Leu Arg Gly Gly Leu Thr Thr Leu Asn Gln Leu Met Ile Val  
85 90 95  
Ile Gly Ser Ser Val Ser Phe Leu Ile Gly Ser Leu Ile Ser Trp Lys  
100 105 110  
Thr Leu Ala Leu Thr Val Leu Ala Pro Cys Ile Val Leu Leu Phe Gly  
115 120 125  
Leu Cys Phe Ile Pro Glu Ser Pro Arg Trp Leu Ala Lys Ala Gly His

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 130                                                             | 135 | 140 |
| Glu Lys Glu Phe Arg Val Ala Leu Gln Lys Leu Arg Gly Lys Asp Ala |     |     |
| 145                                                             | 150 | 155 |
| Asp Ile Thr Asn Glu Ala Asp Gly Ile Gln Val Ser Ile Gln Ala Leu |     | 160 |
|                                                                 | 165 | 170 |
| Glu Ile Leu Pro Lys Ala Arg Ile Gln Asp Leu Val Ser Lys Lys Tyr |     | 175 |
|                                                                 | 180 | 185 |
| Gly Arg Ser Val Ile Ile Gly Val Ser Leu Met Val Phe Gln Gln Phe |     | 190 |
|                                                                 | 195 | 200 |
| Val Gly Ile Asn Gly Ile Gly Phe Tyr Ala Ser Glu Thr Phe Val Lys |     | 205 |
|                                                                 | 210 | 215 |
| Ala Gly Phe Thr Ser Gly Lys Leu Gly Thr Ile Ala Ile Ala Cys Ser |     | 220 |
| 225                                                             | 230 | 235 |
| Gly Ala Asn Asn Cys Ser Trp Asn Asn Leu Asp Arg                 |     | 240 |
|                                                                 | 245 | 250 |

(2) INFORMATION FOR SEQ ID NO:1927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..580
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1927:

|            |             |            |            |             |             |     |
|------------|-------------|------------|------------|-------------|-------------|-----|
| ctgggtggtc | ttaactctctt | tatccgcttg | actaaagaaa | attggcgctgc | agtgatagag  | 60  |
| acgaagaaga | agaagaaaaat | gccgtgcctc | aacctctcca | ccaacgttaa  | ccttgacggc  | 120 |
| gtcgatacat | cttcacattct | ctcggaagct | tctccaccg  | tcgcgaaaaat | catcgccaag  | 180 |
| cctgagaact | atgtgatgat  | tgtcttgaaa | ggctcagtcg | ctatgtcatt  | tggcgggacc  | 240 |
| gaggatcctg | cagcttatgtg | tgaattagtt | tctatcggtg | gccttaatgc  | ggatgtgaac  | 300 |
| aagaagctaa | gcgctgctgt  | tccgcctatt | cttgagacta | agctatcggt  | gcccaagtct  | 360 |
| cgattctctc | tcaagtttta  | tgacaccaag | ggatccttct | ttggttgga   | cgggcggaact | 420 |
| ctttaattcc | gtggtagggtg | attagtgtga | ttgtcttaaa | atgtatgatc  | tactctcacc  | 480 |
| gatcaagtaa | ctttgaacta  | cttcgtattg | taaacataac | taagggttga  | tggagttgca  | 540 |
| taaagaataa | acattttatgc | tatatatgat | gtcacaactc |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1928:

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Leu Gly Gly Leu Thr Leu Phe Ile Arg Leu Thr Lys Glu Asn Trp Arg |    |    |
| 1                                                               | 5  | 10 |
| Arg Val Ile Glu Thr Lys Lys Lys Lys Lys Met Pro Cys Leu Asn Leu |    | 15 |
|                                                                 | 20 | 25 |
| Ser Thr Asn Val Asn Leu Asp Gly Val Asp Thr Ser Ser Ile Leu Ser |    | 30 |
|                                                                 | 35 | 40 |
| Glu Ala Ser Ser Thr Val Ala Lys Ile Ile Gly Lys Pro Glu Asn Tyr |    | 45 |
|                                                                 | 50 | 55 |
| Val Met Ile Val Leu Lys Gly Ser Val Pro Met Ser Phe Gly Gly Thr |    | 60 |
| 65                                                              | 70 | 75 |
| Glu Asp Pro Ala Ala Tyr Gly Glu Leu Val Ser Ile Gly Gly Leu Asn |    | 80 |
|                                                                 | 85 | 90 |
|                                                                 |    | 95 |

Ala Asp Val Asn Lys Lys Leu Ser Ala Ala Val Ser Ala Ile Leu Glu  
100 105 110  
Thr Lys Leu Ser Val Pro Lys Ser Arg Phe Phe Leu Lys Phe Tyr Asp  
115 120 125  
Thr Lys Gly Ser Phe Phe Gly Trp Asn Gly Ala Thr Leu  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1571389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1929:

Met Pro Cys Leu Asn Leu Ser Thr Asn Val Asn Leu Asp Gly Val Asp  
1 5 10 15  
Thr Ser Ser Ile Leu Ser Glu Ala Ser Ser Thr Val Ala Lys Ile Ile  
20 25 30  
Gly Lys Pro Glu Asn Tyr Val Met Ile Val Leu Lys Gly Ser Val Pro  
35 40 45  
Met Ser Phe Gly Gly Thr Glu Asp Pro Ala Ala Tyr Gly Glu Leu Val  
50 55 60  
Ser Ile Gly Gly Leu Asn Ala Asp Val Asn Lys Lys Leu Ser Ala Ala  
65 70 75 80  
Val Ser Ala Ile Leu Glu Thr Lys Leu Ser Val Pro Lys Ser Arg Phe  
85 90 95  
Phe Leu Lys Phe Tyr Asp Thr Lys Gly Ser Phe Phe Gly Trp Asn Gly  
100 105 110  
Ala Thr Leu  
115

(2) INFORMATION FOR SEQ ID NO:1930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1571390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1930:

Met Ile Val Leu Lys Gly Ser Val Pro Met Ser Phe Gly Gly Thr Glu  
1 5 10 15  
Asp Pro Ala Ala Tyr Gly Glu Leu Val Ser Ile Gly Gly Leu Asn Ala  
20 25 30  
Asp Val Asn Lys Lys Leu Ser Ala Ala Val Ser Ala Ile Leu Glu Thr  
35 40 45  
Lys Leu Ser Val Pro Lys Ser Arg Phe Phe Leu Lys Phe Tyr Asp Thr  
50 55 60  
Lys Gly Ser Phe Phe Gly Trp Asn Gly Ala Thr Leu  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single



(A) NAME/KEY: -  
(B) LOCATION: 1..1332  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571391

|             |            |             |             |             |             |      |
|-------------|------------|-------------|-------------|-------------|-------------|------|
| acgacgtttt  | gtttctctct | tctctattaa  | tactatagtt  | ttctctcaac  | tctctgatta  | 60   |
| gctcctaatt  | actcaaacgg | ttgacatttt  | ttttctgata  | aacaatacat  | ggcaagggtca | 120  |
| ctctgttgat  | aggaagcaag | ggggcctgga  | catctgaaga  | ggcaaggaag  |             | 180  |
| ctctgttgact | atatccagaa | actctggttat | ggtaactgtga | ccattctccc  | caaaaattgcc | 240  |
| gtgttgctgaa | gtatggcgaa | aagtgtgtagg | ttaaggtgga  | ctaattctct  | ccgacagagt  | 300  |
| ataagcgaga  | gaaggtttct | ttttgaggaa  | gaagaacaaca | ttatctctg   | tcattgcttc  | 360  |
| tttagaaca   | agtggtctgc | gtgtcgccgc  | cggttaccag  | gaagaacaga  | tatgagatct  | 420  |
| aagaactttt  | ggaacactca | tataaagaag  | aagctactta  | gaatggggat  | tgatccaagt  | 480  |
| actcacagtc  | cacgactoga | tctctctctg  | atctctacca  | tcttgagctt  | atctctatac  | 540  |
| atttcatctt  | cacatcacat | gaacatgtca  | agactcatga  | tggtactcaa  | tcgtcgtcat  | 600  |
| ccacaggcaac | atccattggt | tgaaccggag  | atactcaagc  | tcgtcactct  | tctctctctt  | 660  |
| caaaattcaa  | accaaGaacc | tttgtgttga  | tcatgactcy  | agaaactcaag | ataagcaaac  | 720  |
| agtttatagc  | caaacccgag | taaacccaata | ccaaaccgac  | caatattctc  | agaaacagct  | 780  |
| ctctcaagaa  | ctccaacttt | accatgcacc  | attcccacat  | gaagctcatc  | agtttaacaa  | 840  |
| catggatcat  | cacttcaatg | gtttttgaa   | acaaaattct  | gtttcaactt  | ctatcactgc  | 900  |
| agtcacaagt  | tgctataatc | cgctactcca  | cgattattca  | agttcaaaat  | ttgtctttga  | 960  |
| tctcttctat  | tcggatcaga | gcttcaactt  | cgcaaattcg  | gtcttaaaac  | cgccatctct  | 1020 |
| gagccgcgag  | cgcagctacg | taaacctcgag | ttacataaat  | gagatcagtt  | gcagcactga  | 1080 |
| ggatgaataa  | gaagactatt | cgagtaattc  | catgaagttt  | gatattcccg  | atttcttga   | 1140 |
| cgttaaaggt  | ttatttatat | aattccaaga  | acaaaataat  | aactgagctg  | ggatcactgt  | 1200 |
| ttctttttat  | ttctttgtgt | ttctttaaga  | tttttttttt  | ttgttttcog  | atttgtttac  | 1260 |
| tttgaataa   | ctgttttctg | tttgttgtta  | atttgttata  | tttctctaga  | tctttatagct | 1320 |
| aatcaatttt  | tt         |             |             |             |             |      |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Arg | Ser | Pro | Cys | Cys | Glu | Lys | Asn | Gly | Leu | Lys | Lys | Gly | Pro |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Trp | Thr | Ser | Glu | Glu | Asp | Gln | Lys | Leu | Val | Asp | Tyr | Ile | Gln | Lys | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Tyr | Gly | Asn | Trp | Arg | Thr | Leu | Pro | Lys | Asn | Ala | Gly | Leu | Gln | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Gly | Lys | Ser | Cys | Arg | Leu | Arg | Trp | Thr | Asn | Tyr | Leu | Arg | Pro | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Lys | Arg | Gly | Arg | Phe | Ser | Phe | Glu | Glu | Glu | Glu | Thr | Ile | Ile | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |
| Leu | His | Ser | Phe | Leu | Gly | Asn | Lys | Trp | Ser | Ala | Ile | Ala | Ala | Arg | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Gly | Arg | Thr | Asp | Asn | Glu | Ile | Lys | Asn | Phe | Trp | Asn | Thr | His | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Lys | Lys | Leu | Leu | Arg | Met | Gly | Ile | Asp | Pro | Val | Thr | His | Ser | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Leu | Asp | Leu | Leu | Asp | Ile | Ser | Ser | Ile | Leu | Ala | Ser | Ser | Leu | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Asn | Ser | Ser | Ser | His | His | Met | Asn | Met | Ser | Arg | Leu | Met | Met | Asp | Thr |

(2) INFORMATION FOR SEQ ID NO:1933:

(A) LENGTH: 119 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

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(ix) FEATURE:
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- (A) NAME/KEY: peptide  
(B) LOCATION: 1..119  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571393

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..106  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571394

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | His | His | Phe | Asn | Gly | Phe | Gly | Glu | Gln | Asn | Leu | Val | Ser | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Thr | Thr | Ser | Val | Gln | Asp | Cys | Tyr | Asn | Pro | Ser | Phe | Asn | Asp | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ser | Ser | Asn | Phe | Val | Leu | Asp | Pro | Ser | Tyr | Ser | Asp | Gln | Ser | Phe |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Phe | Ala | Asn | Ser | Val | Leu | Asn | Thr | Pro | Ser | Ser | Ser | Pro | Ser | Pro |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Thr | Leu | Asn | Ser | Ser | Tyr | Ile | Asn | Ser | Ser | Cys | Ser | Thr | Glu |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Glu | Ile | Glu | Ser | Tyr | Cys | Ser | Asn | Leu | Met | Lys | Phe | Asp | Ile | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Phe | Leu | Asp | Val | Asn | Gly | Phe | Ile | Ile |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1461
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1935:

|             |             |            |            |            |            |      |
|-------------|-------------|------------|------------|------------|------------|------|
| actcaactct  | ctttcgaaac  | tcaatcctta | tataacacat | cccatGttaa | gcctataagc | 60   |
| tacaacatc   | agctctctca  | caaaaataaa | atggaggga  | gccagtgac  | cagtgctagg | 120  |
| ctctctctgg  | tgggtgcctgc | tctctgtgga | ggtgagaa   | agccacgaca | gctcacaccc | 180  |
| atggagctag  | ccatgaagct  | ccactacgtc | cgagccgtct | acttcttcaa | gggtgcacgt | 240  |
| gacttcaact  | tcgcccagct  | gaagaacacc | atgtttactc | tacagtctct | actccaatct | 300  |
| tatcaccaac  | tctcaggtcg  | gatccggatg | tccgacaacg | acaacgacac | ttcagctgca | 360  |
| gccataacct  | caactcgtct  | caacgacagt | ggcatacgcg | tggtcgaggc | caacgtcgaa | 420  |
| gagttccacg  | tggagaaagt  | gctcaggttg | gacgaccgtt | ccattgacca | ccgatttctt | 480  |
| gtctacgac   | acgttctctg  | tcttgatctt | acottctcgc | cactcgtttt | ctccagata  | 540  |
| actcagttta  | aatgtgtgtg  | gctctgtatt | gggttgagtt | gggcccatat | tcttggagac | 600  |
| gtgttttcag  | catcaacgtt  | catgaaaaa  | cttggacagc | tggtagtcgg | tcatgcccca | 660  |
| acaaaacccg  | tttaccgcga  | aacccccgaa | ctaacctctc | atgctcgtta | tgatggtgaa | 720  |
| gctattttcca | tfgaaaagat  | agattctggt | ggcgagtatt | ggttacttac | caataaatgc | 780  |
| aagatggggg  | gacacatttt  | taatttttag | ctcaaccaca | ttgatagctt | gatggccaa  | 840  |
| tacacccacg  | gagaccaacc  | ttctctggag | gttgatattt | tgatgacatt | gatatggaag | 900  |
| tcgctactga  | atattccgcg  | cgaaacaaac | acgaattgta | taacaatttg | tgaacgtaaa | 960  |
| aagttttcaa  | ctgtttggaa  | cgaggacttg | gtaataacgc | tagtggaata | gaatgacgaa | 1020 |
| atggtttggg  | tactcgaact  | agctgcactg | attgctggtg | aaaaaagaga | agaaaacggt | 1080 |
| gcgatcaaga  | ggatgataga  | acaagataaa | ggctcttcgg | attttttca  | gtacggtgta | 1140 |
| aatttaacgt  | ttgtgaatct  | tgatgatatg | aatcttgatg | caacggaggg | caacggaggg | 1200 |
| aagccggatt  | tcgtaaaact  | cacgattcat | gggttcggag | acaagagtgt | tgttttggtt | 1260 |
| tttcccaacg  | aaaactttgc  | aaggattgta | agtgtagtga | tgccctga   | agaccttgca | 1320 |
| aaactcaagg  | aggaggtgac  | taatatgatt | atataacttt | gtatctctct | cttgttgtaa | 1380 |
| tacataaatg  | ctgtttttta  | ctctttgtaa | tttcattatc | gaattgttgg | gaagcctatc | 1440 |
| aataaattgt  | ttgaactggt  | t          |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:1936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..451
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1936:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Gln | Leu | Ser | Phe | Glu | Thr | Gln | Ser | Leu | Tyr | Asn | Thr | Ser | His | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Lys | Pro | Ile | Ser | Tyr | Thr | Tyr | Gln | Leu | Ser | His | Lys | Asn | Lys | Met | Glu |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ser | Pro | Val | Thr | Ser | Val | Arg | Leu | Ser | Ser | Val | Pro | Ala | Ser |     |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Val | Val | Gly | Glu | Asn | Lys | Pro | Arg | Gln | Leu | Thr | Pro | Met | Asp | Leu | Ala |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Met | Lys | Leu | His | Tyr | Val | Arg | Ala | Val | Tyr | Phe | Phe | Lys | Gly | Ala | Arg |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     | 80  |     |
| Asp | Phe | Thr | Val | Thr | Ala | Asp | Val | Lys | Asn | Thr | Met | Phe | Thr | Leu | Gln |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |

Leu Leu Gln Ser Tyr His His Val Ser Gly Arg Ile Arg Met Ser Asp  
100 105 110  
Asn Asp Asn Asp Thr Ser Ala Ala Ala Ile Pro Tyr Ile Arg Cys Asn  
115 120 125  
Asp Ser Gly Ile Arg Val Val Glu Ala Asn Val Glu Phe Thr Val  
130 135 140  
Glu Lys Trp Leu Glu Leu Asp Asp Arg Ser Ile Asp His Arg Phe Leu  
145 150 155 160  
Val Tyr Asp His Val Leu Gly Pro Asp Leu Thr Phe Ser Pro Leu Val  
165 170 175  
Phe Leu Gln Ile Thr Gln Phe Lys Cys Gly Gly Leu Cys Ile Gly Leu  
180 185 190  
Ser Trp Ala His Ile Leu Gly Asp Val Phe Ser Ala Ser Thr Phe Met  
195 200 205  
Lys Thr Leu Gly Gln Leu Val Ser Gly His Ala Pro Thr Lys Pro Val  
210 215 220  
Tyr Pro Lys Thr Pro Glu Leu Thr Ser His Ala Arg Asn Asp Gly Glu  
225 230 235 240  
Ala Ile Ser Ile Glu Lys Ile Asp Ser Val Gly Glu Tyr Trp Leu Leu  
245 250 255  
Thr Asn Lys Cys Lys Met Gly Arg His Ile Phe Asn Phe Ser Leu Asn  
260 265 270  
His Ile Asp Ser Leu Met Ala Lys Tyr Thr Thr Arg Asp Gln Pro Phe  
275 280 285  
Ser Glu Val Asp Ile Leu Tyr Ala Leu Ile Trp Lys Ser Leu Leu Asn  
290 295 300  
Ile Arg Gly Glu Thr Asn Thr Asn Val Ile Thr Ile Cys Asp Arg Lys  
305 310 315 320  
Lys Ser Ser Thr Cys Trp Asn Glu Asp Leu Val Ile Ser Val Val Glu  
325 330 335  
Lys Asn Asp Glu Met Val Gly Ile Ser Glu Leu Ala Ala Leu Ile Ala  
340 345 350  
Gly Glu Lys Arg Glu Glu Asn Gly Ala Ile Lys Arg Met Ile Glu Gln  
355 360 365  
Asp Lys Gly Ser Ser Asp Phe Phe Thr Tyr Gly Ala Asn Leu Thr Phe  
370 375 380  
Val Asn Leu Asp Glu Ile Asp Met Tyr Glu Leu Glu Ile Asn Gly Gly  
385 390 395 400  
Lys Pro Asp Phe Val Asn Tyr Thr Ile His Gly Val Gly Asp Lys Gly  
405 410 415  
Val Val Leu Val Phe Pro Lys Gln Asn Phe Ala Arg Ile Val Ser Val  
420 425 430  
Val Met Pro Glu Glu Asp Leu Ala Lys Leu Lys Glu Glu Val Thr Asn  
435 440 445  
Met Ile Ile  
450

(2) INFORMATION FOR SEQ ID NO:1937:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 421 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..421

(D) OTHER INFORMATION: / Ceres Seq. ID 1571397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1937:

Met Glu Gly Ser Pro Val Thr Ser Val Arg Leu Ser Ser Val Val Pro  
1 5 10 15  
Ala Ser Val Val Gly Glu Asn Lys Pro Arg Gln Leu Thr Pro Met Asp

(B) LOCATION: 1..391

(D) OTHER INFORMATION: / Ceres Seq. ID 1571398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1938:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Leu | Ala | Met | Lys | Leu | His | Tyr | Val | Arg | Ala | Val | Tyr | Phe | Phe |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Lys | Gly | Ala | Arg | Asp | Phe | Thr | Val | Ala | Asp | Val | Lys | Asn | Thr | Met | Phe |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Thr | Leu | Gln | Ser | Leu | Leu | Gln | Ser | Tyr | His | His | Val | Ser | Gly | Arg | Ile |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Arg | Met | Ser | Asp | Asn | Asp | Asn | Asp | Thr | Ser | Ala | Ala | Ala | Ile | Pro | Tyr |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Ile | Arg | Cys | Asn | Asp | Ser | Gly | Ile | Arg | Val | Val | Glu | Ala | Asn | Val | Glu |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Glu | Phe | Thr | Val | Glu | Lys | Trp | Leu | Glu | Leu | Asp | Asp | Arg | Ser | Ile | Asp |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| His | Arg | Phe | Leu | Val | Tyr | Asp | His | Val | Leu | Gly | Pro | Asp | Leu | Thr | Phe |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Ser | Pro | Leu | Val | Phe | Leu | Gln | Ile | Thr | Gln | Phe | Lys | Cys | Gly | Gly | Leu |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Cys | Ile | Gly | Leu | Ser | Trp | Ala | His | Ile | Leu | Gly | Asp | Val | Phe | Ser | Ala |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |
| Ser | Thr | Phe | Met | Lys | Thr | Leu | Gly | Gln | Leu | Val | Ser | Gly | His | Ala | Pro |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |     |
| Thr | Lys | Pro | Val | Tyr | Pro | Lys | Thr | Pro | Glu | Leu | Thr | Ser | His | Ala | Arg |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Asn | Asp | Gly | Glu | Ala | Ile | Ser | Ile | Glu | Lys | Ile | Asp | Ser | Val | Gly | Glu |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Tyr | Trp | Leu | Leu | Thr | Asn | Lys | Cys | Lys | Met | Gly | Arg | His | Ile | Phe | Asn |
|     |     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |
| Phe | Ser | Leu | Asn | His | Ile | Asp | Ser | Leu | Met | Ala | Lys | Tyr | Thr | Thr | Arg |
|     |     |     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |
| Asp | Gln | Pro | Phe | Ser | Glu | Val | Asp | Ile | Leu | Tyr | Ala | Leu | Ile | Trp | Lys |
| 225 |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |     |
| Ser | Leu | Leu | Asn | Ile | Arg | Gly | Glu | Thr | Asn | Thr | Asn | Val | Ile | Thr | Ile |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Cys | Asp | Arg | Lys | Lys | Ser | Ser | Thr | Cys | Trp | Asn | Glu | Asp | Leu | Val | Ile |
|     |     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Ser | Val | Val | Glu | Lys | Asn | Asp | Glu | Met | Val | Gly | Ile | Ser | Glu | Leu | Ala |
|     |     |     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |
| Ala | Leu | Ile | Ala | Gly | Glu | Lys | Arg | Glu | Glu | Asn | Gly | Ala | Ile | Lys | Arg |
|     |     |     |     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |
| Met | Ile | Glu | Gln | Asp | Lys | Gly | Ser | Ser | Asp | Phe | Phe | Thr | Tyr | Gly | Ala |
| 305 |     |     |     | 310 |     |     |     | 315 |     |     |     |     |     | 320 |     |
| Asn | Leu | Thr | Phe | Val | Asn | Leu | Asp | Glu | Ile | Asp | Met | Tyr | Glu | Leu | Glu |
|     |     |     |     | 325 |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Ile | Asn | Gly | Gly | Lys | Pro | Asp | Phe | Val | Asn | Tyr | Thr | Ile | His | Gly | Val |
|     |     |     |     | 340 |     |     |     | 345 |     |     |     |     |     | 350 |     |
| Gly | Asp | Lys | Gly | Val | Val | Leu | Val | Phe | Pro | Lys | Gln | Asn | Phe | Ala | Arg |
|     |     |     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |
| Ile | Val | Ser | Val | Val | Met | Pro | Glu | Glu | Asp | Leu | Ala | Lys | Leu | Lys | Glu |
|     |     |     |     | 370 |     |     |     | 375 |     |     |     |     |     | 380 |     |
| Glu | Val | Thr | Asn | Met | Ile | Ile |     |     |     |     |     |     |     |     |     |
| 385 |     |     |     | 390 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1939:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1193 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1193

(D) OTHER INFORMATION: / Ceres Seq. ID 1571418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1939:

|             |             |             |             |            |             |      |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| ctcttttagca | aaaaatctca  | gaactcaRaa  | aaaaaaCaSR  | tcacaaccca | aagacaatgS  | 60   |
| gagatgagtt  | tgcgtctcgc  | ttcatottca  | acctcaaac   | caattgtgtc | actaaacct   | 120  |
| ggaaaaaac   | ttaatttccc  | aatccgaaac  | catagaatcc  | ctaaaaatc  | gaaaccttt   | 180  |
| tgcgttaggt  | cttcaatgag  | cttggtctaaa | ccaccagac   | aaactctatc | tagtaactgg  | 240  |
| gatgtatcta  | gtctctccat  | tgattccggt  | gtcactctc   | cttcaagact | cccaagtttc  | 300  |
| gaagaactcg  | ataccaccaa  | catgttgctc  | cgtcaaaagaa | tcgtctttt  | gggtttctcag | 360  |
| gttgatgata  | tgacggcgga  | tttgggtata  | agtcaagctat | tgttactaga | tgcgtaggac  | 420  |
| tcagaaagag  | acattacgct  | ttttatcaat  | tcaccgggtg  | gatctattac | tgctgggagt  | 480  |
| ggaatatatg  | atgcaatgaa  | acaatgtaag  | gcggatgtat  | ctaactgttg | cttaggggta  | 540  |
| gctgcattcta | tggtgtcggt  | tcttcttgct  | tctggttcaa  | aagggaacg  | gtattgtgat  | 600  |
| ctcaactcta  | aagttaigtat | ccatcagcca  | cttggtactg  | ctggaggcaa | agcaacggaa  | 660  |
| atgagcatac  | gtataagaga  | aatgatgtac  | cacaagatta  | aacttaacaa | aatcttctct  | 720  |
| agaatcactg  | ggagacgtga  | atcagagatc  | gaaagtga    | cagaccgtga | taacttcttg  | 780  |
| aatccatggg  | aggcgaaaga  | atatggttgg  | atcgacgctg  | taatcgatga | tgggaaacgg  | 840  |
| ggactaatcg  | ctccaattgg  | agatggta    | cctctctcta  | aaaccaaagt | ctggggtctt  | 900  |
| tggaagagtc  | aaggaaccaa  | gaaagacaa   | actaacttgc  | catctgagcg | ctccatgaca  | 960  |
| cagaaatggt  | atgccgccat  | tgaatagaac  | tggtgttgca  | gcgtttacgc | cttttatatg  | 1020 |
| tattctgggt  | ggtacctgtg  | accatataac  | gttgcaattc  | ctgtgtttgt | accatttctc  | 1080 |
| tgatagattt  | ttggaataat  | ttgaaggcaa  | aagatagatt  | atttgtgtga | gaagaagcta  | 1140 |
| caaaatttaa  | tgattaaatt  | gaatcatacc  | gccatgagaa  | gctttgtgtt | ttc         |      |

(2) INFORMATION FOR SEQ ID NO:1940:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..328

(D) OTHER INFORMATION: / Ceres Seq. ID 1571419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1940:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Phe | Ser | Lys | Lys | Ser | Gln | Asn | Ser | Xaa | Lys | Lys | Xaa | Xaa | Gln | His |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Arg | Gln | Xaa | Glu | Met | Ser | Leu | Arg | Leu | Ala | Ser | Ser | Ser | Thr | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Pro | Ile | Cys | Leu | Leu | Asn | Pro | Gly | Lys | Asn | Leu | Asn | Phe | Pro | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Asn | His | Arg | Ile | Pro | Lys | Thr | Ser | Lys | Pro | Phe | Cys | Val | Arg | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Met | Ser | Leu | Ser | Lys | Pro | Pro | Arg | Gln | Thr | Leu | Ser | Ser | Asn | Trp |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Val | Ser | Ser | Phe | Ser | Ile | Asp | Ser | Val | Ala | Gln | Ser | Pro | Ser | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Pro | Ser | Phe | Glu | Glu | Leu | Asp | Thr | Thr | Asn | Met | Leu | Leu | Arg | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Ile | Val | Phe | Leu | Gly | Ser | Gln | Val | Asp | Asp | Met | Thr | Ala | Asp | Leu |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Ile | Ser | Gln | Leu | Leu | Leu | Leu | Asp | Ala | Glu | Asp | Ser | Glu | Arg | Asp |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Ile | Thr | Leu | Phe | Ile | Asn | Ser | Pro | Gly | Ser | Ile | Thr | Ala | Gly | Met |     |
|     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Gly | Ile | Tyr | Asp | Ala | Met | Lys | Gln | Cys | Lys | Ala | Asp | Val | Ser | Thr | Val |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Cys | Leu | Gly | Leu | Ala | Ala | Ser | Met | Gly | Ala | Phe | Leu | Leu | Ala | Ser | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Lys | Gly | Lys | Arg | Tyr | Cys | Met | Pro | Asn | Ser | Lys | Val | Met | Ile | His |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gln | Pro | Leu | Gly | Thr | Ala | Gly | Gly | Lys | Ala | Thr | Glu | Met | Ser | Ile | Arg |  |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Ile | Arg | Glu | Met | Met | Tyr | His | Lys | Ile | Lys | Leu | Asn | Lys | Ile | Phe | Ser |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Arg | Ile | Thr | Gly | Lys | Pro | Glu | Ser | Glu | Ile | Glu | Ser | Asp | Thr | Asp | Arg |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Asp | Asn | Phe | Leu | Asn | Pro | Trp | Glu | Ala | Lys | Glu | Tyr | Gly | Leu | Ile | Asp |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Ala | Val | Ile | Asp | Asp | Gly | Lys | Pro | Gly | Leu | Ile | Ala | Pro | Ile | Gly | Asp |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Gly | Thr | Pro | Pro | Pro | Lys | Thr | Lys | Val | Trp | Asp | Leu | Trp | Lys | Val | Glu |  |
| 290 |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |  |
| Gly | Thr | Lys | Lys | Asp | Asn | Thr | Asn | Leu | Pro | Ser | Glu | Arg | Ser | Met | Thr |  |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     |     | 320 |  |
| Gln | Asn | Gly | Tyr | Ala | Ala | Ile | Glu |     |     |     |     |     |     |     |     |  |
|     |     |     |     |     | 325 |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..307
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1941:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Leu | Arg | Leu | Ala | Ser | Ser | Ser | Thr | Ser | Asn | Pro | Ile | Cys | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu | Asn | Pro | Gly | Lys | Asn | Leu | Asn | Phe | Pro | Ile | Arg | Asn | His | Arg | Ile |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro | Lys | Thr | Ser | Lys | Pro | Phe | Cys | Val | Arg | Ser | Ser | Met | Ser | Leu | Ser |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Lys | Pro | Pro | Arg | Gln | Thr | Leu | Ser | Ser | Asn | Trp | Asp | Val | Ser | Ser | Phe |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Ser | Ile | Asp | Ser | Val | Ala | Gln | Ser | Pro | Ser | Arg | Leu | Pro | Ser | Phe | Glu |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Glu | Leu | Asp | Thr | Thr | Asn | Met | Leu | Leu | Arg | Gln | Arg | Ile | Val | Phe | Leu |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Gly | Ser | Gln | Val | Asp | Asp | Met | Thr | Ala | Asp | Leu | Val | Ile | Ser | Gln | Leu |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| Leu | Leu | Leu | Asp | Ala | Glu | Asp | Ser | Glu | Arg | Asp | Ile | Thr | Leu | Phe | Ile |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |  |
| Asn | Ser | Pro | Gly | Gly | Ser | Ile | Thr | Ala | Gly | Met | Gly | Ile | Tyr | Asp | Ala |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Met | Lys | Gln | Cys | Lys | Ala | Asp | Val | Ser | Thr | Val | Cys | Leu | Gly | Leu | Ala |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Ala | Ser | Met | Gly | Ala | Phe | Leu | Leu | Ala | Ser | Gly | Ser | Lys | Gly | Lys | Arg |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |  |
| Tyr | Cys | Met | Pro | Asn | Ser | Lys | Val | Met | Ile | His | Gln | Pro | Leu | Gly | Thr |  |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |
| Ala | Gly | Gly | Lys | Ala | Thr | Glu | Met | Ser | Ile | Arg | Ile | Arg | Glu | Met | Met |  |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |
| Tyr | His | Lys | Ile | Lys | Leu | Asn | Lys | Ile | Phe | Ser | Arg | Ile | Thr | Gly | Lys |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Pro | Glu | Ser | Glu | Ile | Glu | Ser | Asp | Thr | Asp | Arg | Asp | Asn | Phe | Leu | Asn |  |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |  |
| Pro | Trp | Glu | Ala | Lys | Glu | Tyr | Gly | Leu | Ile | Asp | Ala | Val | Ile | Asp | Asp |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |  |
| Gly | Lys | Pro | Gly | Leu | Ile | Ala | Pro | Ile | Gly | Asp | Gly | Thr | Pro | Pro | Pro |  |



(2) INFORMATION FOR SEQ ID NO:1942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

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(ix) FEATURE:
```

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..263  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571421

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1.1191  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1943:

|             |             |            |            |            |            |      |
|-------------|-------------|------------|------------|------------|------------|------|
| taccattctt  | ctgaaaaatga | acacctcaga | agccctaagc | accacaatga | ttttgggcac | 60   |
| cacactagaa  | aaccacagcg  | tgctgtgaag | cctgatgctt | tgaaggagcc | tcacattatt | 120  |
| gatgtgcctg  | cattgtcatt  | ggatgatgtg | aaagaaaaga | ccgataacct | tggatcaaa  | 180  |
| tcattgattg  | gtgaaggatc  | ttacggcaga | gcctattatg | caaccttgaa | agatggaaa  | 240  |
| gctgtgcggg  | tgaagaagct  | tgacaatgca | gcggaacctg | aatcaaatgt | tgagtctctg | 300  |
| actcaggtct  | cgagggtttc  | caagctgaag | cacgataatt | ttgttgagct | cttcgggtat | 360  |
| tgcgttgaag  | ggaatttcgc  | cattcttcgc | tatgagtttg | ctactatggg | atctttacat | 420  |
| gacatcttac  | acggggagaa  | aggagtcaca | ggagcacac  | caggtcactg | gcttgactgg | 480  |
| atccaaaggg  | tcagaataga  | atttgatgca | gctagaggac | ttgagtattt | gcatgagaaa | 540  |
| gttcaacctg  | cagtaataca  | cagagatatt | cgatctagca | atgtgctctt | ctttgaagat | 600  |
| tttaaaagcca | agatcgctga  | ttttaatcta | tcgaaccaat | ctcctgatat | ggctgctcgt | 660  |
| cttcattcta  | ccagagtttt  | gggaatcttc | ggttaccacg | caccagagta | tgcgatgact | 720  |
| ggtaacatga  | cacagaagag  | fgatgtttat | agtttttggt | tggtgctttt | ggagctcttg | 780  |
| actggtagga  | aaccocgtga  | tcatacgatg | cctcgtgtgc | aacaaagtct | tgttactctg | 840  |
| gctactccaa  | ggctaaagtga | agacaaagt  | aagcaatgtg | ttgatccaaa | actaaaggaa | 900  |
| gaatatcctc  | ctaaagctgt  | tgcaaaagct | gctgcagtag | cagcattgtg | tgtgcaaat  | 960  |
| gaatcagagt  | ttagggccaa  | catacgactt | gtggtaaaag | ctctcaacc  | attgtgtgag | 1020 |
| tcatacaacg  | cagcagctgt  | accagtcag  | gaagcctgat | tcttctgtgc | aatagcaaca | 1080 |
| atgggaagatt | gggttcgggt  | tcagttgttg | ccataccgta | taaatgtgtt | cttaaagaga | 1140 |
| gtctttttgt  | cgaggctttt  | cttcagttaa | gagctccaaa | agcaccacac | c          |      |

(2) INFORMATION FOR SEQ ID NO:1944:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1.352  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1944:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | His | Ser | Ser | Glu | Asn | Glu | His | Leu | Arg | Ser | Pro | Lys | His | His | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Phe | Gly | His | His | Thr | Arg | Lys | Pro | Gln | Ala | Ala | Val | Lys | Pro | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Ala | Leu | Lys | Glu | Pro | Pro | Ser | Ile | Asp | Val | Pro | Ala | Leu | Ser | Leu | Asp |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Glu | Leu | Lys | Glu | Lys | Thr | Asp | Asn | Phe | Gly | Ser | Lys | Ser | Leu | Ile | Gly |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Glu | Gly | Ser | Tyr | Gly | Arg | Ala | Tyr | Tyr | Ala | Thr | Leu | Lys | Asp | Gly | Lys |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Ala | Val | Ala | Val | Lys | Lys | Leu | Asp | Asn | Ala | Ala | Glu | Pro | Glu | Ser | Asn |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |     |
| Val | Glu | Phe | Leu | Thr | Gln | Val | Ser | Arg | Val | Ser | Lys | Leu | Lys | His | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Asn | Phe | Val | Glu | Leu | Phe | Gly | Tyr | Cys | Val | Glu | Gly | Asn | Phe | Arg | Ile |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ala | Tyr | Glu | Phe | Ala | Thr | Met | Gly | Ser | Leu | His | Asp | Ile | Leu | His |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Gly | Arg | Lys | Gly | Val | Gln | Gly | Ala | Gln | Pro | Gly | Pro | Thr | Leu | Asp | Trp |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     | 160 |     |
| Ile | Gln | Arg | Val | Arg | Ile | Ala | Val | Asp | Ala | Ala | Arg | Gly | Leu | Glu | Tyr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |     |     |     |
| Leu | His | Glu | Lys | Val | Gln | Pro | Ala | Val | Ile | His | Arg | Asp | Ile | Arg | Ser |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Ser | Asn | Val | Leu | Leu | Phe | Glu | Asp | Phe | Lys | Ala | Lys | Ile | Ala | Asp | Phe |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 195                                                             | 200 | 205 |
| Asn Leu Ser Asn Gln Ser Pro Asp Met Ala Ala Arg Leu His Ser Thr |     |     |
| 210                                                             | 215 | 220 |
| Arg Val Leu Gly Xaa Phe Gly Tyr His Ala Pro Glu Tyr Ala Met Thr |     |     |
| 225                                                             | 230 | 235 |
| Gly Gln Leu Thr Gln Lys Ser Asp Val Tyr Ser Phe Gly Val Val Leu |     |     |
|                                                                 | 245 | 250 |
| Leu Glu Leu Leu Thr Gly Arg Lys Pro Val Asp His Thr Met Pro Arg |     |     |
|                                                                 | 260 | 265 |
| Gly Gln Gln Ser Leu Val Thr Trp Ala Thr Pro Arg Leu Ser Glu Asp |     |     |
|                                                                 | 275 | 280 |
| Lys Val Lys Gln Cys Val Asp Pro Lys Leu Lys Gly Glu Tyr Pro Pro |     |     |
|                                                                 | 290 | 295 |
| Lys Ala Val Ala Lys Leu Ala Ala Val Ala Ala Leu Cys Val Gln Tyr |     |     |
| 305                                                             | 310 | 315 |
| Glu Ser Glu Phe Arg Pro Asn Met Ser Ile Val Val Lys Ala Leu Gln |     |     |
|                                                                 | 325 | 330 |
| Pro Leu Leu Arg Ser Ser Thr Ala Ala Ala Val Pro Val Gln Glu Ala |     |     |
|                                                                 | 340 | 345 |
|                                                                 |     | 350 |

(2) INFORMATION FOR SEQ ID NO:1945:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1571424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1945:

|                                                                 |             |
|-----------------------------------------------------------------|-------------|
| Met Gly Ser Leu His Asp Ile Leu His Gly Arg Lys Gly Val Gln Gly |             |
| 1                                                               | 5 10 15     |
| Ala Gln Pro Gly Pro Thr Leu Asp Trp Ile Gln Arg Val Arg Ile Ala |             |
|                                                                 | 20 25 30    |
| Val Asp Ala Ala Arg Gly Leu Glu Tyr Leu His Glu Lys Val Gln Pro |             |
|                                                                 | 35 40 45    |
| Ala Val Ile His Arg Asp Ile Arg Ser Ser Asn Val Leu Leu Phe Glu |             |
|                                                                 | 50 55 60    |
| Asp Phe Lys Ala Lys Ile Ala Asp Phe Asn Leu Ser Asn Gln Ser Pro |             |
| 65                                                              | 70 75 80    |
| Asp Met Ala Ala Arg Leu His Ser Thr Arg Val Leu Gly Xaa Phe Gly |             |
|                                                                 | 85 90 95    |
| Tyr His Ala Pro Glu Tyr Ala Met Thr Gly Gln Leu Thr Gln Lys Ser |             |
|                                                                 | 100 105 110 |
| Asp Val Tyr Ser Phe Gly Val Val Leu Leu Glu Leu Thr Gly Arg     |             |
|                                                                 | 115 120 125 |
| Lys Pro Val Asp His Thr Met Pro Arg Gly Gln Gln Ser Leu Val Thr |             |
|                                                                 | 130 135 140 |
| Trp Ala Thr Pro Arg Leu Ser Glu Asp Lys Val Lys Gln Cys Val Asp |             |
| 145                                                             | 150 155 160 |
| Pro Lys Leu Lys Gly Glu Tyr Pro Pro Lys Ala Val Ala Lys Leu Ala |             |
|                                                                 | 165 170 175 |
| Ala Val Ala Ala Leu Cys Val Gln Tyr Glu Ser Glu Phe Arg Pro Asn |             |
|                                                                 | 180 185 190 |
| Met Ser Ile Val Val Lys Ala Leu Gln Pro Leu Leu Arg Ser Ser Thr |             |
|                                                                 | 195 200 205 |
| Ala Ala Ala Val Pro Val Gln Glu Ala                             |             |
|                                                                 | 210 215     |

(2) INFORMATION FOR SEQ ID NO:1946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1500
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1946:

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| aacgcttgcga | cagctctctac | accgctcatga | acactgaatc | agttgtcgag  | ttccttggga  | 60   |
| atgtgacctt  | gttcgacggg  | ttacctagtt  | cctctctgaa | gagaatctcc  | gaagtctgtt  | 120  |
| ctctcaaaag  | ttatgacaga  | ggtgattatg  | tggttcgtga | aaatcaaaat  | gtggatggag  | 180  |
| tttatttttc  | cttgcaagga  | caggctcagg  | ttctgagatc | agccgaagag  | gaaaaactac  | 240  |
| aagagttccc  | tttgaacga   | tatgatttct  | tcggccatgg | tattttcggg  | gatgtttaact | 300  |
| cagcagatgt  | tggtgctgtg  | acagagctta  | cctgcttgct | gttgatgtct  | gatcatcgtg  | 360  |
| ctttacttga  | aataaagtca  | gtctcggatt  | cgataaagga | acgctgtctt  | gtggaagaca  | 420  |
| tactatatct  | agaaccatta  | gatttgaatg  | tataccgggg | gttcacccca  | cctaagctc   | 480  |
| caacctatgg  | aaagggttat  | ggaggccaat  | tagttggaca | ggcacttgcc  | gcagcatcaa  | 540  |
| aaactgttga  | aactatgaag  | atagtcata   | attttcattg | ctatttccct  | ctgtgtggag  | 600  |
| atataaatat  | tcccatcata  | tatgatgtta  | acogcttacg | tgacggcaac  | aaacttgcga  | 660  |
| ccagaaagtgt | agatgctaga  | cagaaaaggaa | aaactatatt | ccacttgctc  | gcgtcatttc  | 720  |
| agaaaaagca  | acaaagtttt  | attcaccagg  | agtcgaccat | gcctcataca  | ccagctcctg  | 780  |
| aaacgcttct  | accaaaggag  | gagatgcttg  | aacggctgtg | tactgacctt  | ctgtcactcta | 840  |
| gggattaccg  | aaaccaaagt  | gcaactgaaa  | ttagtgttcc | attccctata  | gatatttcgat | 900  |
| tttctgagcg  | aaactcgttc  | actaaacaga  | ataagctctc | tcacaagacta | aaatatttgtt | 960  |
| ttagagcaaa  | gggaaaaact  | tctgatgatg  | atcaagcttt | gcacagatgt  | gtgggttgcat | 1020 |
| ttgcttcctga | tttgatactc  | gccactatca  | gtttaaaccc | tcaccggaga  | gagggcatga  | 1080 |
| gtgtagctgc  | tcttagcctg  | gaccactcga  | tgtgtgtcca | ccgacctgtg  | agagcagatg  | 1140 |
| attgggttgt  | gtttgtgtga  | gtccaactgc  | gacctaaagc | cgcggttttg  | caactggcga  | 1200 |
| aatgtctcaac | agaaaggggag | agctgggtgt  | atcattgacg | caagaagctg  | tgtaagaga   | 1260 |
| agctgtgact  | atgaagccat  | ccttcggggc  | caagctatga | agccatagga  | ttttgatagt  | 1320 |
| gagagaattg  | ctgcactctg  | tactcctcac  | ggctcacatt | caaaagctcg  | tcacttatca  | 1380 |
| tacattttgca | tatgtttttc  | gatccacaat  | tattattttc | ccctctaaaa  | gggtctacac  | 1440 |
| atcatgttgt  | ttgtaaccac  | gataatgttt  | caacagcaat | gaaaaagcaa  | acagtgtgtc  | 1500 |

(2) INFORMATION FOR SEQ ID NO:1947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..385
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1947:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Phe | Asp | Ser | Leu | Tyr | Thr | Val | Met | Asn | Thr | Glu | Ser | Val | Val | Glu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Phe | Leu | Gly | Asn | Val | Thr | Leu | Leu | Gln | Arg | Leu | Pro | Ser | Ser | Ser | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Lys | Arg | Ile | Ser | Glu | Val | Val | Val | Phe | Lys | Gly | Tyr | Asp | Arg | Gly | Asp |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Tyr | Val | Val | Arg | Glu | Asn | Gln | Asn | Val | Asp | Gly | Val | Tyr | Phe | Leu | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Gln | Gly | Gln | Ala | Gln | Val | Leu | Arg | Ser | Ala | Glu | Glu | Glu | Asn | Tyr | Gln |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     | 80  |     |     |
| Glu | Phe | Pro | Leu | Lys | Arg | Tyr | Asp | Phe | Phe | Gly | His | Gly | Ile | Phe | Gly |

Val  
385

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

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(ix) FEATURE:
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(B) LOCATION: 1..377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1948:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Thr | Glu | Ser | Val | Val | Glu | Phe | Leu | Gly | Asn | Val | Thr | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Arg | Leu | Pro | Ser | Ser | Ser | Leu | Lys | Arg | Ile | Ser | Glu | Val | Val | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Lys | Gly | Tyr | Asp | Arg |     | Gly | Asp | Tyr | Val | Val | Arg | Glu | Asn | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Val | Asp | Gly | Val | Tyr | Phe |     | Leu | Leu | Gln | Gly | Gln | Ala | Gln | Val | Leu |
|     | 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Ser | Ala | Glu | Glu | Glu | Asn |     | Tyr | Gln | Glu | Phe | Pro | Leu | Lys | Arg | Tyr |
| 65  |     |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |

Phe Phe Gly His Gly Ile Phe Gly Asp Val Tyr Ser Ala Asp Val Val  
85 90 95  
Ala Val Thr Glu Leu Thr Cys Leu Leu Met Ser Asp His Arg Ala  
100 105 110  
Leu Leu Glu Ile Lys Ser Val Ser Asp Ser Asp Lys Glu Arg Cys Leu  
115 120 125  
Val Glu Asp Ile Leu Tyr Leu Glu Pro Leu Asp Leu Asn Val Tyr Arg  
130 135 140  
Gly Phe Thr Pro Pro Asn Ala Pro Thr Tyr Gly Lys Val Tyr Gly Gly  
145 150 155 160  
Gln Leu Val Gly Gln Ala Leu Ala Ala Ser Lys Thr Val Glu Thr  
165 170 175  
Met Lys Ile Val His Asn Phe His Cys Tyr Phe Leu Leu Val Gly Asp  
180 185 190  
Ile Asn Ile Pro Ile Ile Tyr Asp Val Asn Arg Leu Arg Asp Gly Asn  
195 200 205  
Asn Phe Ala Thr Arg Ser Val Asp Ala Arg Gln Lys Gly Lys Thr Ile  
210 215 220  
Phe Thr Leu Phe Ala Ser Phe Gln Lys Lys Gln Gln Gly Phe Ile His  
225 230 235 240  
Gln Glu Ser Thr Met Pro His Thr Pro Ala Pro Glu Thr Leu Leu Pro  
245 250 255  
Arg Glu Glu Met Leu Glu Arg Leu Val Thr Glu Pro Leu Leu Pro Arg  
260 265 270  
Asp Tyr Arg Asn Gln Val Ala Thr Glu Ile Ser Val Pro Phe Pro Ile  
275 280 285  
Asp Ile Arg Phe Cys Glu Pro Asn Arg Ser Thr Lys Gln Asn Lys Ser  
290 295 300  
Pro Pro Arg Leu Lys Tyr Trp Phe Arg Ala Lys Gly Lys Leu Ser Asp  
305 310 315 320  
Asp Asp Gln Ala Leu His Arg Cys Val Val Ala Phe Ala Ser Asp Leu  
325 330 335  
Ile Phe Ala Thr Ile Ser Leu Asn Pro His Arg Arg Glu Gly Met Ser  
340 345 350  
Val Ala Ala Leu Ser Leu Asp His Ser Met Trp Phe His Arg Pro Val  
355 360 365  
Arg Ala Asp Asp Trp Leu Leu Phe Val  
370 375

(2) INFORMATION FOR SEQ ID NO:1949:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..271
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1949:

Met Ser Asp His Arg Ala Leu Leu Glu Ile Lys Ser Val Ser Asp Ser  
1 5 10 15  
Asp Lys Glu Arg Cys Leu Val Glu Asp Ile Leu Tyr Leu Glu Pro Leu  
20 25 30  
Asp Leu Asn Val Tyr Arg Gly Phe Thr Pro Pro Asn Ala Pro Thr Tyr  
35 40 45  
Gly Lys Val Tyr Gly Gly Gln Leu Val Gly Gln Ala Leu Ala Ala Ala  
50 55 60  
Ser Lys Thr Val Glu Thr Met Lys Ile Val His Asn Phe His Cys Tyr  
65 70 75 80  
Phe Leu Leu Val Gly Asp Ile Asn Ile Pro Ile Tyr Asp Val Asn

(2) INFORMATION FOR SEQ ID NO:1950:

(A) LENGTH: 1974 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (α

## (ii) MOLECULE TYPE: DNA (genomic)

```
(ix) FEATURE:
```

(A) NAME/KEY: -

{B) LOCATION: 1..1974

(D) OTHER INFORMATION: / Ceres Seq. ID 1571432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1950:

|             |            |            |             |            |             |      |
|-------------|------------|------------|-------------|------------|-------------|------|
| aaaaaagaat  | acacagaca  | gtctctcgtg | gctcgttaat  | ggcgattctc | aaattctgat  | 60   |
| ctcgtacaaa  | caatggcgca | aacctcgga  | ccagtcaacg  | cgacgatgc  | ccaggattgt  | 120  |
| cactcgtctc  | ttctctctcc | ggcgaggagg | ttctcgtctc  | gtaattacgt | cgaaagcgtg  | 180  |
| aaagtgtgac  | gctgtttagg | gaagaagaat | ggatttgtatt | tttcagctcg | tttgctggtg  | 240  |
| ccgtgtcagc  | gggttaactc | acagctgggt | gaagtcacac  | acgagctctc | ttcgaaagtt  | 300  |
| ggtttttgaa  | ttgtttttgt | gtcaggtgat | gaggatgaag  | agtcatttgg | agatttaatt  | 360  |
| agtaaatgac  | ctcgtctcgc | gtcttcgttt | actgatctgg  | aaacccgtga | ccgttttgat  | 420  |
| gagtttgttta | aggttagggg | aataccttca | ctagtgtatg  | ttgatgatgc | tcgttaaaatt | 480  |
| gtgaatgaca  | atggtgtgtg | gctctacaga | agctatggag  | ctgatgctta | ttttttacaa  | 540  |
| ccagagaaaa  | tgaaggagat | caaaaggagt | gaagatagag  | ctcgaggaga | acagacctta  | 600  |
| agatctgaac  | ttgttgactc | ttccagagct | tttgtgtatt  | cgctcagcgc | aaacacagta  | 660  |
| cccgatcacg  | agcttgaggg | aaaaaccatt | ggcctctctc  | ttctctgggc | ctctcacagg  | 720  |
| aaatgcacag  | agcttaactc | aaagcttgtt | ggcttttata  | cgaagctgaa | gggaataaag  | 780  |
| gaggttttgt  | agatttgttt | gatattcttc | gaagatagat  | aggagctttc | taatcaagac  | 840  |
| ttcaagacca  | agcattgctc | gactctgcgc | ttcaacgaca  | aaagtgtgat | aaaatttgct  | 900  |
| cggcatttca  | tgctgtcaac | actaccgaca | ctggctcatt  | tcggcctgta | tggaaaaaat  | 960  |
| cgctcaactga | atgtctcgta | agctattggc | gactattggg  | ttcttcgcta | ctctttcaat  | 1020 |
| ccagagaagc  | ttcaagaact | caaggagcta | gaaaagscac  | aggttagagg | tcaaacgcgc  | 1080 |
| gagtcacttc  | ttgtctcagg | tgactctaac | taagttctac  | gaaaaggatg | ggcaaaagtg  | 1140 |
| cttgtttcgc  | attcgtgtgg | gaagaactat | cttttgtact  | ttctcagcta | ctggtgtctc  | 1200 |
| ccctgtcgcg  | tttttacacc | aaagcttgtt | gaagtatata  | acgagataaa | ggagcggaat  | 1260 |
| gacagcgttt  | aattgatctt | ctctcctagc | gacgcgtacc  | aggaataatt | ctgatgatgc  | 1320 |
| tttgtccaaa  | tgccttggtc | ggctcttcac | tttgtgtatc  | ctaggaaagt | actcttggtc  | 1380 |
| aaaaaccttta | agggctgttg | atcccaaatc | tagcagatct  | gggacacatt | gggcaaaagg  | 1440 |
| taacaaaaga  | acgaaggagc | cttgtctgag | cccatggagc  | cgtgctctat | ccctttctac  | 1500 |
| ttgcgaagac  | ttgaagctta | ttgaagctta | ctcatgatag  | atagcaaaag | attggtctaa  | 1560 |

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gaagggtgaaa catgtttctcc atgaagaaca tgagctagaa ctaactcgtg ttcagggttta 1620
cacatgcgat aagtggtgagg aagaaggagc aatatggtga ccattgcgac gaatgcgact 1680
ttgatcttca cgccaagtgt gctttaaacg agtacacaaa agaaaaacgc gatgaggctg 1740
tgaaagttgg tggcAgacga gtccaaagat ggttgggttt gtgaaggaaa cgtatgcacc 1800
aaggccctgat aggtagcttc aggcacagtt atgtcactat gtgtatgcaa agctatttcc 1860
ttcttttgta taattgctaa tagtgagaat gtgtggttac aactctgat ctgattaaga 1920
ccttggagat aaactctgtt aatctaaagt agtaataaaa gaattcttct attt

```

(2) INFORMATION FOR SEQ ID NO:1951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 470 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..470

(D) OTHER INFORMATION: / Ceres Seq. ID 1571433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1951:

```

Lys Lys Glu Tyr Thr Asp Gln Ser Ser Cys Ala Arg Asn Trp Arg Phe
1 5 10 15
Ser Asn Ser Ile Ser Val Gln Thr Met Ala Glu Thr Ser Lys Gln Val
20 25 30
Asn Gly Asp Asp Ala Gln Asp Leu His Ser Leu Leu Ser Ser Pro Ala
35 40 45
Arg Asp Phe Leu Val Arg Asn Asp Gly Glu Gln Val Lys Val Asp Ser
50 55 60
Leu Leu Gly Lys Lys Ile Gly Leu Tyr Phe Ser Ala Ala Trp Cys Gly
65 70 75 80
Pro Cys Gln Arg Phe Thr Pro Gln Leu Val Glu Val Tyr Asn Glu Leu
85 90 95
Ser Ser Lys Val Gly Phe Glu Ile Val Phe Val Ser Gly Asp Glu Asp
100 105 110
Glu Glu Ser Phe Gly Asp Tyr Phe Ser Lys Met Pro Trp Leu Ala Val
115 120 125
Pro Phe Thr Asp Ser Glu Thr Arg Asp Arg Leu Asp Glu Leu Phe Lys
130 135 140
Val Arg Gly Ile Pro Asn Leu Val Met Val Asp Asp His Gly Lys Leu
145 150 155 160
Val Asn Glu Asn Gly Val Gly Val Ile Arg Ser Tyr Gly Ala Asp Ala
165 170 175
Tyr Pro Phe Thr Pro Glu Lys Met Lys Glu Ile Lys Glu Asp Glu Asp
180 185 190
Arg Ala Arg Arg Glu Gln Thr Leu Arg Ser Val Leu Val Thr Pro Ser
195 200 205
Arg Asp Phe Val Ile Ser Pro Asp Gly Asn Lys Val Pro Val Ser Glu
210 215 220
Leu Glu Gly Lys Thr Ile Gly Leu Leu Phe Ser Val Ala Ser Tyr Arg
225 230 235 240
Lys Cys Thr Glu Leu Thr Pro Lys Leu Val Glu Phe Tyr Thr Lys Leu
245 250 255
Lys Glu Asn Lys Glu Asp Phe Glu Ile Val Leu Ile Ser Leu Glu Asp
260 265 270 275
Asp Glu Glu Ser Phe Asn Gln Asp Phe Lys Thr Lys Pro Trp Leu Ala
280 285
Leu Pro Phe Asn Asp Lys Ser Gly Ser Lys Leu Ala Arg His Phe Met
290 295 300
Leu Ser Thr Leu Pro Thr Leu Val Ile Leu Gly Pro Asp Gly Lys Ile
305 310 315 320
Arg His Ser Asn Val Ala Glu Ala Ile Asp Asp Tyr Gly Val Leu Ala
325 330 335

```



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Pro | Phe | Thr | Pro | Glu | Lys | Phe | Gln | Glu | Leu | Lys | Glu | Leu | Glu | Lys |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ala | Lys | Val | Glu | Ala | Gln | Thr | Leu | Glu | Ser | Leu | Leu | Val | Ser | Gly | Asp |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Leu | Asn | Tyr | Val | Leu | Gly | Lys | Asp | Gly | Ala | Lys | Val | Leu | Val | Ser | Asp |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Leu | Val | Gly | Lys | Thr | Ile | Leu | Met | Tyr | Phe | Ser | Ala | His | Trp | Cys | Pro |
|     | 385 |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Pro | Cys | Arg | Ala | Phe | Thr | Pro | Lys | Leu | Val | Glu | Val | Tyr | Lys | Gln | Ile |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Lys | Glu | Arg | Asn | Glu | Ala | Phe | Glu | Leu | Ile | Phe | Ile | Ser | Ser | Asp | Arg |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Asp | Gln | Glu | Ser | Phe | Asp | Glu | Tyr | Tyr | Ser | Gln | Met | Pro | Trp | Leu | Ala |
|     | 435 |     |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Leu | Pro | Phe | Gly | Asp | Pro | Arg | Lys | Ala | Ser | Leu | Ala | Lys | Thr | Phe | Lys |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Val | Gly | Gly | Ser | Gln | Cys |     |     |     |     |     |     |     |     |     |     |
|     | 465 |     |     |     | 470 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1952:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 446 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..446

(D) OTHER INFORMATION: / Ceres Seq. ID 1571434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1952:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Thr | Ser | Lys | Gln | Val | Asn | Gly | Asp | Asp | Ala | Gln | Asp | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| His | Ser | Leu | Leu | Ser | Ser | Pro | Ala | Arg | Asp | Phe | Leu | Val | Arg | Asn | Asp |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Glu | Gln | Val | Lys | Val | Asp | Ser | Leu | Leu | Gly | Lys | Lys | Ile | Gly | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Phe | Ser | Ala | Ala | Trp | Cys | Gly | Pro | Cys | Gln | Arg | Phe | Thr | Pro | Gln |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Leu | Val | Glu | Val | Tyr | Asn | Glu | Leu | Ser | Ser | Lys | Val | Gly | Phe | Glu | Ile |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Phe | Val | Ser | Gly | Asp | Glu | Asp | Glu | Ser | Phe | Gly | Asp | Tyr | Phe |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |     |
| Ser | Lys | Met | Pro | Trp | Leu | Ala | Val | Pro | Phe | Thr | Asp | Ser | Glu | Thr | Arg |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Arg | Leu | Asp | Glu | Leu | Phe | Lys | Val | Arg | Gly | Ile | Pro | Asn | Leu | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Met | Val | Asp | Asp | His | Gly | Lys | Leu | Val | Asn | Glu | Asn | Gly | Val | Gly | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Ile | Arg | Ser | Tyr | Gly | Ala | Asp | Ala | Tyr | Pro | Phe | Thr | Pro | Glu | Lys | Met |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Lys | Glu | Ile | Lys | Glu | Asp | Glu | Asp | Arg | Ala | Arg | Arg | Glu | Gln | Thr | Leu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Arg | Ser | Val | Leu | Val | Thr | Pro | Ser | Arg | Asp | Phe | Val | Ile | Ser | Pro | Asp |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Asn | Lys | Val | Pro | Val | Ser | Glu | Leu | Glu | Gly | Lys | Thr | Ile | Gly | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Phe | Ser | Val | Ala | Ser | Tyr | Arg | Lys | Cys | Thr | Glu | Leu | Thr | Pro | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Val | Glu | Phe | Tyr | Thr | Lys | Leu | Lys | Glu | Asn | Lys | Glu | Asp | Phe | Glu |
|     | 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     | 240 |     |
| Ile | Val | Leu | Ile | Ser | Leu | Glu | Asp | Asp | Glu | Glu | Ser | Phe | Asn | Gln | Asp |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Trp | Leu | Ala | Val | Pro | Phe | Thr | Asp | Ser | Glu | Thr | Arg | Asp | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Asp | Glu | Leu | Phe | Lys | Val | Arg | Gly | Ile | Pro | Asn | Leu | Val | Met | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Asp | His | Gly | Lys | Leu | Val | Asn | Glu | Asn | Gly | Val | Gly | Val | Ile | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Tyr | Gly | Ala | Asp | Ala | Tyr | Pro | Phe | Thr | Pro | Glu | Lys | Met | Lys | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Lys | Glu | Asp | Glu | Asp | Arg | Ala | Arg | Arg | Glu | Gln | Thr | Leu | Arg | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Leu | Val | Thr | Pro | Ser | Arg | Asp | Phe | Val | Ile | Ser | Pro | Asp | Gly | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Val | Pro | Val | Ser | Glu | Leu | Glu | Gly | Lys | Thr | Ile | Gly | Leu | Phe |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Val | Ala | Ser | Tyr | Arg | Lys | Cys | Thr | Glu | Leu | Thr | Pro | Lys | Leu | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Phe | Tyr | Thr | Lys | Leu | Lys | Glu | Asn | Lys | Glu | Asp | Phe | Glu | Ile | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Ile | Ser | Leu | Glu | Asp | Asp | Glu | Glu | Ser | Phe | Asn | Gln | Asp | Phe | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Lys | Pro | Trp | Leu | Ala | Leu | Pro | Phe | Asn | Asp | Lys | Ser | Gly | Ser | Lys |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Ala | Arg | His | Phe | Met | Leu | Ser | Thr | Leu | Pro | Thr | Leu | Val | Ile | Leu |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |

Gly Pro Asp Gly Lys Ile Arg His Ser Asn Val Ala Glu Ala Ile Asp  
195 200 205  
Asp Tyr Gly Val Leu Ala Tyr Pro Phe Thr Pro Glu Lys Phe Gln Glu  
210 215 220  
Leu Lys Glu Leu Glu Lys Ala Lys Val Glu Ala Gln Thr Leu Glu Ser  
225 230 235 240  
Leu Leu Val Ser Gly Asp Leu Asn Tyr Val Leu Gly Lys Asp Gly Ala  
245 250 255  
Lys Val Leu Val Ser Asp Leu Val Gly Lys Thr Ile Leu Met Tyr Phe  
260 265 270  
Ser Ala His Trp Cys Pro Pro Cys Arg Ala Phe Thr Pro Lys Leu Val  
275 280 285  
Glu Val Tyr Lys Gln Ile Lys Glu Arg Asn Glu Ala Phe Glu Leu Ile  
290 295 300  
Phe Ile Ser Ser Asp Arg Asp Gln Glu Ser Phe Asp Glu Tyr Tyr Ser  
305 310 315 320  
Gln Met Pro Trp Leu Ala Leu Pro Phe Gly Asp Pro Arg Lys Ala Ser  
325 330 335  
Leu Ala Lys Thr Phe Lys Val Gly Gly Ser Gln Cys  
340 345

(2) INFORMATION FOR SEQ ID NO:1954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1954:

|             |             |            |            |            |            |      |
|-------------|-------------|------------|------------|------------|------------|------|
| ctctgctaaa  | tctgtgtcga  | tctaaaaaat | caacgaacac | aaaactcatc | aaagctcctc | 60   |
| aaaaaccctaa | acacagctctc | tccatcttct | tcaactctct | tctcgttcgg | attctcatct | 120  |
| cttcttctgg  | tttcagattg  | agtcttggta | ctgtgtttca | taagactalt | gaagttaaga | 180  |
| tgtctggagc  | attgaatatg  | actcttggat | agattgttaa | gaggggtaaa | actgcaaggt | 240  |
| ctggggggaag | agggaattct  | cgtgggcgtg | gtcgtggacg | tgtgtgtgtg | ggaagaggag | 300  |
| ctggaccctgc | tagaagaggt  | cctcttgcTG | gtgaatgctc | gtccatcatc | tttcaccatt | 360  |
| aacaagcctg  | tcgtaSggt   | caggagcttg | ccatggcmaa | gcggttttgt | tgaagatggc | 420  |
| ctaagagctg  | ccggggcatc  | aggagttgaa | gttggaacca | ggctccatgt | tacaaatctg | 480  |
| gaccaggtg   | tgacaaatga  | agatataaag | gaactcttct | ctgagattgt | ggaggtagag | 540  |
| cgttatgcga  | ttcattatga  | caaaaatggg | cgtccaagtg | gcacagctga | agtgtgtgat | 600  |
| ccaaagaagaa | gtgattgcat  | tcaagctctg | aagaaatata | acaatgtgct | attgtagtga | 660  |
| aggccaatga  | gcattgagat  | tttgggtggc | aacaattctt | ccgaggctcc | tttatcttgt | 720  |
| cgctggaatg  | tgaatgtcac  | tggactcaat | ggaaggctga | agaggacggt | tgttatccaa | 780  |
| caaggaggag  | gagggagagg  | aggaagaggt | ccagctccta | ctgtcactgc | ccgccttcca | 840  |
| attcataacc  | agcagggagg  | agggatgaga | ggaggaagag | gcgggttttg | tgcataaggg | 900  |
| cgtggtaatg  | gtggccctgg  | tcgtgtgggt | ggaagaggaa | atggaaaaga | gccagtgga  | 960  |
| aagtgcagctg | ctgatcttga  | caaagatctt | gagagctatc | acgctgatgc | catgaacacc | 1020 |
| tcttaaatcg  | tgtttgtgtg  | ttcttactaa | actagtttca | gatgaaatca | tgcttctctt | 1080 |
| tttttcatgc  | tcttcgttgg  | ttttgttgga | tgttgattgt | aaagtaaatg | gaagcctttt | 1140 |

agaatc

(2) INFORMATION FOR SEQ ID NO:1955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..272  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571441  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1955:

```

Met Arg Leu Leu Arg Gly Val Lys Leu Gln Gly Leu Gly Glu Glu Gly
1 5 10 15
Phe Leu Val Gly Val Val Val Asp Val Val Val Val Glu Glu Glu Leu
20 25 30
Asp Leu Leu Glu Glu Val Leu Leu Val Val Asn Ala Arg Pro Ser Ser
35 40 45
Phe Thr Ile Asn Lys Pro Val Arg Xaa Val Arg Ser Leu Pro Trp Gln
50 55 60
Ser Gly Leu Phe Glu Asp Gly Leu Arg Ala Ala Gly Ala Ser Gly Val
65 70 75 80
Glu Val Gly Thr Arg Leu His Val Thr Asn Leu Asp Gln Gly Val Thr
85 90 95
Asn Glu Asp Ile Arg Glu Leu Phe Ser Glu Ile Gly Glu Val Glu Arg
100 105 110
Tyr Ala Ile His Tyr Asp Lys Asn Gly Arg Pro Ser Gly Thr Ala Glu
115 120 125
Val Val Tyr Pro Arg Arg Ser Asp Ala Phe Gln Ala Leu Lys Lys Tyr
130 135 140
Asn Asn Val Leu Leu Asp Gly Arg Pro Met Arg Leu Glu Ile Leu Gly
145 150 155 160
Gly Asn Asn Ser Ser Glu Ala Pro Leu Ser Gly Arg Val Asn Val Asn
165 170 175
Val Thr Gly Leu Asn Gly Arg Leu Lys Arg Thr Val Val Ile Gln Gln
180 185 190
Gly Gly Gly Gly Arg Gly Gly Arg Gly Pro Ala Pro Thr Val Ser Arg
195 200 205
Arg Leu Pro Ile His Asn Gln Gln Gly Gly Gly Met Arg Gly Gly Arg
210 215 220
Gly Gly Phe Arg Ala Arg Gly Arg Gly Asn Gly Gly Arg Gly Arg Gly
225 230 235 240
Gly Gly Arg Gly Asn Gly Lys Lys Pro Val Glu Lys Ser Ala Ala Asp
245 250 255
Leu Asp Lys Asp Leu Glu Ser Tyr His Ala Asp Ala Met Asn Thr Ser
260 265 270

```

(2) INFORMATION FOR SEQ ID NO:1956:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1569 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1569

(D) OTHER INFORMATION: / Ceres Seq. ID 1571445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1956:

```

aaaaaaacaa aaacagagcc aggaataatg tcaagtcttc ctgtttcttc ctgcctcttta 60
ccoccttatct taattctctt gaaaaatctc aaaccatcga aatggaagct tcctccaggcc 120
ccaaagaagc ttccgatcat cgggaactta caccaacgcc gggaattaca tcccaggaac 180
agtcggaatc tttccgaaaa gtacggacca atcgtgtttc tccgatacgg attcgtcccc 240
gtggtcgtga tctcgtcaaa agaagcagca gaggaagttc tcaagaccac gatcttgagt 300
gttgtagccg accagagacg gttgggacca gagcaatctc ttacaacttt aaagacatcg 360
gattcgcaac gtgcggtgaa gattggagaa cgatgcggaa gctctcgggt gtcgagctct 420
tcagctcgaa aaagcttcaa tctttcaggt atatcagaga ggaagagaac gacttctgtg 480
tcaagaaact ctctgattta gcttcagac gatctttggt gaatcttgag aaaaaccttt 540
ttacttttagt cggaagtata gtgtgtagga taggggtttg gataaatctc cgtgagtgtg 600

```

|            |            |            |             |            |            |      |
|------------|------------|------------|-------------|------------|------------|------|
| agtctgttga | tgaagatagc | atcgatgac  | ttgtgcacaa  | gtctgaagat | gtcataagga | 660  |
| attctatctt | ctctgtattc | tttcccggt  | taatgggtag  | gtctcatgag | tggatctcca | 720  |
| gtgagaggaa | gagattgaat | agactttact | cggaaagtaga | cactttcttt | cagaatattc | 780  |
| ttgatgatca | tctcaagcct | ggaagagaga | gctctgatata | catcgatgtg | atgattgata | 840  |
| tgatgaagaa | gcaagagaaa | gagggagact | ctttcaagtt  | caccactgat | catctcaaa  | 900  |
| ggatgatctc | ggacatatct | ctagcaggag | ttggaacaag  | ctccactaca | ttgatatggg | 960  |
| cgatgaccga | gctgatccga | aacccgagag | tgatgaagaa  | agttcaagac | gagattcgga | 1020 |
| caacacttgg | ggacaagaag | gagagaatca | cagaagaaga  | tttaaacacc | cttcactact | 1080 |
| tcaagctcat | ggctcaagag | atatctcagg | tacatccagc  | agctccaact | ttgctcccaa | 1140 |
| gagagacatt | gtctcatgtc | aagatccaag | gctacgatata | tcctgtctaa | acacagatca | 1200 |
| tgatcaaaCG | ttacgcgatt | gcacgtgatc | caaaactatg  | gacaaaccc  | gatgagttaa | 1260 |
| accctgatag | gttcccttgc | agctccatag | attacagagg  | actgaacttt | gagctattac | 1320 |
| cgtttggtac | tggtaggagg | atatgtccag | ggatgacaat  | ggggatcgcc | attgttgaat | 1380 |
| tgggactatt | gaatttgcct | tactttcttc | actgggggct  | accagagaag | gaagaagcca | 1440 |
| aggagatcat | caccgggaat | gaagttgctc | ttgacctgtt  | tcaagttttt | ctccactgaa | 1500 |
| tatgtgtttt | ggttatgcaa | tgtttgtact | acactaagct  | tgattctaaa | ttataacat  | 1560 |
| cttacaagc  |            |            |             |            |            |      |

(2) INFORMATION FOR SEQ ID NO:1957:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 498 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..498

(D) OTHER INFORMATION: / Ceres Seq. ID 1571446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1957:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asn | Lys | Asn | Arg | Ala | Arg | Asn | Asn | Val | Ser | Leu | Pro | Leu | Phe | Pro |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Pro | Leu | Thr | Pro | Tyr | Leu | Asn | Leu | Leu | Glu | Lys | Ser | Gln | Thr | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Met | Glu | Ala | Ser | Ser | Arg | Pro | Lys | Glu | Ala | Ser | Asp | His | Arg | Glu |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Leu | Thr | Pro | Thr | Pro | Gly | Ile | Thr | Ser | Gln | Glu | Gln | Ser | Glu | Ser | Phe |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Lys | Val | Arg | Thr | Asn | Arg | Val | Ser | Pro | Ile | Arg | Ile | Arg | Pro | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Arg | Asp | Leu | Val | Lys | Arg | Ser | Ser | Arg | Gly | Ser | Ser | Gln | Asp | His |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Leu | Glu | Cys | Cys | Ser | Arg | Pro | Glu | Thr | Val | Gly | Thr | Arg | Ala | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Tyr | Asn | Phe | Lys | Asp | Ile | Gly | Phe | Ala | Pro | Cys | Gly | Glu | Asp | Trp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Thr | Met | Arg | Lys | Leu | Ser | Val | Val | Glu | Leu | Phe | Ser | Ser | Lys | Lys |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Gln | Ser | Phe | Arg | Tyr | Ile | Arg | Glu | Glu | Glu | Asn | Asp | Leu | Cys | Val |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Lys | Lys | Leu | Ser | Asp | Leu | Ala | Ser | Arg | Arg | Ser | Leu | Val | Asn | Leu | Glu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Thr | Leu | Phe | Thr | Leu | Val | Gly | Ser | Ile | Val | Cys | Arg | Ile | Gly | Phe |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Gly | Ile | Asn | Leu | Arg | Glu | Cys | Glu | Phe | Val | Asp | Glu | Asp | Ser | Ile | Asp |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asp | Leu | Val | His | Lys | Ser | Glu | Asp | Val | Ile | Arg | Asn | Ser | Ile | Phe | Ser |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asp | Phe | Phe | Pro | Gly | Leu | Met | Gly | Arg | Leu | Ile | Glu | Trp | Ile | Phe | Ser |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Glu | Arg | Lys | Arg | Leu | Asn | Arg | Leu | Tyr | Ser | Glu | Val | Asp | Thr | Phe | Phe |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |

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Gln Asn Ile Leu Asp Asp His Leu Lys Pro Gly Arg Glu Ser Ser Asp
 260 265 270
Ile Ile Asp Val Met Ile Asp Met Met Lys Lys Gln Glu Lys Glu Gly
 275 280 285
Asp Ser Phe Lys Phe Thr Thr Asp His Leu Lys Gly Met Ile Ser Asp
 290 295 300
Ile Phe Leu Ala Gly Val Gly Thr Ser Ser Thr Thr Leu Ile Trp Ala
 305 310 315 320
Met Thr Glu Leu Ile Arg Asn Pro Arg Val Met Lys Lys Val Gln Asp
 325 330 335
Glu Ile Arg Thr Thr Leu Gly Asp Lys Lys Glu Arg Ile Thr Glu Glu
 340 345 350
Asp Leu Asn Gln Leu His Tyr Phe Lys Leu Met Val Lys Glu Ile Phe
 355 360 365
Arg Leu His Pro Ala Ala Pro Leu Leu Pro Arg Glu Thr Leu Ser
 370 375 380
His Val Lys Ile Gln Gly Tyr Asp Ile Pro Ala Lys Thr Gln Ile Met
 385 390 395 400
Ile Asn Ala Tyr Ala Ile Ala Arg Asp Pro Lys Leu Trp Thr Asn Pro
 405 410 415
Asp Glu Phe Asn Pro Asp Arg Phe Leu Asp Ser Ser Ile Asp Tyr Arg
 420 425 430
Gly Leu Asn Phe Glu Leu Leu Pro Phe Gly Ser Gly Arg Arg Ile Cys
 435 440 445
Pro Gly Met Thr Met Gly Ile Ala Ile Val Glu Leu Gly Leu Leu Asn
 450 455 460
Leu Leu Tyr Phe Phe Asp Trp Gly Leu Pro Glu Lys Glu Glu Ala Lys
 465 470 475 480
Glu Ile Ile Thr Gly Asn Glu Val Ala Leu Asp Leu Val Gln Val Phe
 485 490 495
Leu His

```

(2) INFORMATION FOR SEQ ID NO:1958:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..465
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1958:

```

Met Glu Ala Ser Ser Arg Pro Lys Glu Ala Ser Asp His Arg Glu Leu
 1 5 10 15
Thr Pro Thr Pro Gly Ile Thr Ser Gln Glu Gln Ser Glu Ser Phe Arg
 20 25 30
Lys Val Arg Thr Asn Arg Val Ser Pro Ile Arg Ile Arg Pro Arg Gly
 35 40 45
Arg Asp Leu Val Lys Arg Ser Ser Arg Gly Ser Ser Gln Asp His Asp
 50 55 60
Leu Glu Cys Cys Ser Arg Pro Glu Thr Val Gly Thr Arg Ala Ile Ser
 65 70 75 80
Tyr Asn Phe Lys Asp Ile Gly Phe Ala Pro Cys Gly Glu Asp Trp Arg
 85 90 95
Thr Met Arg Lys Leu Ser Val Val Glu Leu Phe Ser Ser Lys Lys Leu
 100 105 110
Gln Ser Phe Arg Tyr Ile Arg Glu Glu Glu Asn Asp Leu Cys Val Lys
 115 120 125
Lys Leu Ser Asp Leu Ala Ser Arg Arg Ser Leu Val Asn Leu Glu Lys

```

|                                                                     |     |     |
|---------------------------------------------------------------------|-----|-----|
| 130                                                                 | 135 | 140 |
| Thr Leu Phe Thr Leu Val Gly Ser Ile Val Cys Arg Ile Gly Phe Gly     |     |     |
| 145                                                                 | 150 | 155 |
| Ile Asn Leu Arg Glu Cys Glu Phe Val Asp Glu Asp Ser Ile Asp Asp     |     |     |
|                                                                     | 165 | 170 |
| Leu Val His Lys Ser Ser Glu Asp Val Ile Arg Asn Ser Ile Phe Ser Asp |     |     |
|                                                                     | 180 | 185 |
| Phe Phe Pro Gly Leu Met Gly Arg Leu Ile Glu Trp Ile Phe Ser Glu     |     |     |
|                                                                     | 195 | 200 |
| Arg Lys Arg Leu Asn Arg Leu Tyr Ser Glu Val Asp Thr Phe Phe Gln     |     |     |
|                                                                     | 210 | 215 |
| Asn Ile Leu Asp Asp His Leu Lys Pro Gly Arg Glu Ser Ser Asp Ile     |     |     |
| 225                                                                 | 230 | 235 |
| Ile Asp Val Met Ile Asp Met Met Lys Lys Gln Glu Lys Glu Gly Asp     |     |     |
|                                                                     | 245 | 250 |
| Ser Phe Lys Phe Thr Thr Asp His Leu Lys Gly Met Ile Ser Asp Ile     |     |     |
|                                                                     | 260 | 265 |
| Phe Leu Ala Gly Val Gly Thr Ser Ser Thr Thr Leu Ile Trp Ala Met     |     |     |
|                                                                     | 275 | 280 |
| Thr Glu Leu Ile Arg Asn Pro Arg Val Met Lys Lys Val Gln Asp Glu     |     |     |
|                                                                     | 290 | 295 |
| Ile Arg Thr Thr Leu Gly Asp Lys Lys Glu Arg Ile Thr Glu Glu Asp     |     |     |
| 305                                                                 | 310 | 315 |
| Leu Asn Gln Leu His Tyr Phe Lys Leu Met Val Lys Glu Ile Phe Arg     |     |     |
|                                                                     | 325 | 330 |
| Leu His Pro Ala Ala Pro Leu Leu Leu Pro Arg Glu Thr Leu Ser His     |     |     |
|                                                                     | 340 | 345 |
| Val Lys Ile Gln Gly Tyr Asp Ile Pro Ala Lys Thr Gln Ile Met Ile     |     |     |
|                                                                     | 355 | 360 |
| Asn Ala Tyr Ala Ile Ala Arg Asp Pro Lys Leu Trp Thr Asn Pro Asp     |     |     |
|                                                                     | 370 | 375 |
| Glu Phe Asn Pro Asp Arg Phe Leu Asp Ser Ser Ile Asp Tyr Arg Gly     |     |     |
| 385                                                                 | 390 | 395 |
| Leu Asn Phe Glu Leu Leu Pro Phe Gly Ser Gly Arg Arg Ile Cys Pro     |     |     |
|                                                                     | 405 | 410 |
| Gly Met Thr Met Gly Ile Ala Ile Val Glu Leu Gly Leu Leu Asn Leu     |     |     |
|                                                                     | 420 | 425 |
| Leu Tyr Phe Phe Asp Trp Gly Leu Pro Glu Lys Glu Glu Ala Lys Glu     |     |     |
|                                                                     | 435 | 440 |
| Ile Ile Thr Gly Asn Glu Val Ala Leu Asp Leu Val Gln Val Phe Leu     |     |     |
|                                                                     | 450 | 455 |
|                                                                     |     | 460 |

His  
465

(2) INFORMATION FOR SEQ ID NO:1959:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..368

(D) OTHER INFORMATION: / Ceres Seq. ID 1571448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1959:

|                                                                 |
|-----------------------------------------------------------------|
| Met Arg Lys Leu Ser Val Val Glu Leu Phe Ser Ser Lys Lys Leu Gln |
| 1 5 10 15                                                       |
| Ser Phe Arg Tyr Ile Arg Glu Glu Glu Asn Asp Leu Cys Val Lys Lys |
| 20 25 30                                                        |
| Leu Ser Asp Leu Ala Ser Arg Arg Ser Leu Val Asn Leu Glu Lys Thr |
| 35 40 45                                                        |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Phe | Thr | Leu | Val | Gly | Ser | Ile | Val | Cys | Arg | Ile | Gly | Phe | Gly | Ile |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Leu | Arg | Glu | Cys | Glu | Phe | Val | Asp | Glu | Asp | Ser | Ile | Asp | Asp | Leu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Val | His | Lys | Ser | Glu | Asp | Val | Ile | Arg | Asn | Ser | Ile | Phe | Ser | Asp | Phe |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Pro | Gly | Leu | Met | Gly | Arg | Leu | Ile | Glu | Trp | Ile | Phe | Ser | Glu | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Lys | Arg | Leu | Asn | Arg | Leu | Tyr | Ser | Glu | Val | Asp | Thr | Phe | Phe | Gln | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     | 125 |     |
| Ile | Leu | Asp | Asp | His | Leu | Lys | Pro | Gly | Arg | Glu | Ser | Ser | Asp | Ile | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Val | Met | Ile | Asp | Met | Met | Lys | Lys | Gln | Glu | Lys | Glu | Gly | Asp | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Phe | Lys | Phe | Thr | Thr | Asp | His | Leu | Lys | Gly | Met | Ile | Ser | Asp | Ile | Phe |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Ala | Gly | Val | Gly | Thr | Ser | Ser | Thr | Thr | Leu | Ile | Trp | Ala | Met | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Glu | Leu | Ile | Arg | Asn | Pro | Arg | Val | Met | Lys | Lys | Val | Gln | Asp | Glu | Ile |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| Arg | Thr | Thr | Leu | Gly | Asp | Lys | Lys | Glu | Arg | Ile | Thr | Glu | Glu | Asp | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asn | Gln | Leu | His | Tyr | Phe | Lys | Leu | Met | Val | Lys | Glu | Ile | Phe | Arg | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| His | Pro | Ala | Ala | Pro | Leu | Leu | Leu | Pro | Arg | Glu | Thr | Leu | Ser | His | Val |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Ile | Gln | Gly | Tyr | Asp | Ile | Pro | Ala | Lys | Thr | Gln | Ile | Met | Ile | Asn |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Ala | Tyr | Ala | Ile | Ala | Arg | Asp | Pro | Lys | Leu | Trp | Thr | Asn | Pro | Asp | Glu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     |     | 285 |     |
| Phe | Asn | Pro | Asp | Arg | Phe | Leu | Asp | Ser | Ser | Ile | Asp | Tyr | Arg | Gly | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asn | Phe | Glu | Leu | Leu | Pro | Phe | Gly | Ser | Gly | Arg | Arg | Ile | Cys | Pro | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Met | Thr | Met | Gly | Ile | Ala | Ile | Val | Glu | Leu | Gly | Leu | Leu | Asn | Leu | Leu |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Tyr | Phe | Phe | Asp | Trp | Gly | Leu | Pro | Glu | Lys | Glu | Glu | Ala | Lys | Glu | Ile |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ile | Thr | Gly | Asn | Glu | Val | Ala | Leu | Asp | Leu | Val | Gln | Val | Phe | Leu | His |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     |     |     | 365 |     |

(2) INFORMATION FOR SEQ ID NO:1960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1221
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1960:

|             |             |             |            |            |             |     |
|-------------|-------------|-------------|------------|------------|-------------|-----|
| atattttcttc | ttctcttccaa | tttacagttc  | tctgcacctt | ttactttccc | ctgtttttttg | 60  |
| atcctcaatc  | accaaaacct  | agcttggtct  | tctgttgatt | atttcgaaaa | gggggtttgt  | 120 |
| ttgtttttctg | ggaatcagca  | aaaatcacga  | aatggttgcc | ttaatatctc | aatcgggata  | 180 |
| aaatcgatcg  | aaaatgagtc  | agccttctgt  | gattcttgct | acggttagct | atgatcacac  | 240 |
| catccgattc  | tgggaagccg  | aamctggctg  | ctgttacccg | accattcagt | atctcgattc  | 300 |
| gcattgaaat  | aggcttgaga  | taaccccgaga | taagcattat | ctagctgcag | cttgcaatcc  | 360 |
| tcataattcga | ctctttgatg  | tcaattccaa  | tagtctccaa | cctgtgatga | cttacgattc  | 420 |



```

acacaccaac aatgtttatg cagtaggatt tcaatgtgat gcaaaatgga tgtattcagg 480
atcagaagat ggcacagtta agatctggga cttaagggct ccgggttgcc aaaaggagta 540
tgaaagtgtt gcagcggtta atacagttgt ttacaccca aatcagactg aattgatatc 600
tggagaccaa aatggaata tacgtgtatg ggatctcaga gcaaatctgt gtactgtgga 660
actggtacca gaagttgata cagctgtacg gtctttaact gttatgtggg atgggacaat 720
ggtagtcgct gctaacaacc gtggCaacat gttatgtatg gcgcttggg cgtgghaaac 780
agacaatgac agagtttgag ccccttcata agctgcaagc tcataatgac cacatcctta 840
aatgtctcct ctctcctgca aacaaatata tagcgactgc atcatctgat aaaactgtca 900
aaatatggaa cgtcgatggt ttcaaaactg agaaaagttt aacaggacat caaagatggg 960
tttGggactg cgtctctcca gtggatggag aatttcttgt aacagcatca tcggacatga 1020
cggctagatt gtggtcgatg ccagcaggca aagaagttaa agtataccaa ggctatcaca 1080
aagccactgt gtgctgtgca ctccacgact aaaaccttaa taagaatgaa agctaaatta 1140
tgaacaaact acgattgtgt ttttgtgt ttagttaaact ctgtacatt tcaatcgaat 1200
tcgttcaaat tgctcttatg t

```

(2) INFORMATION FOR SEQ ID NO:1961:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..201

(D) OTHER INFORMATION: / Ceres Seq. ID 1571461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1961:

```

Met Ser Gln Pro Ser Val Ile Leu Ala Thr Ala Ser Tyr Asp His Thr
1 5 10 15
Ile Arg Phe Trp Glu Ala Glu Xaa Gly Arg Cys Tyr Arg Thr Ile Gln
 20 25 30
Tyr Pro Asp Ser His Val Asn Arg Leu Glu Ile Thr Pro Asp Lys His
 35 40 45
Tyr Leu Ala Ala Ala Cys Asn Pro His Ile Arg Leu Phe Asp Val Asn
50 55 60
Ser Asn Ser Pro Gln Pro Val Met Thr Tyr Asp Ser His Thr Asn Asn
65 70 75
Val Met Ala Val Gly Phe Gln Cys Asp Ala Lys Trp Met Tyr Ser Gly
 85 90 95
Ser Glu Asp Gly Thr Val Lys Ile Trp Asp Leu Arg Ala Pro Gly Cys
 100 105 110
Gln Lys Glu Tyr Glu Ser Val Ala Ala Val Asn Thr Val Val Leu His
 115 120 125
Pro Asn Gln Thr Glu Leu Ile Ser Gly Asp Gln Asn Gly Asn Ile Arg
130 135 140
Val Trp Asp Leu Arg Ala Asn Ser Cys Ser Cys Glu Leu Val Pro Glu
145 150 155 160
Val Asp Thr Ala Val Arg Ser Leu Thr Val Met Trp Asp Gly Thr Met
 165 170 175
Val Val Ala Ala Asn Asn Arg Gly Asn Met Leu Cys Met Ala Leu Val
 180 185 190
Ala Trp Xaa Thr Asp Asn Asp Arg Val
 195 200

```

(2) INFORMATION FOR SEQ ID NO:1962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1571462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1962:

```
Met Thr Tyr Asp Ser His Thr Asn Asn Val Met Ala Val Gly Phe Gln
1 5 10 15
Cys Asp Ala Lys Trp Met Tyr Ser Gly Ser Glu Asp Gly Thr Val Lys
 20 25 30
Ile Trp Asp Leu Arg Ala Pro Gly Cys Gln Lys Glu Tyr Glu Ser Val
 35 40 45
Ala Ala Val Asn Thr Val Val Leu His Pro Asn Gln Thr Glu Leu Ile
 50 55 60
Ser Gly Asp Gln Asn Gly Asn Ile Arg Val Trp Asp Leu Arg Ala Asn
 65 70 75 80
Ser Cys Ser Cys Glu Leu Val Pro Glu Val Asp Thr Ala Val Arg Ser
 85 90 95
Leu Thr Val Met Trp Asp Gly Thr Met Val Val Ala Ala Asn Asn Arg
 100 105 110
Gly Asn Met Leu Cys Met Ala Leu Val Ala Trp Xaa Thr Asp Asn Asp
 115 120 125
Arg Val
 130
```

(2) INFORMATION FOR SEQ ID NO:1963:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1571463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1963:

```
Met Ala Val Gly Phe Gln Cys Asp Ala Lys Trp Met Tyr Ser Gly Ser
1 5 10 15
Glu Asp Gly Thr Val Lys Ile Trp Asp Leu Arg Ala Pro Gly Cys Gln
 20 25 30
Lys Glu Tyr Glu Ser Val Ala Ala Val Asn Thr Val Val Leu His Pro
 35 40 45
Asn Gln Thr Glu Leu Ile Ser Gly Asp Gln Asn Gly Asn Ile Arg Val
 50 55 60
Trp Asp Leu Arg Ala Asn Ser Cys Ser Cys Glu Leu Val Pro Glu Val
 65 70 75 80
Asp Thr Ala Val Arg Ser Leu Thr Val Met Trp Asp Gly Thr Met Val
 85 90 95
Val Ala Ala Asn Asn Arg Gly Asn Met Leu Cys Met Ala Leu Val Ala
 100 105 110
Trp Xaa Thr Asp Asn Asp Arg Val
 115 120
```

(2) INFORMATION FOR SEQ ID NO:1964:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1636 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1636

(D) OTHER INFORMATION: / Ceres Seq. ID 1571464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1964:

```

acttcccttt gttcccaaaa ttctcgaaat cgaaacacga cttaaaacga aaaagacgag 60
acttttaaca ctcagacact aaccaacact ctctctcttt ctatctctct ctgcgcgcatc 120
ggaagcagat ttctctcaaa aggtggattt caacgaagct tagtgagcta aaggtcttcta 180
tcgatcaaat caagtctgac ccttcctctt tcaactactcc ttcaactctcc ttcttccgtg 240
actatctcga gagctcttgt gctaagatac ctacttgtgt ccatgaagaa gacaaagaca 300
ctaagccgag gagtttctga gtggaagaga gtgatgatga tatggatgaa actgaagaag 360
taaaaccgaa agtggaggaa gaagaagaag aggtatgagat tgttgaatct gatgtagagc 420
ttgaaggaga cactgttgag cctgataatg atctctctca gaagatgggg gattcatcag 480
tgagggtgac tgatgagaat cgtgaagctg ctcaagaagc taaggggcaaa gcCatggagg 540
ccctttctga aggaaacttt gatgaagcaa ttgagcattt aactcgggca ataacgttga 600
accgcacttc agctattatg tatgaaacaa gagctagtgt ctacattaaq ttgaagaagc 660
caaacctgcg tattcgaagt gcaaacgcag cattggagat taacctgatg tctgccaag 720
gatacaagtc acgagggtatg gctcgtgcca tgcttgagaa atgggcagag gctgcaaaag 780
accttcacct tgcactctac atagactatg atgaggaaat tagtgctgtt ctcaaaaagg 840
ttgaacctaa tgcacataag cttgaggagc accgtagaaa gtatgacaga ttacgttaagg 900
aaaagagaga caaaaaagct gaacgggata gattactctg ccgtgctgaa gcacagcgtg 960
cctatgataa agctaagaaa caagaacagt catcacttag cagaccatca ggagcggtt 1020
tcccaggagg tatgcccggt gggttccccag gaggatgccc cgggtgagtc ccaggaggaa 1080
tgaggagcat gcccgcgga gttccgggag gaatgggtgg tatggcggtt atggccggtg 1140
gattccagag aggaatgggc ggtggtatgc ctgcaggaaat gggcggtggt atggccggaa 1200
tgggcggtgg taatgcctgt ggaatgggtg gtggcggtat gccagggtga ggcggtggt 1260
tgccgtggtg tgccggtatg cctggtggtg tggaacttcag caaaatatgt aatgatcctg 1320
agctaatagc ggcatttagc gaacctgaag tcaatggctg tctcaagaat gtgatgaaga 1380
accctgcgaa cctagcgaag catcaggcga atccgaaggt ggctcccgtg attgcaaga 1440
tgatggcga atttgacaga cctcagtaaa caaaacaaga agcttgcttt tctttgcgaa 1500
ttctgtgtt taattgcgtg agataagaga tatgttggag aacttttttt tctttttat 1560
ttgtcgttc agaggaactt taacaggaa aaaaactctt tctcttcgtt agtaactcac 1620
ctctctctct tttttt

```

(2) INFORMATION FOR SEQ ID NO:1965:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..441

(D) OTHER INFORMATION: / Ceres Seq. ID 1571465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1965:

```

Met Asp Ser Thr Lys Leu Ser Glu Leu Lys Val Phe Ile Asp Gln Cys
1 5 10 15
Lys Ser Asp Pro Ser Leu Leu Thr Thr Pro Ser Leu Ser Phe Phe Arg
20 25 30
Asp Tyr Leu Glu Ser Leu Gly Ala Lys Ile Pro Thr Gly Val His Glu
35 40 45
Glu Asp Lys Asp Thr Lys Pro Arg Ser Phe Val Val Glu Glu Ser Asp
50 55 60
Asp Asp Met Asp Glu Thr Glu Glu Val Lys Pro Lys Val Glu Glu Glu
65 70 75 80
Glu Glu Glu Asp Glu Ile Val Glu Ser Asp Val Glu Leu Glu Gly Asp
85 90 95
Thr Val Glu Pro Asp Asn Asp Pro Pro Gln Lys Met Gly Asp Ser Ser
100 105 110
Val Glu Val Thr Asp Glu Asn Arg Glu Ala Ala Gln Glu Ala Lys Gly
115 120 125
Lys Ala Met Glu Ala Leu Ser Glu Gly Asn Phe Asp Glu Ala Ile Glu
130 135 140
His Leu Thr Arg Ala Ile Thr Leu Asn Pro Thr Ser Ala Ile Met Tyr
145 150 155 160
Gly Asn Arg Ala Ser Val Tyr Ile Lys Leu Lys Lys Pro Asn Ala Ala

```

(2) INFORMATION FOR SEQ ID NO:1966:

(A) LENGTH: 375 amino acids

(C) STRANDEDNESS:

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..375

(D) OTHER INFORMATION: / Ceres Seq. ID 1571466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1966:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Glu | Thr | Glu | Glu | Val | Lys | Pro | Lys | Val | Glu | Glu | Glu | Glu | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Asp | Glu | Ile | Val | Glu | Ser | Asp | Val | Glu | Leu | Glu | Gly | Asp | Thr | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Pro | Asp | Asn | Asp | Pro | Pro | Gln | Lys | Met | Gly | Asp | Ser | Ser | Val | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Thr | Asp | Glu | Asn | Arg | Glu | Ala | Gln | Glu | Ala | Lys | Gly | Lys | Ala |     |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Met | Glu | Ala | Leu | Ser | Glu | Gly | Asn | Phe | Asp | Glu | Ala | Ile | Glu | His | Leu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Arg | Ala | Ile | Thr | Leu | Asn | Pro | Thr | Ser | Ala | Ile | Met | Tyr | Gly | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Arg | Ala | Ser | Val | Tyr | Ile | Lys | Leu | Lys | Lys | Pro | Asn | Ala | Ala | Ile | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Asp Ala Asn Ala Ala Leu Glu Ile Asn Pro Asp Ser Ala Lys Gly Tyr  
115 120 125  
Lys Ser Arg Gly Met Ala Arg Ala Met Leu Gly Glu Trp Ala Glu Ala  
130 135 140  
Ala Lys Asp Leu His Leu Ala Ser Thr Ile Asp Tyr Asp Glu Glu Ile  
145 150 155 160  
Ser Ala Val Leu Lys Lys Val Glu Pro Asn Ala His Lys Leu Glu Glu  
165 170 175  
His Arg Arg Lys Tyr Asp Arg Leu Arg Lys Glu Arg Glu Asp Lys Lys  
180 185 190  
Ala Glu Arg Asp Arg Leu Arg Arg Ala Glu Ala Gln Ala Ala Tyr  
195 200 205  
Asp Lys Ala Lys Lys Glu Glu Gln Ser Ser Ser Ser Arg Pro Ser Gly  
210 215 220  
Gly Gly Phe Pro Gly Gly Met Pro Gly Gly Phe Pro Gly Gly Met Pro  
225 230 235 240  
Gly Gly Phe Pro Gly Gly Met Gly Gly Met Pro Gly Gly Phe Pro Gly  
245 250 255  
Gly Met Gly Gly Met Gly Gly Met Pro Gly Gly Phe Pro Gly Gly Met  
260 265 270  
Gly Gly Gly Met Pro Ala Gly Met Gly Gly Met Pro Gly Met Gly  
275 280 285  
Gly Gly Met Pro Ala Gly Met Gly Gly Gly Gly Met Pro Gly Ala Gly  
290 295 300  
Gly Gly Met Pro Gly Gly Gly Met Pro Gly Gly Met Asp Phe Ser  
305 310 315 320  
Lys Ile Leu Asn Asp Pro Glu Leu Met Thr Ala Phe Ser Asp Pro Glu  
325 330 335  
Val Met Ala Ala Leu Gln Asp Val Met Lys Asn Pro Ala Asn Leu Ala  
340 345 350  
Lys His Gln Ala Asn Pro Lys Val Ala Pro Val Ile Ala Lys Met Met  
355 360 365  
Gly Lys Phe Ala Gly Pro Gln  
370 375

(2) INFORMATION FOR SEQ ID NO:1967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..334
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1967:

Met Gly Asp Ser Ser Val Glu Val Thr Asp Glu Asn Arg Glu Ala Ala  
1 5 10 15  
Gln Glu Ala Lys Gly Lys Ala Met Glu Ala Leu Ser Glu Gly Asn Phe  
20 25 30  
Asp Glu Ala Ile Glu His Leu Thr Arg Ala Ile Thr Leu Asn Pro Thr  
35 40 45  
Ser Ala Ile Met Tyr Gly Asn Arg Ala Ser Val Tyr Ile Lys Leu Lys  
50 55 60  
Lys Pro Asn Ala Ala Ile Arg Asp Ala Asn Ala Ala Leu Glu Ile Asn  
65 70 75 80  
Pro Asp Ser Ala Lys Gly Tyr Lys Ser Arg Gly Met Ala Arg Ala Met  
85 90 95  
Leu Gly Glu Trp Ala Glu Ala Ala Lys Asp Leu His Leu Ala Ser Thr  
100 105 110  
Ile Asp Tyr Asp Glu Glu Ile Ser Ala Val Leu Lys Lys Val Glu Pro

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 115                                                             | 120 | 125 |
| Asn Ala His Lys Leu Glu Glu His Arg Arg Lys Tyr Asp Arg Leu Arg |     |     |
| 130                                                             | 135 | 140 |
| Lys Glu Arg Glu Asp Lys Lys Ala Glu Arg Asp Arg Leu Arg Arg Arg |     |     |
| 145                                                             | 150 | 155 |
| Ala Glu Ala Gln Ala Ala Tyr Asp Lys Ala Lys Lys Glu Glu Gln Ser |     |     |
| 165                                                             | 170 | 175 |
| Ser Ser Ser Arg Pro Ser Gly Gly Gly Phe Pro Gly Gly Met Pro Gly |     |     |
| 180                                                             | 185 | 190 |
| Gly Phe Pro Gly Gly Met Pro Gly Gly Phe Pro Gly Gly Met Gly Gly |     |     |
| 195                                                             | 200 | 205 |
| Met Pro Gly Gly Phe Pro Gly Gly Met Gly Gly Met Gly Met Pro     |     |     |
| 210                                                             | 215 | 220 |
| Gly Gly Phe Pro Gly Gly Met Gly Gly Gly Met Pro Ala Gly Met Gly |     |     |
| 225                                                             | 230 | 235 |
| Gly Gly Met Pro Gly Met Gly Gly Gly Met Pro Ala Gly Met Gly Gly |     |     |
| 245                                                             | 250 | 255 |
| Gly Gly Met Pro Gly Ala Gly Gly Gly Met Pro Gly Gly Gly Gly Met |     |     |
| 260                                                             | 265 | 270 |
| Pro Gly Gly Met Asp Phe Ser Lys Ile Leu Asn Asp Pro Glu Leu Met |     |     |
| 275                                                             | 280 | 285 |
| Thr Ala Phe Ser Asp Pro Glu Val Met Ala Ala Leu Gln Asp Val Met |     |     |
| 290                                                             | 295 | 300 |
| Lys Asn Pro Ala Asn Leu Ala Lys His Gln Asn Pro Lys Val Ala     |     |     |
| 305                                                             | 310 | 315 |
| Pro Val Ile Ala Lys Met Met Gly Lys Phe Ala Gly Pro Gln         |     |     |
| 325                                                             | 330 |     |

(2) INFORMATION FOR SEQ ID NO:1968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1968:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| acattccctca | ccaaaccctc  | tccaaaacac  | accacacagt  | acgcacacac  | acaaagacaa  | 60   |
| tgctcccttt  | caaaatatct  | ttcttcacga  | ctctctctgt  | gcggcggttt  | tcagtgctcg  | 120  |
| ctgtcgattt  | caacactgac  | gtcaacgtag  | cttggggaaa  | tgcccggtgg  | aagatactca  | 180  |
| acaaagccca  | gcttcttact  | ctctccctag  | acaaatccct  | tggttccgtt  | tttcaatcca  | 240  |
| aaacagagta  | tttgtttgga  | aagattgata  | tgcagattaa  | gcttgttctt  | ggtaactctg  | 300  |
| caggaaacgt  | cacaactttt  | taoctgagtt  | tatatatttt  | ctttaggagt  | tttaagtgat  | 360  |
| tttggaattg  | gtttttatat  | tgagacttca  | tcttgacatt  | tttgtgtatt  | tcagctctaa  | 420  |
| atccgaagga  | tccactttgg  | atgagattga  | ttttgagttc  | ttgggttaata | tgagtgaggga | 480  |
| tccttatact  | ttcacactta  | atgttttacac | tcaaggtaaa  | ggtagcagaag | agcaacaatt  | 540  |
| ccatctctgg  | ttcgaccctaa | cgcgcaattt  | ccacacttac  | tcaatctctt  | ggaaacctcca | 600  |
| aagaatcata  | ttgaccgtcg  | atgacacacc  | cattagagag  | tttaaaaaat  | atgagtctctt | 660  |
| cggtgtcttg  | tttccaaaga  | acaagccgat  | gaggatgtac  | gcgagtttat  | ggaaagcaga  | 720  |
| cgattggcca  | acaagaggcg  | gtcttgttaa  | aactgattgg  | tctaaagctc  | cattcatggc  | 780  |
| ttcttacaga  | aacattaaaga | ttgactcgaa  | accaaaactcc | aatttggtaca | ctcaagaaat  | 840  |
| ggattcaaca  | agccaagcta  | gactcaaatg  | ggttcagaag  | aattacatga  | tctacaatta  | 900  |
| ttgtactcag  | catagagggt  | ttccacaggg  | agctccctaag | gaatgcacaa  | caagctcata  | 960  |
| gaactcaca   | ttatatctta  | tttatttatc  | tacacttctc  | ctcttctctt  | tatgtgaaaa  | 1020 |
| tttgtgaatc  | tetgttttcta | gcttgtctat  | tatgtccogag | aatttctttt  | tctgtttttg  | 1080 |
| attctttttg  | ttgtakatct  | ttgtccarta  | aaggaaatga  | tgtgtcttta  | cc          |      |

(2) INFORMATION FOR SEQ ID NO:1969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..118  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571469  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1969:  
Ile Pro His Gln Thr Leu Ser Lys Thr His Pro His Val Arg Thr His  
1 5 10 15  
Thr Lys Thr Met Ser Pro Phe Lys Ile Phe Phe Thr Thr Leu Leu  
20 25 30  
Val Ala Ala Phe Ser Val Ser Ala Ala Asp Phe Asn Thr Asp Val Asn  
35 40 45  
Val Ala Trp Gly Asn Gly Arg Gly Lys Ile Leu Asn Asn Gly Gln Leu  
50 55 60  
Leu Thr Leu Ser Leu Asp Lys Ser Ser Gly Ser Gly Phe Gln Ser Lys  
65 70 75 80  
Thr Glu Tyr Leu Phe Gly Lys Ile Asp Met Gln Ile Lys Leu Val Pro  
85 90 95  
Gly Asn Ser Ala Gly Thr Val Thr Thr Phe Tyr Val Ser Leu Tyr Ile  
100 105 110  
Xaa Phe Arg Ser Phe Lys  
115

(2) INFORMATION FOR SEQ ID NO:1970:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 99 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..99  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571470  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1970:  
Met Ser Pro Phe Lys Ile Phe Phe Phe Thr Thr Leu Leu Val Ala Ala  
1 5 10 15  
Phe Ser Val Ser Ala Ala Asp Phe Asn Thr Asp Val Asn Val Ala Trp  
20 25 30  
Gly Asn Gly Arg Gly Lys Ile Leu Asn Asn Gly Gln Leu Leu Thr Leu  
35 40 45  
Ser Leu Asp Lys Ser Ser Gly Ser Gly Phe Gln Ser Lys Thr Glu Tyr  
50 55 60  
Leu Phe Gly Lys Ile Asp Met Gln Ile Lys Leu Val Pro Gly Asn Ser  
65 70 75 80  
Ala Gly Thr Val Thr Thr Phe Tyr Val Ser Leu Tyr Ile Xaa Phe Arg  
85 90 95  
Ser Phe Lys

(2) INFORMATION FOR SEQ ID NO:1971:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 163 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1571471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1971:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gly | Asp | Pro | Tyr | Thr | Leu | His | Thr | Asn | Val | Tyr | Thr | Gln | Gly |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Gly | Asp | Lys | Glu | Gln | Gln | Phe | His | Leu | Trp | Phe | Asp | Pro | Thr | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Phe | His | Thr | Tyr | Ser | Ile | Leu | Trp | Asn | Pro | Gln | Arg | Ile | Ile | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Val | Asp | Asp | Thr | Pro | Ile | Arg | Glu | Phe | Lys | Asn | Tyr | Glu | Ser | Leu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Val | Leu | Phe | Pro | Lys | Asn | Lys | Pro | Met | Arg | Met | Tyr | Ala | Ser | Leu |
| 65  |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Trp | Asn | Ala | Asp | Asp | Trp | Ala | Thr | Arg | Gly | Gly | Leu | Val | Lys | Thr | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Trp | Ser | Lys | Ala | Pro | Phe | Met | Ala | Ser | Tyr | Arg | Asn | Ile | Lys | Ile | Asp |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ser | Lys | Pro | Asn | Ser | Asn | Trp | Tyr | Thr | Gln | Glu | Met | Asp | Ser | Thr | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Ala | Arg | Leu | Lys | Trp | Val | Gln | Lys | Asn | Tyr | Met | Ile | Tyr | Asn | Tyr |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Cys | Thr | Asp | His | Arg | Arg | Phe | Pro | Gln | Gly | Ala | Pro | Lys | Glu | Cys | Thr |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Thr | Ser | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1972:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 733 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..733

(D) OTHER INFORMATION: / Ceres Seq. ID 1571472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1972:

|             |             |             |             |             |              |     |
|-------------|-------------|-------------|-------------|-------------|--------------|-----|
| cccggttcaa  | aaacccaaaa  | ttctagagat  | agaggacggc  | aatgcgatgg  | gggtcatcttt  | 60  |
| ctcgcgcctcc | tttactaaact | ccaccaccgc  | cgccgcgcgtt | cctcctccgt  | cgccaccccttc | 120 |
| atcgccgtca  | cgttccaaatg | taaaatctaa  | cggagaagag  | agacctcgtt  | tcttcgatggg  | 180 |
| aaaggcgaag  | aacaagtgtct | gggctaatagc | tgacatcgta  | cctggctcgac | atcccgcagag  | 240 |
| gtggcgtaaa  | gacgtcgccg  | gtaacatagt  | ctgcaaacgc  | ttcggaattt  | gcaatggttg   | 300 |
| tctctgtttc  | gagtatgata  | acattgtttc  | ttattccaaa  | gggtggagagt | cgaatagcgga  | 360 |
| gaattgtcag  | attcttccaa  | caagagttaa  | caagattcaaa | tcagctccaag | aaaatggtta   | 420 |
| tgccaccact  | cttaagagagt | gtGgcggaag  | ctacggtgtg  | ggaagacggt  | arggaggagg   | 480 |
| atacggttgt  | ggtgaaggag  | gaggttacgg  | aggaagcggt  | gggtgtggag  | gatggtaatt   | 540 |
| cttttaatta  | ggTtttggga  | ttaccaatga  | atgtctctct  | tctcgcttgt  | tatgtctcta   | 600 |
| cttgggtttt  | tgtgtttctc  | attttgtttc  | gggtctgctt  | tagatttgat  | gtaacagcttc  | 660 |
| gtgattaggt  | attttgggat  | ctggaaacgt  | aattttaagt  | cacttgatcat | tctctaaata   | 720 |
| acaaatttct  | tgc         |             |             |             |              |     |

(2) INFORMATION FOR SEQ ID NO:1973:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1571473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1973:



Pro Val Gln Lys Pro Lys Ile Leu Glu Ile Glu Asp Gly Asn Ala Met  
1 5 10 15  
Gly Ser Ser Phe Ser Ala Ser Phe Thr Asn Ser Thr Thr Ala Ala Ala  
20 25 30  
Val Pro Pro Pro Ser Pro Ser Pro Ser Arg Ser Asn Val Lys  
35 40 45  
Ser Asn Gly Glu Glu Arg Pro Arg Phe Phe Asp Gly Lys Ala Lys Asn  
50 55 60  
Lys Cys Trp Ala Asn Ala Asp Ile Val Pro Gly Arg His Pro Glu Arg  
65 70 75 80  
Trp Arg Lys Asp Val Ala Gly Asn Ile Val Cys Lys Arg Phe Gly Asn  
85 90 95  
Cys Asn Gly Cys Leu Cys Phe Glu Tyr Asp His Ile Val Pro Tyr Ser  
100 105 110  
Lys Gly Gly Glu Ser Ile Ala Glu Asn Cys Gln Ile Leu Gln Thr Arg  
115 120 125  
Val Asn Arg Phe Lys Ser Ala Gln Glu Asn Val Asp Ala Thr Thr Leu  
130 135 140  
Lys Ser Gly Gly Gly Ser Tyr Gly Gly Gly Arg Xaa Gly Gly Gly  
145 150 155 160  
Tyr Gly Gly Gly Glu Gly Gly Tyr Gly Gly Ser Gly Gly Gly Gly  
165 170 175  
Gly Trp

(2) INFORMATION FOR SEQ ID NO:1974:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1571474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1974:

Met Gly Ser Ser Phe Ser Ala Ser Phe Thr Asn Ser Thr Thr Ala Ala  
1 5 10 15  
Ala Val Pro Pro Pro Ser Pro Pro Ser Ser Pro Ser Arg Ser Asn Val  
20 25 30  
Lys Ser Asn Gly Glu Glu Arg Pro Arg Phe Phe Asp Gly Lys Ala Lys  
35 40 45  
Asn Lys Cys Trp Ala Asn Ala Asp Ile Val Pro Gly Arg His Pro Glu  
50 55 60  
Arg Trp Arg Lys Asp Val Ala Gly Asn Ile Val Cys Lys Arg Phe Gly  
65 70 75 80  
Asn Cys Asn Gly Cys Leu Cys Phe Glu Tyr Asp His Ile Val Pro Tyr  
85 90 95  
Ser Lys Gly Gly Glu Ser Ile Ala Glu Asn Cys Gln Ile Leu Gln Thr  
100 105 110  
Arg Val Asn Arg Phe Lys Ser Ala Gln Glu Asn Val Asp Ala Thr Thr  
115 120 125  
Leu Lys Ser Gly Gly Gly Ser Tyr Gly Gly Gly Arg Arg Xaa Gly Gly  
130 135 140  
Gly Tyr Gly Gly Gly Glu Gly Gly Gly Tyr Gly Gly Ser Gly Gly Gly  
145 150 155 160  
Gly Gly Trp

(2) INFORMATION FOR SEQ ID NO:1975:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1406 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1406

(D) OTHER INFORMATION: / Ceres Seq. ID 1571479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1975:

|             |            |            |             |             |             |      |
|-------------|------------|------------|-------------|-------------|-------------|------|
| aatttttttga | gtttttgtct | cgaaaccgg  | tttaacccaa  | gaaccccaag  | atctctctct  | 60   |
| atttggtttgc | ctttctcttt | ctttctgact | caaacctctta | aatcaattct  | cgcgatttaa  | 120  |
| caaaacctta  | gatttattct | actcttcgaa | gtcgatttca  | atggaagggt  | ctctgcgcgc  | 180  |
| catcgcgagg  | aagacatggg | agctagagaa | caacattctc  | cgagtggaa   | caaccgattc  | 240  |
| agcctccgac  | agtatattcc | actacgagca | cgcttcacaa  | gccaaaaatcc | agcaggagaa  | 300  |
| gccattggcc  | tcggatccca | actacttcaa | gcgcgttcc   | atctcagccc  | ttgctctctt  | 360  |
| caagatgggt  | gttcacgcgt | gtcccggtgg | cacaatcgag  | atcatggggt  | ttatgcaggg  | 420  |
| taaaacgcag  | gggtatatac | tcactgttat | ggatgctttt  | gctttgctgt  | ttgaagggtac | 480  |
| tgagactagg  | gttaatgctc | agtctgatgc | ctatgagtat  | atgggttgat  | actctcagac  | 540  |
| cagcaagctg  | gctggggagg | tgagaaacgt | tgttggtgg   | tatcactctc  | accttcgggt  | 600  |
| tggatgtttg  | ctctcgggta | ttgatgtttc | gacacagatg  | cttaaccaac  | agtatcagga  | 660  |
| gccattctta  | gctgtttgta | ttgatccaac | aaggactgtt  | tcggctggta  | aggttgagat  | 720  |
| tggggcattc  | agaacatatt | cagagggaca | taagatctcg  | gatgatcatg  | tttctgagta  | 780  |
| tcagactatc  | ccctttaaca | agattgagga | ctttggtgta  | ctttgcaaac  | agactactc   | 840  |
| attggacatc  | acttatttca | agtcactctc | cgaatgctac  | catttgagtc  | tcctttggaa  | 900  |
| caagtatctg  | gtgaacactc | ttctctcttc | cccactgttg  | ggcaaatggag | actatgttgc  | 960  |
| cgggcaaatc  | tcagactttg | ctgagaagct | cgagcaagcg  | gagagtacgc  | tcgttaactc  | 1020 |
| ccggtatggA  | aggaatttcg | Cccagccggt | caccAaaagg  | aggaagagg   | atgagctcA   | 1080 |
| aactccgcaa  | gataactcgg | gatagtgcaa | agataactgt  | cagcagctc   | atggactaa   | 1140 |
| tgtcacaggt  | tatcaagag  | atctgtttca | attccgctcg  | tcagtccaag  | aagtctgctg  | 1200 |
| acgactcatc  | agatccagag | cccatgatta | ctcgtgaa    | ttggtctatt  | ctttgtttt   | 1260 |
| ttggctcggg  | aaattgacta | tcggtttgac | ccggtttatg  | agggcaatgc  | cattgttccc  | 1320 |
| tatatctcta  | gtgtagtatt | tgcttcagac | aaagatcttt  | gggttattaa  | atgacattaa  | 1380 |
| cataaatcga  | cttaattggt | tttgcg     |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1976:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..314

(D) OTHER INFORMATION: / Ceres Seq. ID 1571480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1976:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Gly | Ser | Ser | Ser | Ala | Ile | Ala | Arg | Lys | Thr | Trp | Glu | Leu | Glu |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asn | Asn | Ile | Leu | Arg | Val | Glu | Pro | Thr | Asp | Ser | Ala | Ser | Asp | Ser | Ile |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Phe | His | Tyr | Asp | Asp | Ala | Ser | Gln | Ala | Lys | Ile | Gln | Gln | Glu | Lys | Pro |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Trp | Ala | Ser | Asp | Pro | Asn | Tyr | Phe | Lys | Arg | Val | His | Ile | Ser | Ala | Leu |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ala | Leu | Leu | Lys | Met | Val | Val | His | Ala | Arg | Ser | Gly | Gly | Thr | Ile | Glu |  |
|     |     |     | 65  |     |     | 70  |     |     |     |     | 75  |     |     | 80  |     |  |
| Ile | Met | Gly | Leu | Met | Gln | Gly | Lys | Thr | Glu | Gly | Asp | Thr | Ile | Ile | Val |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Met | Asp | Ala | Phe | Ala | Leu | Pro | Val | Glu | Gly | Thr | Glu | Thr | Arg | Val | Asn |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ala | Gln | Ser | Asp | Ala | Tyr | Glu | Tyr | Met | Val | Glu | Tyr | Ser | Gln | Thr | Ser |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |

Lys Leu Ala Gly Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His  
130 135 140  
Pro Gly Tyr Gly Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Met  
145 150 155 160  
Leu Asn Gln Gln Tyr Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro  
165 170 175  
Thr Arg Thr Val Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr  
180 185 190  
Tyr Pro Glu Gly His Lys Ile Ser Asp Asp His Val Ser Glu Tyr Gln  
195 200 205  
Thr Ile Pro Leu Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln  
210 215 220  
Tyr Tyr Ser Leu Asp Ile Thr Tyr Phe Lys Ser Ser Leu Asp Ser His  
225 230 235 240  
Leu Leu Asp Leu Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser  
245 250 255  
Ser Pro Leu Leu Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp  
260 265 270  
Leu Ala Glu Lys Leu Glu Gln Ala Glu Ser Gln Leu Ala Asn Ser Arg  
275 280 285  
Tyr Gly Arg Asn Cys Ala Gln Pro Val Thr Lys Arg Arg Lys Glu Asp  
290 295 300  
Glu Pro Gln Thr Arg Glu Asp Asn Ser Gly  
305 310

(2) INFORMATION FOR SEQ ID NO:1977:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..246

(D) OTHER INFORMATION: / Ceres Seq. ID 1571481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1977:

Met Val Val His Ala Arg Ser Gly Gly Thr Ile Glu Ile Met Gly Leu  
1 5 10 15  
Met Gln Gly Lys Thr Glu Gly Asp Thr Ile Ile Val Met Asp Ala Phe  
20 25 30  
Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn Ala Gln Ser Asp  
35 40 45  
Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Ser Lys Leu Ala Gly  
50 55 60  
Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His Pro Gly Tyr Gly  
65 70 75 80  
Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Met Leu Asn Gln Gln  
85 90 95  
Tyr Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro Thr Arg Thr Val  
100 105 110  
Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr Tyr Pro Glu Gly  
115 120 125  
His Lys Ile Ser Asp Asp His Val Ser Glu Tyr Gln Thr Ile Pro Leu  
130 135 140  
Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln Tyr Tyr Ser Leu  
145 150 155 160  
Asp Ile Thr Tyr Phe Lys Ser Ser Leu Asp Ser His Leu Leu Asp Leu  
165 170 175  
Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser Ser Pro Leu Leu  
180 185 190  
Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp Leu Ala Glu Lys

195 200 205  
Leu Gly Gln Ala Glu Ser Gln Leu Ala Asn Ser Arg Tyr Gly Arg Asn  
210 215 220  
Cys Ala Gln Pro Val Thr Lys Arg Arg Lys Glu Asp Glu Pro Gln Thr  
225 230 235 240  
Arg Glu Asp Asn Ser Gly  
245

(2) INFORMATION FOR SEQ ID NO:1978:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..233

(D) OTHER INFORMATION: / Ceres Seq. ID 1571482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1978:

Met Gly Leu Met Gln Gly Lys Thr Glu Gly Asp Thr Ile Ile Val Met  
1 5 10 15  
Asp Ala Phe Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn Ala  
20 25 30  
Gln Ser Asp Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Ser Lys  
35 40 45  
Leu Ala Gly Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His Pro  
50 55 60  
Gly Tyr Gly Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Met Leu  
65 70 75 80  
Asn Gln Gln Tyr Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro Thr  
85 90 95  
Arg Thr Val Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr Tyr  
100 105 110  
Pro Glu Gly His Lys Ile Ser Asp Asp His Val Ser Glu Tyr Gln Thr  
115 120 125  
Ile Pro Leu Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln Tyr  
130 135 140  
Tyr Ser Leu Asp Ile Thr Tyr Phe Lys Ser Ser Leu Asp Ser His Leu  
145 150 155 160  
Leu Asp Leu Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser Ser  
165 170 175  
Pro Leu Leu Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp Leu  
180 185 190  
Ala Glu Lys Leu Glu Gln Ala Glu Ser Gln Leu Ala Asn Ser Arg Tyr  
195 200 205  
Gly Arg Asn Cys Ala Gln Pro Val Thr Lys Arg Arg Lys Glu Asp Glu  
210 215 220  
Pro Gln Thr Arg Glu Asp Asn Ser Gly  
225 230

(2) INFORMATION FOR SEQ ID NO:1979:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1654 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1654

(D) OTHER INFORMATION: / Ceres Seq. ID 1571483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1979:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| acmatwacyt  | agaacatcct  | aatacaaaact | gcttcgcgcca | ttgctcgaaa  | atcgcgctctt | 60   |
| ctgacaatgt  | gctgaacagt  | agtcacgcgc  | cgagtttagca | aagtgaacact | tcgaagatttc | 120  |
| tctttaccta  | atctcaaggtt | tctggattttg | taagaaacccg | cgtttacaaa  | atgttcaagt  | 180  |
| tgaagcaatg  | gttgatttat  | ttgggtgtatt | cgtttagtaat | aatgaacaca  | gaaggactgt  | 240  |
| ttgtcaaat   | tacatttgtt  | cgaaacgcag  | tcgctaaagg  | ggcggttgt   | ttagatggaa  | 300  |
| gtccaccagc  | ttatcatttg  | gatagaggtt  | ctggaactgg  | aatcaatagt  | tggttgatc   | 360  |
| agcttgaggg  | aggaggatgg  | tgcaataatg  | taacaaattg  | cgtttagtcg  | atgcatactc  | 420  |
| gattagggtc  | atcgaaagaa  | atgggtggaga | accttgcttt  | ctcagctatt  | cttagcaata  | 480  |
| agaaacaata  | taactcctgat | ttttacaatt  | ggaatagagt  | gaaagttaga  | tactgtgacg  | 540  |
| gggcacatt   | cacaggagat  | gtagaagcag  | tgaacctgcg  | tactaatctt  | cacttcagag  | 600  |
| gtgctcgagt  | ttggttagcc  | gttatgcaag  | agctgctagc  | taaaagcgatg | ataaacgcgc  | 660  |
| agaattcgctg | ttgtctgtgc  | gttctgtcgt  | gcgggttagc  | ttcgctgatg  | ctattgtgata | 720  |
| gtttccgtgc  | tctattaccg  | atgggaacca  | aagtaaaatg  | tctttcagat  | gctgggtttt  | 780  |
| ttctcaacac  | aagagacgct  | tcaggagctc  | aatacattaa  | aacatacttc  | gaagatgttg  | 840  |
| ttactcttca  | tggaacagca  | aagaacttgc  | cgaggctcag  | cacatcaaga  | tttaactcctg | 900  |
| caatgtgttt  | ctttccgcgaa | tatgtggctc  | gccagattag  | aactcctctg  | ttcattcttta | 960  |
| atgcccgttta | tgaactcttg  | cagataaaga  | acattttggc  | tcgcgcgagca | gctgatcctt  | 1020 |
| acggaaaaat  | gcaaaagtgt  | caactagaca  | tcaagaattg  | ccatccaagt  | cagatcaaa   | 1080 |
| ttatgcaaga  | tttcagggtta | gagttcttga  | gtgcagtgat  | aggtttagg   | agatcttcat  | 1140 |
| caagagggat  | gttcatagat  | tcttgcctga  | ctcaactgca  | aaccagagca  | caaatcttcat | 1200 |
| ggttcttgcca | agattctcca  | attctaaacc  | gaacgacaa   | agcaaaagct  | gttgagagatt | 1260 |
| gggtttatga  | cagaaacattg | tttcagaaga  | tagattgtcc  | ttacctctgt  | aacctactct  | 1320 |
| gccaccacag  | ggTttttcac  | tctctagat   | gctcctccaa  | tttaagtgat  | tcatacatat  | 1380 |
| acagatagata | tttattatta  | ttttgaaaag  | aaaattttgct | tataaatatg  | tcatttgtta  | 1440 |
| gatacatata  | gtgaaatatt  | cctagggttt  | agctatagaa  | gatgaaaaag  | aaaaagagt   | 1500 |
| tgataattc   | ttgagtggtg  | agaataagca  | ataggagtaa  | ttttcttcag  | cactgttctt  | 1560 |
| gtgtgctgtt  | taattgtctc  | tgtttctctt  | ctattctgat  | gtaaaatgca  | aattgttacc  | 1620 |

(2) INFORMATION FOR SEQ ID NO:1980:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..411

(D) OTHER INFORMATION: / Ceres Seq. ID 1571484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1980:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Lys | Leu | Lys | Gln | Trp | Leu | Ile | Tyr | Leu | Val | Tyr | Ser | Leu | Val |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Met | Asn | Thr | Glu | Gly | Leu | Phe | Val | Asn | Ile | Thr | Phe | Val | Arg | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ala | Val | Ala | Lys | Gly | Ala | Val | Cys | Leu | Asp | Gly | Ser | Pro | Pro | Ala | Tyr |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| His | Leu | Asp | Arg | Gly | Ser | Gly | Thr | Gly | Ile | Asn | Ser | Trp | Leu | Ile | Gln |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Leu | Glu | Gly | Gly | Gly | Trp | Cys | Asn | Asn | Val | Thr | Asn | Cys | Val | Ser | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Met | His | Thr | Arg | Leu | Gly | Ser | Ser | Lys | Lys | Met | Val | Glu | Asn | Leu | Ala |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Ser | Ala | Ile | Leu | Ser | Asn | Lys | Lys | Gln | Tyr | Asn | Pro | Asp | Phe | Tyr |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Asn | Trp | Asn | Arg | Val | Lys | Val | Arg | Tyr | Cys | Asp | Gly | Ala | Ser | Phe | Thr |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Gly | Asp | Val | Glu | Ala | Val | Asn | Pro | Ala | Thr | Asn | Leu | His | Phe | Arg | Gly |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |
| Ala | Arg | Val | Trp | Leu | Ala | Val | Met | Gln | Glu | Leu | Leu | Ala | Lys | Gly | Met |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ile | Asn | Ala | Glu | Asn | Ala | Val | Leu | Ser | Gly | Cys | Ser | Ala | Gly | Gly | Leu |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Thr | Glu | Gly | Leu | Phe | Val | Asn | Ile | Thr | Phe | Val | Arg | Asn | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ala | Lys | Gly | Ala | Val | Cys | Leu | Asp | Gly | Ser | Pro | Pro | Ala | Tyr | His |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Asp | Arg | Gly | Ser | Gly | Thr | Gly | Ile | Asn | Ser | Trp | Leu | Ile | Gln | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Gly | Gly | Gly | Trp | Cys | Asn | Asn | Val | Thr | Asn | Cys | Val | Ser | Arg | Met |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His | Thr | Arg | Leu | Gly | Ser | Lys | Lys | Met | Val | Glu | Asn | Leu | Ala | Phe |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Ala | Ile | Leu | Ser | Asn | Lys | Lys | Gln | Tyr | Asn | Pro | Asp | Phe | Tyr | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Trp | Asn | Arg | Val | Lys | Val | Arg | Tyr | Cys | Asp | Gly | Ala | Ser | Phe | Thr | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Val | Glu | Ala | Val | Asn | Pro | Ala | Thr | Asn | Leu | His | Phe | Arg | Gly | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Val | Trp | Leu | Ala | Val | Met | Gln | Glu | Leu | Leu | Ala | Lys | Gly | Met | Ile |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ala | Glu | Asn | Ala | Val | Leu | Ser | Gly | Cys | Ser | Ala | Gly | Gly | Leu | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Leu | Met | His | Cys | Asp | Ser | Phe | Arg | Ala | Leu | Leu | Pro | Met | Gly | Thr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |
| Lys | Val | Lys | Cys | Leu | Ser | Asp | Ala | Gly | Phe | Phe | Leu | Asn | Thr | Arg | Asp |
|     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |
| Val | Ser | Gly | Val | Gln | Tyr | Ile | Lys | Thr | Tyr | Phe | Glu | Asp | Val | Val | Thr |
|     |     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Leu | His | Gly | Ser | Ala | Lys | Asn | Leu | Pro | Arg | Ser | Cys | Thr | Ser | Arg | Leu |
|     |     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |
| Thr | Pro | Ala | Met | Cys | Phe | Phe | Pro | Gln | Tyr | Val | Ala | Arg | Gln | Ile | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Thr | Pro | Leu | Phe | Ile | Leu | Asn | Ala | Ala | Tyr | Asp | Ser | Trp | Gln | Ile | Lys |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |
| Asn | Ile | Leu | Ala | Pro | Arg | Ala | Ala | Asp | Pro | Tyr | Gly | Lys | Trp | Gln | Ser |
|     |     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Cys | Gln | Leu | Asp | Ile | Lys | Asn | Cys | His | Pro | Ser | Gln | Ile | Lys | Val | Met |
|     |     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |
| Gln | Asp | Phe | Arg | Leu | Glu | Phe | Leu | Ser | Ala | Val | Ile | Gly | Leu | Gly | Arg |
|     |     |     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |
| Ser | Ser | Ser | Arg | Gly | Met | Phe | Ile | Asp | Ser | Cys | Tyr | Thr | His | Cys | Gln |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Thr | Glu | Thr | Gln | Thr | Ser | Trp | Phe | Trp | Gln | Asp | Ser | Pro | Ile | Leu | Asn |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |
| Arg | Thr | Thr | Ile | Ala | Lys | Ala | Val | Gly | Asp | Trp | Val | Tyr | Asp | Arg | Thr |
|     |     |     |     | 340 |     |     |     |     | 345 |     |     |     |     |     |     |
| Leu | Phe | Gln | Lys | Ile | Asp | Cys | Pro | Tyr | Pro | Cys | Asn | Pro | Thr | Cys | His |
|     |     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |
| His | Arg | Val | Phe | His | Ser | Ser | Arg | Cys | Ser | Ser | Asn | Leu | Ser | Asp | Ser |
|     |     |     |     | 370 |     |     |     | 375 |     |     |     | 380 |     |     |     |
| Thr | Ile | Tyr | Ser | Ile | Asp | Leu | Leu | Leu | Phe |     |     |     |     |     |     |
| 385 |     |     |     |     | 390 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1982:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..331

(D) OTHER INFORMATION: / Ceres Seq. ID 1571486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1982:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Thr | Arg | Leu | Gly | Ser | Ser | Lys | Lys | Met | Val | Glu | Asn | Leu | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Phe | Ser | Ala | Ile | Leu | Ser | Asn | Lys | Lys | Gln | Tyr | Asn | Pro | Asp | Phe | Tyr |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Asn | Trp | Asn | Arg | Val | Lys | Val | Arg | Tyr | Cys | Asp | Gly | Ala | Ser | Phe | Thr |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Gly | Asp | Val | Glu | Ala | Val | Asn | Pro | Ala | Thr | Asn | Leu | His | Phe | Arg | Gly |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Ala | Arg | Val | Trp | Leu | Ala | Val | Met | Gln | Glu | Leu | Leu | Ala | Lys | Gly | Met |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     | 75  |     | 80  |
| Ile | Asn | Ala | Glu | Asn | Ala | Val | Leu | Ser | Gly | Cys | Ser | Ala | Gly | Gly | Leu |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Ser | Leu | Met | His | Cys | Asp | Ser | Phe | Arg | Ala | Leu | Leu | Pro | Met | Gly |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Lys | Val | Lys | Cys | Leu | Ser | Asp | Ala | Gly | Phe | Phe | Leu | Asn | Thr | Arg |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Asp | Val | Ser | Gly | Val | Gln | Tyr | Ile | Lys | Thr | Tyr | Phe | Glu | Asp | Val | Val |

|                     |                         |                         |
|---------------------|-------------------------|-------------------------|
| 130                 | 135                     | 140                     |
| Thr Leu His Gly Ser | Ala Lys Asn Leu Pro Arg | Ser Cys Thr Ser Arg     |
| 145                 | 150                     | 155                     |
| Leu Thr Pro Ala Met | Cys Phe Phe Pro Gln Tyr | Val Ala Arg Gln Ile     |
| 165                 | 170                     | 175                     |
| Arg Thr Pro Leu Phe | Ile Leu Asn Ala Ala Tyr | Asp Ser Trp Gln Ile     |
| 180                 | 185                     | 190                     |
| Lys Asn Ile Leu Ala | Pro Arg Ala Ala Asp Pro | Tyr Gly Lys Trp Gln     |
| 195                 | 200                     | 205                     |
| Ser Cys Gln Leu Asp | Ile Lys Asn Cys His Pro | Ser Gln Ile Lys Val     |
| 210                 | 215                     | 220                     |
| Met Gln Asp Phe Arg | Leu Glu Phe Leu Ser Ala | Val Ile Gly Leu Gly     |
| 225                 | 230                     | 235                     |
| Arg Ser Ser Ser Arg | Gly Met Phe Ile Asp Ser | Cys Tyr Thr His Cys     |
| 245                 | 250                     | 255                     |
| Gln Thr Glu Thr Gln | Thr Ser Trp Phe Trp     | Gln Asp Ser Pro Ile Leu |
| 260                 | 265                     | 270                     |
| Asn Arg Thr Thr Ile | Ala Lys Ala Val Gly Asp | Trp Val Tyr Asp Arg     |
| 275                 | 280                     | 285                     |
| Thr Leu Phe Gln Lys | Ile Asp Cys Pro Tyr Pro | Cys Asn Pro Thr Cys     |
| 290                 | 295                     | 300                     |
| His His Arg Val Phe | His Ser Ser Arg Cys Ser | Asn Leu Ser Asp         |
| 305                 | 310                     | 315                     |
| Ser Thr Ile Tyr Ser | Ile Asp Leu Leu Leu Phe |                         |
| 325                 | 330                     |                         |

(2) INFORMATION FOR SEQ ID NO:1983:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1649 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1649

(D) OTHER INFORMATION: / Ceres Seq. ID 1571487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1983:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| tccatttaata | ctctctctccc | ctcatcctct  | cttctctct   | catcatcatc  | ttcttcttca  | 60   |
| atgccctctca | cgcgtttttct | ctctctctccc | ttcttcctatg | ccgccggtt   | ctctctccta  | 120  |
| ctccgcgcgta | cacgttaccg  | tcggatgggt  | cttctctcgg  | gaagccttgg  | ttctctctat  | 180  |
| ataggagaga  | cttttcaagt  | gatcgagct   | tacaaaacag  | agaaccctga  | gcctttcatc  | 240  |
| gacgagagag  | tagccccgta  | cGgttcgggt  | ttcatgacgc  | atctttttgg  | tgaaccgacg  | 300  |
| attttctcag  | ctgaccgcga  | aacgaaccgg  | ttgtgtcttc  | agaacgaagg  | gaagcttttt  | 360  |
| gagtgttctt  | atcctgtctc  | catttgtaac  | cttttgggga  | aaactctct   | gcttcttatg  | 420  |
| aaaggtctct  | tgccataaacg | tatgcactct  | ctccaccatga | gctttgtctaa | ttcttcaact  | 480  |
| attaaagacc  | atctcatgct  | tgatattgac  | cggttagtcc  | ggtttaattc  | tgattcttgg  | 540  |
| ctctctcgtg  | ttctctctcat | ggaagaagcc  | aaaaagataa  | cgtttgagct  | aacggtgaag  | 600  |
| cagttgatga  | gcctttgatcc | aggggaattg  | agtgaagagt  | taaggaaaaga | gtatctctct  | 660  |
| gtcatcgaag  | gcttctctctc | ctctctctct  | ccaccactta  | ccgcaaaagc  |             | 720  |
| atccaagcgc  | ggaggaaggt  | tgacggaggc  | ttgagcgttg  | aaggaggagg  |             | 780  |
| gaggaggaag  | aaggagcgga  | gagaaagaaa  | gatatgcttg  | cgccgcttgc  | tcggcggagt  | 840  |
| gatggatttt  | ccgatgaaga  | gattgttgac  | ttcttgggtg  | cttactgtg   | cgcccggttat | 900  |
| gaaacaacct  | ccaagatcat  | gaactctgcc  | gtcaaaattc  | tcaccgagac  | ttctttagct  | 960  |
| cttgcctcaac | tcaaggaaaga | gcattgaaag  | attagggcac  | tgaaagattga | ttcgttatagt | 1020 |
| cttgaaatgga | gtgattacaa  | gtcaatgcc   | ttcacacaa   | gtgtgggttaa | tgagacgcta  | 1080 |
| cgagtggtcta | acatcatcgg  | cggtgttttc  | agacgtgcac  | tgacgagatt  | tgagatcaaa  | 1140 |
| ggttataaaa  | ttccaaaagt  | ttccaaagt   | ttctcatcgt  | ttagacgggt  | ctatttagac  | 1200 |
| ccaaacacct  | tcaaagaatg  | tcgcactttc  | aacccttgga  | gatggcagag  | caactcggta  | 1260 |
| acgacagggc  | cttcttaagt  | ttctcacacc  | tttggtggag  | ggccaaagct  | atgtcccggt  | 1320 |
| tacgagctgg  | ctaggggttc  | actctctgtt  | ttctctcacc  | gcctagtgc   | aggcttcaat  | 1380 |
| tgggttctcg  | cagagcaaga  | caagctgggt  | ttctttccaa  | ctacaagaac  | gcagaaacgg  | 1440 |



(2) INFORMATION FOR SEO ID NO:1984:

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 492 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..492

(D) OTHER INFORMATION: / Ceres Seq. ID 1571488

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1984:
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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   | er  | le  | Asn | Thr | 5   | eu  | Ser | Pro | Ser | Ser | Ser | 10  | Leu | Leu | Leu | Ser | Ser | Ser |
| 1   | Ser | Ser | Ser | Ser | 20  | Met | Ala | Phe | Thr | 25  | Ala | Phe | Leu | Leu | Leu | Leu | Ser | Ser |
| Ile | Ala | Ala | Ala | Gly |     | Phe | Leu | Leu | Leu | 40  | Leu | Arg | Arg | Thr | 45  | Arg | Tyr | Arg |
| Met | Gly | Leu | Pro | Pro | Gly |     | Ser | Leu | Gly | 55  | Leu | Leu | Pro | Leu | 60  | Ile | Gly | Glu |
| Phe | Gln | Leu | Ile | Gly | Ala | 70  | Tyr | Lys | Thr |     | Glu | Asn | Pro | Glu | Pro | Phe | Ile |     |
| 65  | Asp | Glu | Arg | Val | Ala | 85  | Arg | Tyr | Gly |     | Ser | Val | 75  | Phe | Met | Thr | His | Leu |
| Gly | Glu | Pro | Thr | Ile | Phe |     | Ser | Ala | Asp | 90  | Pro | Glu | Thr | Asn | Arg | 110 | Phe | Val |
| Leu | Gln | Asn | Glu | Gly | Lys |     | Leu | Phe | Glu | 105 | Cys | Ser | Tyr | Pro | 125 | Ala | Ser | Ile |
| Cys | Asn | Leu | Leu | Gly | Lys |     | His | Ser | Leu | 120 | Leu | Leu | Met | Lys | Gly | Ser | Leu |     |
| 130 | His | Lys | Arg | Met | His |     | Ser | Leu | Thr | 135 | Met | Ser | Phe | Ala | Asn | Ser | Ser | Ile |
| 145 | Ile | Lys | Asp | His | Leu | 165 | Met | Leu | Asp | Ile | Asp | Arg | 155 | Ala | Val | Arg | Phe | Asn |
| Leu | Asp | Ser | Trp | Ser | Ser |     | Arg | Val | Leu | 185 | Leu | Met | Glu | Glu | Ala | Lys | Lys |     |
| Ile | Thr | Phe | Glu | Leu | Thr |     | Val | Lys | Gln | 200 | Leu | Met | Ser | Phe | Asp | Pro | Gly |     |
| Glu | Trp | Ser | Glu | Ser | Leu |     | Arg | Lys | Glu | 215 | Tyr | Leu | Leu | Val | Ile | Glu | Gly |     |
| 225 | Phe | Phe | Ser | Leu | Pro |     | Leu | Pro | Phe | Ser | Thr | Thr | Tyr | Arg | Lys | Ala | 240 |     |
| Ile | Gln | Ala | Arg | Arg | Lys |     | Val | Ala | Glu | 250 | Ala | Leu | Thr | Val | Val | Val | Met |     |
| Lys | Arg | Arg | Glu | Glu | Glu |     | Glu | Glu | Gly | 265 | Ala | Glu | Arg | Lys | Lys | Asp | Met |     |
| Leu | Ala | Ala | Leu | Leu | Ala |     | Ala | Asp | Asp | 280 | Gly | Phe | Ser | Asp | Glu | Glu | Ile |     |
| Val | Asp | Phe | Leu | Val | Ala |     | Leu | Leu | Val | 295 | Ala | Gly | Tyr | Glu | Thr | Thr | Ser |     |
| Thr | Ile | Met | Thr | Leu | Ala |     | Val | Lys | Phe | 310 | Leu | Thr | 315 | Glu | Thr | Pro | Leu | Ala |
| 305 | Leu | Ala | Gln | Leu | Lys |     | Glu | Glu | His | 325 | Glu | Lys | Ile | Arg | Ala | Met | Lys | Ser |
| Asp | Ser | Tyr | Ser | Leu | Glu |     | Trp | Ser | Asp | 340 | Tyr | Lys | Ser | Met | Pro | Phe | Phe | Thr |
| Gln | Cys | Val | Val | Asn | Glu |     | Thr | Leu | Arg | 350 | Val | Ala | Asn | Ile | Ile | Gly | Gly |     |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 355                                                             | 360 | 365 |
| Val Phe Arg Arg Ala Met Thr Asp Val Glu Ile Lys Gly Tyr Lys Ile |     |     |
| 370                                                             | 375 | 380 |
| Pro Lys Gly Trp Lys Val Phe Ser Ser Phe Arg Ala Val His Leu Asp |     |     |
| 385                                                             | 390 | 395 |
| Pro Asn His Phe Lys Asp Ala Arg Thr Phe Asn Pro Trp Arg Trp Gln |     |     |
| 405                                                             | 410 | 415 |
| Ser Asn Ser Val Thr Thr Gly Pro Ser Asn Val Phe Thr Pro Phe Gly |     |     |
| 420                                                             | 425 | 430 |
| Gly Gly Pro Arg Leu Cys Pro Gly Tyr Glu Leu Ala Arg Val Ala Leu |     |     |
| 435                                                             | 440 | 445 |
| Ser Val Phe Leu His Arg Leu Val Thr Gly Phe Ser Trp Val Pro Ala |     |     |
| 450                                                             | 455 | 460 |
| Glu Gln Asp Lys Leu Val Phe Phe Pro Thr Thr Arg Thr Gln Lys Arg |     |     |
| 465                                                             | 470 | 475 |
| Tyr Pro Ile Phe Val Lys Arg Arg Asp Phe Ala Thr                 |     |     |
| 485                                                             | 490 |     |

(2) INFORMATION FOR SEQ ID NO:1985:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 472 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..472

(D) OTHER INFORMATION: / Ceres Seq. ID 1571489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1985:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Ala Phe Thr Ala Phe Leu Leu Leu Leu Ser Ser Ile Ala Ala Gly |     |
| 1                                                               | 5   |
| Phe Leu Leu Leu Arg Arg Thr Arg Tyr Arg Arg Met Gly Leu Pro     | 10  |
| 20                                                              | 25  |
| Pro Gly Ser Leu Gly Leu Pro Leu Ile Gly Glu Thr Phe Gln Leu Ile | 30  |
| 35                                                              | 40  |
| Gly Ala Tyr Lys Thr Glu Asn Pro Glu Pro Phe Ile Asp Glu Arg Val | 45  |
| 50                                                              | 55  |
| Ala Arg Tyr Gly Ser Val Phe Met Thr His Leu Phe Gly Glu Pro Thr | 60  |
| 65                                                              | 70  |
| Ile Phe Ser Ala Asp Pro Glu Thr Asn Arg Phe Val Leu Gln Asn Glu | 75  |
| 85                                                              | 90  |
| Gly Lys Leu Phe Glu Cys Ser Tyr Pro Ala Ser Ile Cys Asn Leu Leu | 95  |
| 100                                                             | 105 |
| Gly Lys His Ser Leu Leu Leu Met Lys Gly Ser Leu His Lys Arg Met | 110 |
| 115                                                             | 120 |
| His Ser Leu Thr Met Ser Phe Ala Asn Ser Ser Ile Ile Lys Asp His | 125 |
| 130                                                             | 135 |
| Leu Met Leu Asp Ile Asp Arg Leu Val Arg Phe Asn Leu Asp Ser Trp | 140 |
| 145                                                             | 150 |
| Ser Ser Arg Val Leu Leu Met Glu Glu Ala Lys Lys Ile Thr Phe Glu | 155 |
| 165                                                             | 170 |
| Leu Thr Val Lys Gln Leu Met Ser Phe Asp Pro Gly Glu Trp Ser Glu | 175 |
| 180                                                             | 185 |
| Ser Leu Arg Lys Glu Tyr Leu Leu Val Ile Glu Gly Phe Ser Leu     | 190 |
| 195                                                             | 200 |
| Pro Leu Pro Leu Phe Ser Thr Thr Tyr Arg Lys Ala Ile Gln Ala Arg | 205 |
| 210                                                             | 215 |
| Arg Lys Val Ala Glu Ala Leu Thr Val Val Val Met Lys Arg Arg Glu | 220 |
| 225                                                             | 230 |
| Glu Glu Glu Glu Gly Ala Glu Arg Lys Lys Asp Met Leu Ala Ala Leu | 235 |
| 245                                                             | 250 |
|                                                                 | 255 |

2025 RELEASE UNDER E.O. 14176

Leu Ala Ala Asp Asp Gly Phe Ser Asp Glu Glu Ile Val Asp Phe Leu  
260 265 270  
Val Ala Leu Leu Val Ala Gly Tyr Glu Thr Thr Ser Thr Ile Met Thr  
275 280 285  
Leu Ala Val Lys Phe Leu Thr Glu Thr Pro Leu Ala Leu Ala Gln Leu  
290 295 300  
Lys Glu Glu His Glu Lys Ile Arg Ala Met Lys Ser Asp Ser Tyr Ser  
305 310 315 320  
Leu Glu Trp Ser Asp Tyr Lys Ser Met Pro Phe Thr Gln Cys Val Val  
325 330 335  
Asn Glu Thr Leu Arg Val Ala Asn Ile Ile Gly Gly Val Phe Arg Arg  
340 345 350  
Ala Met Thr Asp Val Glu Ile Lys Gly Tyr Lys Ile Pro Lys Gly Trp  
355 360 365  
Lys Val Phe Ser Ser Phe Arg Ala Val His Leu Asp Pro Asn His Phe  
370 375 380  
Lys Asp Ala Arg Thr Phe Asn Pro Trp Arg Trp Gln Ser Asn Ser Val  
385 390 395 400  
Thr Thr Gly Pro Ser Asn Val Phe Thr Pro Phe Gly Gly Gly Pro Arg  
405 410 415  
Leu Cys Pro Gly Tyr Glu Leu Ala Arg Val Ala Leu Ser Val Phe Leu  
420 425 430  
His Arg Leu Val Thr Gly Phe Ser Trp Val Pro Ala Glu Gln Asp Lys  
435 440 445  
Leu Val Phe Phe Pro Thr Thr Arg Thr Gln Lys Arg Tyr Pro Ile Phe  
450 455 460  
Val Lys Arg Arg Asp Phe Ala Thr  
465 470

(2) INFORMATION FOR SEQ ID NO:1986:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 444 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..444

(D) OTHER INFORMATION: / Ceres Seq. ID 1571490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1986:

Met Gly Leu Pro Pro Gly Ser Leu Gly Leu Pro Leu Ile Gly Glu Thr  
1 5 10 15  
Phe Gln Leu Ile Gly Ala Tyr Lys Thr Glu Asn Pro Glu Pro Phe Ile  
20 25 30  
Asp Glu Arg Val Ala Arg Tyr Gly Ser Val Phe Met Thr His Leu Phe  
35 40 45  
Gly Glu Pro Thr Ile Phe Ser Ala Asp Pro Glu Thr Asn Arg Phe Val  
50 55 60  
Leu Gln Asn Glu Gly Lys Leu Phe Glu Cys Ser Tyr Pro Ala Ser Ile  
65 70 75 80  
Cys Asn Leu Leu Gly Lys His Ser Leu Leu Leu Met Lys Gly Ser Leu  
85 90 95  
His Lys Arg Met His Ser Leu Thr Met Ser Phe Ala Asn Ser Ser Ile  
100 105 110  
Ile Lys Asp His Leu Met Leu Asp Ile Asp Arg Leu Val Arg Phe Asn  
115 120 125  
Leu Asp Ser Trp Ser Ser Arg Val Leu Leu Met Glu Glu Ala Lys Lys  
130 135 140  
Ile Thr Phe Glu Leu Thr Val Lys Gln Leu Met Ser Phe Asp Pro Gly  
145 150 155 160  
Glu Trp Ser Glu Ser Leu Arg Lys Glu Tyr Leu Leu Val Ile Glu Gly

|             |             |            |             |             |            |     |
|-------------|-------------|------------|-------------|-------------|------------|-----|
| amcatccwaa  | tcgaaaaaatt | ttaaccagca | tatacaaaaa  | acttcgcgat  | ccctctagcg | 60  |
| ttctctctctc | cggcgatatt  | ctctctcttc | ggctcacatt  | gcatcgtctc  | tcactcgatc | 120 |
| ctctggtctct | tacgggcacaa | tcatcttcga | aacatgcgag  | ctcagaagat  | tgaaacgggt | 180 |
| catgaggaca  | tgtccatga   | tgatcagatg | gattactatg  | gaagcggaat  | tgcacatgca | 240 |
| tcaatcgtac  | gcacatccaa  | gtacaccggt | gtcagaacaa  | cggcggtgat  | cgacgaacta | 300 |
| gcacatcaatc | ccggccaccg  | tgtgctctgc | tgtggaagtgc | cggtggccaca | ccaaagatat | 360 |
| ggacaactac  | tgtcttcagt  | ctctcatgat | ggtcagatca  | tgtcttgaaa  | aggaaggcac | 420 |
| cagaaccaat  | ggaccacaaga | ctatgctttc | acagaccaca  | aatcttcagt  | caactcaatt | 480 |
| catcggggct  | ctcatgatat  | cggactactc | tgtggcctgg  | ggctcatgca  | tggcaacatt | 540 |
| tcggttttcaa | cagcccgctgc | cgcgggtggc | tgggaacacat | caaggattga  | ccaagcacat | 600 |
| ccggtttgag  | tcaacttcagt | ctcatggggc | ccagccacag  | cgcctggtgc  | tcttgtgagc | 660 |
| ttctggtctc  | tcgatccggt  | ttaacaagat | gcttcttggtg | tgatcgataa  | tacogtgaaa | 720 |
| tgctgggaagc | tcgcatacgg  | gtcatggaa  | atggattgct  | tctcagctct  | tcaaaagcac | 780 |
| actgatggg   | tcgatgatgt  | gctctgggca | ccaactctgg  | gtctccctca  | gtccaccata | 840 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| gccagtggtt | cccaagatgg | gaaagttatc | atatggacag | tgggaaaaga | aggtgagcaa | 900  |
| tgggaaggtg | aggtttctca | ggacttttat | actcctgtgt | ggcgggtctc | gtcgtcgttg | 960  |
| accggtaact | tattggccgt | atccgatggg | aacaacaacg | tgactgtgtg | gAaagaggct | 1020 |
| gttgatggag | agtgggaaca | agtttactgt | gttgagcctt | aggtttttga | tgcttttcta | 1080 |
| tctctctgct | cttctcttta | aggaactgaa | tcaaacattt | tttctttact | cttttcttag | 1140 |
| tcgggtttgg | tggtcttttt | cagggaatgt | tgaattgggt | ttcttaaaga | cttttggatt | 1200 |
| atcttttttc | ttattctttt | catagagacc | attttaaaat | tcc        |            |      |

(2) INFORMATION FOR SEQ ID NO:1988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..302
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571500

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1988:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Gly | Gln | Lys | Ile | Glu | Thr | Gly | His | Glu | Asp | Ile | Val | His | Asp |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Gln | Met | Asp | Tyr | Tyr | Gly | Lys | Arg | Ile | Ala | Thr | Ala | Ser | Ser | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Thr | Ile | Lys | Ile | Thr | Gly | Val | Ser | Asn | Asn | Gly | Gly | Ser | Gln | Gln |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Ala | Thr | Leu | Thr | Gly | His | Arg | Gly | Pro | Val | Trp | Glu | Val | Ala | Trp |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ala | His | Pro | Lys | Tyr | Gly | Ser | Ile | Leu | Ala | Ser | Cys | Ser | Tyr | Asp | Gly |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     |     | 80  |     |
| Gln | Val | Ile | Leu | Trp | Lys | Glu | Gly | Asn | Gln | Asn | Gln | Trp | Thr | Gln | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| His | Val | Phe | Thr | Asp | His | Lys | Ser | Ser | Val | Asn | Ser | Ile | Ala | Trp | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | His | Asp | Ile | Gly | Leu | Ser | Leu | Ala | Cys | Gly | Ser | Ser | Asp | Gly | Asn |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Ser | Val | Phe | Thr | Ala | Arg | Ala | Asp | Gly | Gly | Trp | Asp | Thr | Ser | Arg |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Ile | Asp | Gln | Ala | His | Pro | Val | Gly | Val | Thr | Ser | Val | Ser | Trp | Ala | Pro |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     | 160 |     |
| Ala | Thr | Ala | Pro | Gly | Ala | Leu | Val | Ser | Ser | Gly | Leu | Leu | Asp | Pro | Val |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Tyr | Lys | Leu | Ala | Ser | Gly | Gly | Cys | Asp | Asn | Thr | Val | Lys | Val | Trp | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Ala | Asn | Gly | Ser | Trp | Lys | Met | Asp | Cys | Phe | Pro | Ala | Leu | Gln | Lys |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| His | Thr | Asp | Trp | Val | Arg | Asp | Val | Ala | Trp | Ala | Pro | Asn | Leu | Gly | Leu |
|     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Pro | Lys | Ser | Thr | Ile | Ala | Ser | Gly | Ser | Gln | Asp | Gly | Lys | Val | Ile | Ile |
|     |     |     | 225 |     |     |     | 230 |     |     | 235 |     |     |     | 240 |     |
| Trp | Thr | Val | Gly | Lys | Glu | Gly | Glu | Gln | Trp | Glu | Gly | Lys | Val | Leu | Lys |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Asp | Phe | Met | Thr | Pro | Val | Trp | Arg | Val | Ser | Ser | Ser | Leu | Thr | Gly | Asn |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Leu | Leu | Ala | Val | Ser | Asp | Gly | Asn | Asn | Val | Thr | Val | Trp | Lys | Glu |     |
|     |     |     | 275 |     |     |     | 280 |     |     |     | 285 |     |     |     |     |
| Ala | Val | Asp | Gly | Glu | Trp | Glu | Gln | Val | Thr | Ala | Val | Glu | Pro |     |     |
|     |     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1989:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..284  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571501  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1989:

```

Met Asp Tyr Tyr Gly Lys Arg Ile Ala Thr Ala Ser Ser Asp Cys Thr
1 5 10 15
Ile Lys Ile Thr Gly Val Ser Asn Asn Gly Gly Ser Gln Gln Leu Ala
20 25 30
Thr Leu Thr Gly His Arg Gly Pro Val Trp Glu Val Ala Trp Ala His
35 40 45
Pro Lys Tyr Gly Ser Ile Leu Ala Ser Cys Ser Tyr Asp Gly Gln Val
50 55 60
Ile Leu Trp Lys Glu Gly Asn Gln Trp Thr Gln Asp His Val
65 70 75
Phe Thr Asp His Lys Ser Ser Val Asn Ser Ile Ala Trp Ala Pro His
85 90 95
Asp Ile Gly Leu Ser Leu Ala Cys Gly Ser Ser Asp Gly Asn Ile Ser
100 105 110
Val Phe Thr Ala Arg Ala Asp Gly Trp Asp Thr Ser Arg Ile Asp
115 120 125
Gln Ala His Pro Val Gly Val Thr Ser Val Ser Trp Ala Pro Ala Thr
130 135 140
Ala Pro Gly Ala Leu Val Ser Ser Gly Leu Leu Asp Pro Val Tyr Lys
145 150 155
Leu Ala Ser Gly Gly Cys Asp Asn Thr Val Lys Val Trp Lys Leu Ala
165 170 175
Asn Gly Ser Trp Lys Met Asp Cys Phe Pro Ala Leu Gln Lys His Thr
180 185 190
Asp Trp Val Arg Asp Val Ala Trp Ala Pro Asn Leu Gly Leu Pro Lys
195 200 205
Ser Thr Ile Ala Ser Gly Ser Gln Asp Gly Lys Val Ile Ile Trp Thr
210 215 220
Val Gly Lys Glu Gly Glu Gln Trp Glu Gly Lys Val Leu Lys Asp Phe
225 230 235
Met Thr Pro Val Trp Arg Val Ser Ser Ser Leu Thr Gly Asn Leu Leu
245 250 255
Ala Val Ser Asp Gly Asn Asn Asn Val Thr Trp Lys Glu Ala Val
260 265 270
Asp Gly Glu Trp Glu Gln Val Thr Ala Val Glu Pro
275 280

```

(2) INFORMATION FOR SEQ ID NO:1990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1194 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1194  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1990:

```

gacaacaatg gcgccttcct cgtcgagcgg tctcacgttc aagctacatc ctctgggtgat 60
gcttaacata tccgatcact tcactagggt taaaactcag cttaatcctc ccgcgcgttc 120
ttgcgccacc ggggaatggct ccaacaacgc cgacgcgatg ttactgcaaa accctagggt 180
ttatggctgc gtcacgggtc tccagagagg tcgtacgggt gagatcttca acagtcttca 240
gctgatattc gatcctgcgc ttgatactct cgacagatcc ttcttcgaga agaagcaaga 300

```

|            |             |             |             |            |            |      |
|------------|-------------|-------------|-------------|------------|------------|------|
| actctataag | aaggtgttcc  | ctgacttcta  | cgtattggga  | tggatttcta | cggaagtga  | 360  |
| cgctaccgaa | tctgatatgc  | atatccacaa  | agctctgatg  | gacattaatg | aatctctgtg | 420  |
| gtatgttctt | ttaaactcctg | ctatcaatca  | tgacacagaag | gatcttctgt | tgactatcta | 480  |
| cgaaagcgaa | tttcattgta  | ttgatggaat  | tctctcagtcg | atttctgtgc | ataccagcta | 540  |
| cacaattgag | acagttgaag  | ctgaaaagaat | atctgttgat  | catgtTgcac | atcttaagcc | 600  |
| atctgatgga | ggctcagctg  | cgactcagtt  | ggctgctcat  | cttactggaa | tacatagtgc | 660  |
| catcaagatg | cttaaatagca | gaatcagagt  | gctataccag  | catattgtcg | ctatgcagaa | 720  |
| aggtgataaa | ccttgtgaga  | actcagttct  | gagacaagta  | tctagtctgc | tcagaagtgt | 780  |
| gcctgcgcga | gaatcagaga  | agttcaatga  | aaatttcttg  | atggagtaca | acgacaaatt | 840  |
| gctgatgtct | tacctagcaa  | tgatcacgaa  | ttgtaccagc  | aacatgaacg | aggtgggtga | 900  |
| caaattcaac | actgcatacg  | acaaacacag  | ccgaagaggt  | ggtaggactg | cggtcaatga | 960  |
| aagattagtt | tcaatgtaaa  | aaaacctttt  | ctttcttttg  | gtggctcggt | ccctaagtga | 1020 |
| aaatttagaa | ctcttttaag  | gcatttctac  | tttcggaacc  | aaacaaacag | ctaggaagct | 1080 |
| tttctctctg | ttaagctttg  | tctagacaga  | agctaaagtt  | aggcctaact | aaattttgct | 1140 |
| acaagactgt | aaaaacaaaa  | cagctttttac | cttctctcaa  | tttttcat   | attc       |      |

(2) INFORMATION FOR SEQ ID NO:1991:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..319

(D) OTHER INFORMATION: / Ceres Seq. ID 1571503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1991:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Thr | Met | Ala | Pro | Ser | Ser | Ser | Ser | Ser | Gly | Leu | Thr | Phe | Lys | Leu | His |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Leu | Val | Met | Leu | Asn | Ile | Ser | Asp | His | Phe | Thr | Arg | Val | Lys | Thr |     |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Gln | Leu | Asn | Pro | Pro | Ala | Ala | Ser | Cys | Ala | Thr | Gly | Asn | Gly | Ser | Asn |     |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Ala | Asp | Ala | Met | Leu | Leu | Gln | Asn | Pro | Arg | Val | Tyr | Gly | Cys | Val |     |
|     |     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Gly | Leu | Gln | Arg | Gly | Arg | Thr | Val | Glu | Ile | Phe | Asn | Ser | Phe | Glu |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Ile | Phe | Asp | Pro | Ala | Leu | Asp | Thr | Leu | Asp | Arg | Ser | Phe | Leu | Glu |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |     |
| Lys | Lys | Gln | Glu | Leu | Tyr | Lys | Lys | Val | Phe | Pro | Asp | Phe | Tyr | Val | Leu |     |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Gly | Trp | Tyr | Ser | Thr | Gly | Ser | Asp | Ala | Thr | Glu | Ser | Asp | Met | His | Ile |     |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| His | Lys | Ala | Leu | Met | Asp | Ile | Asn | Glu | Ser | Pro | Val | Tyr | Val | Leu | Leu |     |
|     |     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Pro | Ala | Ile | Asn | His | Ala | Gln | Lys | Asp | Leu | Pro | Val | Thr | Ile | Tyr |     |
|     |     |     |     | 145 |     |     | 150 |     |     | 155 |     |     |     | 160 |     |     |
| Glu | Ser | Glu | Phe | His | Val | Ile | Asp | Gly | Ile | Pro | Gln | Ser | Ile | Phe | Val |     |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     | 175 |     |     |     |
| His | Thr | Ser | Tyr | Thr | Ile | Glu | Thr | Val | Glu | Ala | Glu | Arg | Ile | Ser | Val |     |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Asp | His | Val | Ala | His | Leu | Lys | Pro | Ser | Asp | Gly | Gly | Ser | Ala | Ala | Thr |     |
|     |     |     |     | 195 |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Gln | Leu | Ala | Ala | His | Leu | Thr | Gly | Ile | His | Ser | Ala | Ile | Lys | Met | Leu |     |
|     |     |     |     | 210 |     |     | 215 |     |     |     | 220 |     |     |     |     |     |
| Asn | Ser | Arg | Ile | Arg | Val | Leu | Tyr | Gln | His | Ile | Val | Ala | Met | Gln | Lys |     |
|     |     |     |     | 225 |     |     | 230 |     |     | 235 |     |     |     |     | 240 |     |
| Gly | Asp | Lys | Pro | Cys | Glu | Asn | Ser | Val | Leu | Arg | Gln | Val | Ser | Ser | Leu |     |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     | 255 |     |     |     |
| Leu | Arg | Ser | Leu | Pro | Ala | Ala | Glu | Ser | Glu | Lys | Phe | Asn | Glu | Asn | Phe |     |
|     |     |     |     | 260 |     |     | 265 |     |     |     |     | 270 |     |     |     |     |





(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..300  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1571505  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1993:  
Met Leu Asn Ile Ser Asp His Phe Thr Arg Val Lys Thr Gln Leu Asn  
1                  5                  10                  15  
Pro Pro Ala Ala Ser Cys Ala Thr Gly Asn Gly Ser Asn Asn Ala Asp  
                  20                  25                  30  
Ala Met Leu Leu Gln Asn Pro Arg Val Tyr Gly Cys Val Ile Gly Leu  
                  35                  40                  45  
Gln Arg Gly Arg Thr Val Glu Ile Phe Asn Ser Phe Glu Leu Ile Phe  
50                  55                  60  
Asp Pro Ala Leu Asp Thr Leu Asp Arg Ser Phe Leu Glu Lys Lys Gln  
65                  70                  75                  80  
Glu Leu Tyr Lys Lys Val Phe Pro Asp Phe Tyr Val Leu Gly Trp Tyr  
                  85                  90                  95  
Ser Thr Gly Ser Asp Ala Thr Glu Ser Asp Met His Ile His Lys Ala  
                  100                  105                  110  
Leu Met Asp Ile Asn Glu Ser Pro Val Tyr Val Leu Leu Asn Pro Ala  
                  115                  120                  125  
Ile Asn His Ala Gln Lys Asp Leu Pro Val Thr Ile Tyr Glu Ser Glu  
130                  135                  140  
Phe His Val Ile Asp Gly Ile Pro Gln Ser Ile Phe Val His Thr Ser  
145                  150                  155                  160  
Tyr Thr Ile Glu Thr Val Glu Ala Glu Arg Ile Ser Val Asp His Val  
                  165                  170                  175  
Ala His Leu Lys Pro Ser Asp Gly Gly Ser Ala Ala Thr Gln Leu Ala  
                  180                  185                  190  
Ala His Leu Thr Gly Ile His Ser Ala Ile Lys Met Leu Asn Ser Arg  
                  195                  200                  205  
Ile Arg Val Leu Tyr Gln His Ile Val Ala Met Gln Lys Gly Asp Lys  
210                  215                  220  
Pro Cys Glu Asn Ser Val Leu Arg Gln Val Ser Ser Leu Leu Arg Ser  
225                  230                  235                  240  
Leu Pro Ala Ala Glu Ser Glu Lys Phe Asn Glu Asn Phe Leu Met Glu  
                  245                  250                  255  
Tyr Asn Asp Lys Leu Leu Met Ser Tyr Leu Ala Met Ile Thr Asn Cys  
260                  265                  270  
Thr Ser Asn Met Asn Glu Val Val Asp Lys Phe Asn Thr Ala Tyr Asp  
275                  280                  285  
Lys His Ser Arg Arg Gly Gly Arg Thr Ala Phe Met  
290                  295                  300

(2) INFORMATION FOR SEQ ID NO:1994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1965 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1965  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1994:

aaaacacaaa catatctctt atcaaacacc aacagctcta ttctctacct catttctcat 60  
catacaaaag agagagaaaa aaactatgga attgacactg aattcctcga gttctcttat 120

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| caaacgtaaa  | gatgccaa    | gttctagaaa  | caaagaaagt  | tctccaaca   | acatgacctt  | 180  |
| tgccgaagat  | aagccgcaca  | catatcaatt  | caaagcaaa   | aactcgggta  | agggaaatgaa | 240  |
| gttcactcac  | gagaagaact  | tccgcgcaga  | aggtgaaacc  | cttgagaaact | gggagaaagct | 300  |
| ccacgtttct  | tcatccaccac | actccaagaa  | cgacgctagc  | gttccggtgt  | tcgtcatggt  | 360  |
| accgctgcac  | acagtaacaa  | tgctcagggca | tttgaacaaa  | ccacgagcca  | tgaacgctag  | 420  |
| tttgatggcc  | ctgaaaaggag | ctgggtgtga  | aggtgtgatg  | gtggatgctt  | ggtggggatt  | 480  |
| ggtggagaaa  | gatggacctt  | tgaattataa  | ctgggaaggg  | tatgcccagc  | ttatacacat  | 540  |
| ggttcaaaa   | cacaggtctca | aactccaggt  | cgttatgtca  | ttccatcaat  | gtggaggagaa | 600  |
| cgtaggagac  | tcttgccagta | tcccttggc   | tccatgggtg  | cttgaagaga  | tcagacaagaa | 660  |
| ccctgatctt  | gtctacacag  | acaaatctgg  | gagaagggaac | cctgaatata  | tctccttggg  | 720  |
| atgtgatctt  | gtgcctgtcc  | taagaggaag  | aacacctatc  | caggtctcat  | cagatttcat  | 780  |
| gaggagcttc  | cgtgaacagt  | ttgaaggcta  | cataggagga  | gttattgcgg  | aaattcaagt  | 840  |
| aggaatggga  | ctctgtggag  | aattgagata  | cccatcatc   | cctgagagca  | acgggaacctg | 900  |
| gagatctccc  | ggaattggag  | agttccagtg  | ctacgacaag  | tatatgaact  | cgtcacttca  | 960  |
| agcatatgct  | gagtcaatcg  | ggaaaactaa  | ctgggggaaca | agtggacctc  | atgatgccgg  | 1020 |
| cgagtacaag  | aacctccacg  | aagatactga  | atttttcagg  | agagacggaa  | catggaatag  | 1080 |
| cgagtatgct  | aagtttttca  | tggaaatggt  | ctccgggaag  | cgctagaaac  | atggagacca  | 1140 |
| actctatctt  | tcagcgaaag  | gtatctttca  | aggaagcggg  | gcaaaagctat | caggaagaagt | 1200 |
| agctggaaat  | cactggcact  | acaacaccag  | gtcacacgca  | gctgagctaa  | ccgctggata  | 1260 |
| ctacacaaca  | agaaatccat  | acgggtatct  | gccaatagct  | aagatgttca  | acaaaacatg  | 1320 |
| agtttgtctc  | aacttcacct  | gcattggagat | gaagacgggg  | gagcaacctg  | agcaccggaa  | 1380 |
| ttgtccacca  | gaaggtctgg  | tcaagcaagt  | acagaacggc  | acaagggcag  | ccggaaccga  | 1440 |
| actagcaggg  | gagaacgcgc  | tagaacgata  | tgactcaagc  | gcattccggc  | aagtggttag  | 1500 |
| aacaaaatagg | tcatattctg  | gaaatgggtt  | aaccgcattt  | acttacctaa  | gaatgaacaa  | 1560 |
| cgcggttatt  | gagggtcaaa  | attggcagca  | gttagtggag  | tttgttaaga  | acatgaagga  | 1620 |
| aggtggctcat | gggaggagac  | tctcaaaaga  | agacacaact  | gggaagtgac  | tttatgttgg  | 1680 |
| atttttcaaa  | ggcaagatcg  | ctgagaatgt  | ggaggaggct  | gcttttagtg  | aatttcccac  | 1740 |
| Rataggtaca  | tacatatagt  | tgggtgttta  | ttgtattcct  | ctctgataaa  | taactagaga  | 1800 |
| gatcaaacca  | gtaagagtgt  | taaagctata  | ttgttcacaa  | attctgggct  | agagtcagag  | 1860 |
| caaaagagaag | caaaatcaag  | atgatgtaca  | cttagatgtt  | tctcatgagt  | tttcttctgt  | 1920 |
| catcatcttc  | atattcttaa  | tctcaaatac  | ttagcttttt  | tctccc      |             |      |

(2) INFORMATION FOR SEQ ID NO:1995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..576
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1995:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | His | Lys | His | Ile | Phe | Tyr | Gln | Thr | Pro | Thr | Ala | Leu | Phe | Ser | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Phe | Leu | Ile | Ile | Thr | Lys | Arg | Glu | Lys | Lys | Thr | Met | Glu | Leu | Thr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Asn | Ser | Ser | Ser | Ser | Leu | Ile | Lys | Arg | Lys | Asp | Ala | Lys | Ser | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Arg | Asn | Gln | Glu | Ser | Ser | Ser | Asn | Met | Thr | Phe | Ala | Lys | Met | Lys |     |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Pro | Pro | Thr | Tyr | Gln | Phe | Gln | Ala | Lys | Asn | Ser | Val | Lys | Glu | Met | Lys |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Phe | Thr | His | Glu | Lys | Thr | Phe | Thr | Pro | Glu | Gly | Glu | Thr | Leu | Glu | Lys |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Trp | Glu | Lys | Leu | His | Val | Leu | Ser | Tyr | Pro | His | Ser | Lys | Asn | Asp | Ala |
|     |     | 100 |     |     |     | 105 |     |     |     |     |     |     | 110 |     |     |
| Ser | Val | Pro | Val | Phe | Val | Met | Leu | Pro | Leu | Asp | Thr | Val | Thr | Met | Ser |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Gly | His | Leu | Asn | Lys | Pro | Arg | Ala | Met | Asn | Ala | Ser | Leu | Met | Ala | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Gly | Ala | Gly | Val | Glu | Gly | Val | Met | Val | Asp | Ala | Trp | Trp | Gly | Leu | 145 | 150 | 155 | 160 |
| Val | Glu | Lys | Asp | Gly | Pro | Met | Asn | Tyr | Asn | Trp | Glu | Gly | Tyr | Ala | Glu | 165 | 170 | 175 |     |
| Leu | Ile | Gln | Met | Val | Gln | Lys | His | Gly | Leu | Lys | Leu | Gln | Val | Val | Met | 180 | 185 | 190 |     |
| Ser | Phe | His | Gln | Cys | Gly | Gly | Asn | Val | Gly | Asp | Ser | Cys | Ser | Ile | Pro | 195 | 200 | 205 |     |
| Leu | Pro | Pro | Trp | Val | Leu | Glu | Glu | Ile | Ser | Lys | Asn | Pro | Asp | Leu | Val | 210 | 215 | 220 |     |
| Tyr | Thr | Asp | Lys | Ser | Gly | Arg | Arg | Asn | Pro | Glu | Tyr | Ile | Ser | Leu | Gly | 225 | 230 | 235 |     |
| Cys | Asp | Ser | Val | Pro | Val | Leu | Arg | Gly | Arg | Thr | Pro | Ile | Gln | Val | Tyr | 245 | 250 | 255 |     |
| Ser | Asp | Phe | Met | Arg | Ser | Phe | Arg | Glu | Arg | Phe | Glu | Gly | Tyr | Ile | Gly | 260 | 265 | 270 |     |
| Gly | Val | Ile | Ala | Glu | Ile | Gln | Val | Gly | Met | Gly | Pro | Cys | Gly | Glu | Leu | 275 | 280 | 285 |     |
| Arg | Tyr | Pro | Ser | Tyr | Pro | Glu | Ser | Asn | Gly | Thr | Trp | Arg | Phe | Pro | Gly | 290 | 295 | 300 |     |
| Ile | Gly | Glu | Phe | Gln | Cys | Tyr | Asp | Lys | Tyr | Met | Lys | Ser | Ser | Leu | Gln | 305 | 310 | 315 |     |
| Ala | Tyr | Ala | Glu | Ser | Ile | Gly | Lys | Thr | Asn | Trp | Gly | Thr | Ser | Gly | Pro | 325 | 330 | 335 |     |
| His | Asp | Ala | Gly | Glu | Tyr | Lys | Asn | Leu | Pro | Glu | Asp | Thr | Glu | Phe | Phe | 340 | 345 | 350 |     |
| Arg | Arg | Asp | Gly | Thr | Trp | Asn | Ser | Glu | Tyr | Gly | Lys | Phe | Phe | Met | Glu | 355 | 360 | 365 |     |
| Trp | Tyr | Ser | Gly | Lys | Leu | Leu | Glu | His | Gly | Asp | Gln | Leu | Leu | Ser | Ser | 370 | 375 | 380 |     |
| Ala | Lys | Gly | Ile | Phe | Gln | Gly | Ser | Gly | Ala | Lys | Leu | Ser | Gly | Lys | Val | 385 | 390 | 395 |     |
| Ala | Gly | Ile | His | Trp | His | Tyr | Asn | Thr | Arg | Ser | His | Ala | Ala | Glu | Leu | 405 | 410 | 415 |     |
| Thr | Ala | Gly | Tyr | Tyr | Asn | Thr | Arg | Asn | His | Asp | Gly | Tyr | Leu | Pro | Ile | 420 | 425 | 430 |     |
| Ala | Lys | Met | Phe | Asn | Lys | His | Gly | Val | Val | Leu | Asn | Phe | Thr | Cys | Met | 435 | 440 | 445 |     |
| Glu | Met | Lys | Asp | Gly | Glu | Gln | Pro | Glu | His | Ala | Asn | Cys | Ser | Pro | Glu | 450 | 455 | 460 |     |
| Gly | Leu | Val | Lys | Gln | Val | Gln | Asn | Ala | Thr | Arg | Gln | Ala | Gly | Thr | Glu | 465 | 470 | 475 |     |
| Leu | Ala | Gly | Glu | Asn | Ala | Leu | Glu | Arg | Tyr | Asp | Ser | Ser | Ala | Phe | Gly | 485 | 490 | 495 |     |
| Gln | Val | Val | Ala | Thr | Asn | Arg | Ser | Asp | Ser | Gly | Asn | Gly | Leu | Thr | Ala | 500 | 505 | 510 |     |
| Phe | Thr | Tyr | Leu | Arg | Met | Asn | Lys | Arg | Leu | Phe | Glu | Gly | Gln | Asn | Trp | 515 | 520 | 525 |     |
| Gln | Gln | Leu | Val | Glu | Phe | Val | Lys | Asn | Met | Lys | Glu | Gly | Gly | His | Gly | 530 | 535 | 540 |     |
| Arg | Arg | Leu | Ser | Lys | Glu | Asp | Thr | Thr | Gly | Ser | Asp | Leu | Tyr | Val | Gly | 545 | 550 | 555 |     |
| Phe | Val | Lys | Gly | Lys | Ile | Ala | Glu | Asn | Val | Glu | Glu | Ala | Ala | Leu | Val | 565 | 570 | 575 |     |

(2) INFORMATION FOR SEQ ID NO:1996:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 548 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..548  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1996:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Thr | Leu | Asn | Ser | Ser | Ser | Ser | Leu | Ile | Lys | Arg | Lys | Asp |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Ala | Lys | Ser | Ser | Arg | Asn | Gln | Glu | Ser | Ser | Asn | Asn | Met | Thr | Phe |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Ala | Lys | Met | Lys | Pro | Pro | Thr | Tyr | Gln | Phe | Gln | Ala | Lys | Asn | Ser | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Glu | Met | Lys | Phe | Thr | His | Glu | Lys | Thr | Phe | Thr | Pro | Glu | Gly | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Leu | Glu | Lys | Trp | Glu | Lys | Leu | His | Val | Leu | Ser | Tyr | Pro | His | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Asn | Asp | Ala | Ser | Val | Pro | Val | Phe | Val | Met | Leu | Pro | Leu | Asp | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Val | Thr | Met | Ser | Gly | His | Leu | Asn | Lys | Pro | Arg | Ala | Met | Asn | Ala | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Met | Ala | Leu | Lys | Gly | Ala | Gly | Val | Glu | Gly | Val | Met | Val | Asp | Ala |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Trp | Trp | Gly | Leu | Val | Glu | Lys | Asp | Gly | Pro | Met | Asn | Tyr | Asn | Trp | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Tyr | Ala | Glu | Leu | Ile | Gln | Met | Val | Gln | Lys | His | Gly | Leu | Lys | Leu |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Gln | Val | Val | Met | Ser | Phe | His | Gln | Cys | Gly | Gly | Asn | Val | Gly | Asp | Ser |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Cys | Ser | Ile | Pro | Leu | Pro | Pro | Trp | Val | Leu | Glu | Glu | Ile | Ser | Lys | Asn |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Asp | Leu | Val | Tyr | Thr | Asp | Lys | Ser | Gly | Arg | Arg | Asn | Pro | Glu | Tyr |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Ser | Leu | Gly | Cys | Asp | Ser | Val | Pro | Val | Leu | Arg | Gly | Arg | Thr | Pro |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Gln | Val | Tyr | Ser | Asp | Phe | Met | Arg | Ser | Phe | Arg | Glu | Arg | Phe | Glu |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Gly | Tyr | Ile | Gly | Gly | Val | Ile | Ala | Glu | Ile | Gln | Val | Gly | Met | Gly | Pro |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Cys | Gly | Glu | Leu | Arg | Tyr | Pro | Ser | Tyr | Pro | Glu | Ser | Asn | Gly | Thr | Trp |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Arg | Phe | Pro | Gly | Ile | Gly | Glu | Phe | Gln | Cys | Tyr | Asp | Lys | Tyr | Met | Lys |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ser | Ser | Leu | Gln | Ala | Tyr | Ala | Glu | Ser | Ile | Gly | Lys | Thr | Asn | Trp | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Thr | Ser | Gly | Pro | His | Asp | Ala | Gly | Glu | Tyr | Lys | Asn | Leu | Pro | Glu | Asp |
|     | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Thr | Glu | Phe | Phe | Arg | Arg | Asp | Gly | Thr | Trp | Asn | Ser | Glu | Tyr | Gly | Lys |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Phe | Phe | Met | Glu | Trp | Tyr | Ser | Gly | Lys | Leu | Glu | His | Gly | Asp | Gln |     |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Leu | Leu | Ser | Ser | Ala | Lys | Gly | Ile | Phe | Gln | Gly | Ser | Gly | Ala | Lys | Leu |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Ser | Gly | Lys | Val | Ala | Gly | Ile | His | Trp | His | Tyr | Asn | Thr | Arg | Ser | His |
|     | 370 |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |     |
| Ala | Ala | Glu | Leu | Thr | Ala | Gly | Tyr | Tyr | Asn | Thr | Arg | Asn | His | Asp | Gly |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |     |
| Tyr | Leu | Pro | Ile | Ala | Lys | Met | Phe | Asn | Lys | His | Gly | Val | Val | Leu | Asn |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     | 415 |     |     |
| Phe | Thr | Cys | Met | Glu | Met | Lys | Asp | Gly | Glu | Gln | Pro | Glu | His | Ala | Asn |
|     |     |     | 420 |     |     |     | 425 |     |     |     |     |     | 430 |     |     |

Cys Ser Pro Glu Gly Leu Val Lys Gln Val Gln Asn Ala Thr Arg Gln  
435 440 445  
Ala Gly Thr Glu Leu Ala Gly Glu Asn Ala Leu Glu Arg Tyr Asp Ser  
450 455 460  
Ser Ala Phe Gly Gln Val Val Ala Thr Asn Arg Ser Asp Ser Gly Asn  
465 470 475 480  
Gly Leu Thr Ala Phe Thr Tyr Leu Arg Met Asn Lys Arg Leu Phe Glu  
485 490 495  
Gly Gln Asn Trp Gln Gln Leu Val Glu Phe Val Lys Asn Met Lys Glu  
500 505 510  
Gly Gly His Gly Arg Arg Leu Ser Lys Glu Asp Thr Thr Gly Ser Asp  
515 520 525  
Leu Tyr Val Gly Phe Val Lys Gly Lys Ile Ala Glu Asn Val Glu Glu  
530 535 540  
Ala Ala Leu Val  
545

(2) INFORMATION FOR SEQ ID NO:1997:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..519
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1997:

Met Thr Phe Ala Lys Met Lys Pro Pro Thr Tyr Gln Phe Gln Ala Lys  
1 5 10 15  
Asn Ser Val Lys Glu Met Lys Phe Thr His Glu Lys Thr Phe Thr Pro  
20 25 30  
Glu Gly Glu Thr Leu Glu Lys Trp Glu Lys Leu His Val Leu Ser Tyr  
35 40 45  
Pro His Ser Lys Asn Asp Ala Ser Val Pro Val Phe Val Met Leu Pro  
50 55 60  
Leu Asp Thr Val Thr Met Ser Gly His Leu Asn Lys Pro Arg Ala Met  
65 70 75 80  
Asn Ala Ser Leu Met Ala Leu Lys Gly Ala Gly Val Glu Gly Val Met  
85 90 95  
Val Asp Ala Trp Trp Gly Leu Val Glu Lys Asp Gly Pro Met Asn Tyr  
100 105 110  
Asn Trp Glu Gly Tyr Ala Glu Leu Ile Gln Met Val Gln Lys His Gly  
115 120 125  
Leu Lys Leu Gln Val Val Met Ser Phe His Gln Cys Gly Gly Asn Val  
130 135 140  
Gly Asp Ser Cys Ser Ile Pro Leu Pro Pro Thr Val Leu Glu Glu Ile  
145 150 155 160  
Ser Lys Asn Pro Asp Leu Val Tyr Thr Asp Lys Ser Gly Arg Arg Asn  
165 170 175  
Pro Glu Tyr Ile Ser Leu Gly Cys Asp Ser Val Pro Val Leu Arg Gly  
180 185 190  
Arg Thr Pro Ile Gln Val Tyr Ser Asp Phe Met Arg Ser Phe Arg Glu  
195 200 205  
Arg Phe Glu Gly Tyr Ile Gly Gly Val Ile Ala Glu Ile Gln Val Gly  
210 215 220  
Met Gly Pro Cys Gly Glu Leu Arg Tyr Pro Ser Tyr Pro Glu Ser Asn  
225 230 235 240  
Gly Thr Trp Arg Phe Pro Gly Ile Gly Glu Phe Gln Cys Tyr Asp Lys  
245 250 255  
Tyr Met Lys Ser Ser Leu Gln Ala Tyr Ala Glu Ser Ile Gly Lys Thr

260 265 270  
Asn Trp Gly Thr Ser Gly Pro His Asp Ala Gly Glu Tyr Lys Asn Leu  
275 280  
Pro Glu Asp Thr Glu Phe Phe Arg Arg Asp Gly Thr Trp Asn Ser Glu  
290 295 300  
Tyr Gly Lys Phe Phe Met Glu Trp Tyr Ser Gly Lys Leu Leu Glu His  
305 310 315 320  
Gly Asp Gln Leu Leu Ser Ser Ala Lys Gly Ile Phe Gln Gly Ser Gly  
325 330 335  
Ala Lys Leu Ser Gly Lys Val Ala Gly Ile His Trp His Tyr Asn Thr  
340 345 350  
Arg Ser His Ala Ala Glu Leu Thr Ala Gly Tyr Tyr Asn Thr Arg Asn  
355 360 365  
His Asp Gly Tyr Leu Pro Ile Ala Lys Met Phe Asn Lys His Gly Val  
370 375 380  
Val Leu Asn Phe Thr Cys Met Glu Met Lys Asp Gly Glu Gln Pro Glu  
385 390 395 400  
His Ala Asn Cys Ser Pro Glu Gly Leu Val Lys Gln Val Gln Asn Ala  
405 410 415  
Thr Arg Gln Ala Gly Thr Glu Leu Ala Gly Glu Asn Ala Leu Glu Arg  
420 425 430  
Tyr Asp Ser Ser Ala Phe Gly Gln Val Val Ala Thr Asn Arg Ser Asp  
435 440 445  
Ser Gly Asn Gly Leu Thr Ala Phe Thr Tyr Leu Arg Met Asn Lys Arg  
450 455 460  
Leu Phe Glu Gly Gln Asn Trp Gln Gln Leu Val Glu Phe Val Lys Asn  
465 470 475 480  
Met Lys Glu Gly Gly His Gly Arg Arg Leu Ser Lys Glu Asp Thr Thr  
485 490 495  
Gly Ser Asp Leu Tyr Val Gly Phe Val Lys Gly Lys Ile Ala Glu Asn  
500 505 510  
Val Glu Glu Ala Ala Leu Val  
515

(2) INFORMATION FOR SEQ ID NO:1998:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1446
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1998:

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| gacacgacgc | atccaaagaa | acttcaattt | tgggggtttc | cttcgtcttc  | ttcttcttct  | 60  |
| ttcttcttct | gatcgagagg | gacatgggtc | ttaccagccg | ccgttgacga  | ctacgacgac  | 120 |
| catctctctc | ctcttcatct | ttctctcttc | tgcttttctc | tatttctcat  | ttcttccaaa  | 180 |
| ttccaccatt | ccttccacca | ctcagagatc | ttcctttctt | attagctatg  | ttcttcttca  | 240 |
| acaagccatc | ttctagcgcc | gccgctgcgc | gatcgataga | ttcttccgcc  | gcccgagaaa  | 300 |
| attccaaagg | acccaagtat | tcgaaattta | ctcagcagga | gcttctctgt  | tgcaaaccaa  | 360 |
| ttcttaccgc | tggttggttg | atttcaacgt | ttttgatcat | tagtgtttatc | ttcatctccc  | 420 |
| ttggtgttat | ttctctcttt | gcttctccag | atgttgttga | gatcgttgat  | cgttatgata  | 480 |
| gtgcgatcat | acctctatct | gatagggtca | acaagggtgc | atacattcca  | ggaaactggaa | 540 |
| ataaatcttg | taccggagcg | ctaatgtgct | ctaaagctat | gaagcagcct  | attctatgat  | 600 |
| attaccagct | tgagaaactc | taccagaatc | accgcaggta | tgtgaaaagc  | cgaagtgtat  | 660 |
| cgcaattgag | aagtgtgaaa | gatgagaatc | aaatagacgc | atgcaagcct  | gaggatgatt  | 720 |
| ttggtgggca | gccaatgtgt | ccatgtggtc | taattgcttg | gagttctctt  | aatgacacat  | 780 |
| acgttctcat | aagaaataac | cagggtttta | cggtaaacaa | gaaagggaat  | gcattggaaga | 840 |
| gcgacaagga | acacaagtgt | gggaaaaatg | tgtttcccaa | gaactttcag  | aagggcaatc  | 900 |
| tcactgtgtg | tgccagctca | gatccaaata | aaccattgag | tgatcaagag  | gatctgatcg  | 960 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| tgtggatgag | gactgctgcg | ttgccaacat | ttagaaaatt | atacgggaag | atagagagtg | 1020 |
| acttgagaa  | gggtgagaac | atacaagtga | ctctgcagaa | caactacaac | acatacagtt | 1080 |
| tcagtgagaa | gaagaagcct | gttctgtcaa | caacaagtgt | gcttggtgga | aagaacgact | 1140 |
| tcctcgccat | tgcttacctc | accgttgggg | gaatctgttt | cgctctggca | cttgcattta | 1200 |
| cgcctcatga | tcttctgaaa | cccaggcgac | tcggtgatcc | tacctactgt | tcgtggaaac | 1260 |
| gaattccctg | aggctcgtaa | acagatgact | gcacatctcg | cgtatataaa | tctacttata | 1320 |
| tctgtgtgta | atttgatcca | aaattgaaa  | tgatgatctt | ttttttttta | atatagatgt | 1380 |
| gaaatgtatg | tatgatgtta | cagttggaat | atgctcatta | catagaatga | ttgatgcTtt | 1440 |
| cctatc     |            |            |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:1999:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..350

(D) OTHER INFORMATION: / Ceres Seq. ID 1571530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1999:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ser | Ser | Asn | Thr | Pro | Ser | Ser | Ser | Ala | Ala | Ala | Ala | Gly | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Asp | Ser | Ser | Ala | Ala | Arg | Arg | Asn | Ser | Lys | Arg | Pro | Lys | Tyr | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Phe | Thr | Gln | Gln | Glu | Leu | Pro | Ala | Cys | Lys | Pro | Ile | Leu | Thr | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Trp | Val | Ile | Ser | Thr | Phe | Leu | Ile | Ile | Ser | Val | Ile | Phe | Ile | Pro |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Leu | Gly | Val | Ile | Ser | Leu | Phe | Ala | Ser | Gln | Asp | Val | Val | Glu | Ile | Val |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     |     | 80  |     |
| Asp | Arg | Tyr | Asp | Ser | Ala | Cys | Ile | Pro | Leu | Ser | Asp | Arg | Ala | Asn | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Ala | Tyr | Ile | Gln | Gly | Thr | Gly | Asn | Lys | Ser | Cys | Thr | Arg | Thr | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Val | Pro | Lys | Arg | Met | Lys | Gln | Pro | Ile | Tyr | Val | Tyr | Tyr | Gln | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Glu | Asn | Phe | Tyr | Gln | Asn | His | Arg | Arg | Tyr | Val | Lys | Ser | Arg | Ser | Asp |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Ser | Gln | Leu | Arg | Ser | Val | Lys | Asp | Glu | Asn | Gln | Ile | Asp | Ala | Cys | Lys |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Pro | Glu | Asp | Asp | Phe | Gly | Gly | Gln | Pro | Ile | Val | Pro | Cys | Gly | Leu | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ala | Trp | Ser | Leu | Phe | Asn | Asp | Thr | Tyr | Val | Leu | Ser | Arg | Asn | Asn | Gln |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Leu | Thr | Val | Asn | Lys | Lys | Gly | Ile | Ala | Trp | Lys | Ser | Asp | Lys | Glu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| His | Lys | Phe | Gly | Lys | Asn | Val | Phe | Pro | Lys | Asn | Phe | Gln | Lys | Gly | Asn |
|     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Leu | Thr | Gly | Gly | Ala | Ser | Leu | Asp | Pro | Asn | Lys | Pro | Leu | Ser | Asp | Gln |
|     |     |     | 225 |     |     | 230 |     |     |     | 235 |     |     |     | 240 |     |
| Glu | Asp | Leu | Ile | Val | Trp | Met | Arg | Thr | Ala | Ala | Leu | Pro | Thr | Phe | Arg |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Lys | Leu | Tyr | Gly | Lys | Ile | Glu | Ser | Asp | Leu | Glu | Lys | Gly | Glu | Asn | Ile |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gln | Val | Thr | Leu | Gln | Asn | Asn | Tyr | Asn | Thr | Tyr | Ser | Phe | Ser | Gly | Lys |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Lys | Lys | Leu | Val | Leu | Ser | Thr | Thr | Ser | Trp | Leu | Gly | Gly | Lys | Asn | Asp |
|     |     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Phe | Leu | Gly | Ile | Ala | Tyr | Leu | Thr | Val | Gly | Gly | Ile | Cys | Phe | Val | Leu |
|     |     |     | 305 |     |     | 310 |     |     |     | 315 |     |     |     | 320 |     |

Ala Leu Ala Phe Thr Val Met Tyr Leu Val Lys Pro Arg Arg Leu Gly  
325 330 335  
Asp Pro Thr Tyr Leu Ser Trp Asn Arg Ile Pro Gly Gly Arg  
340 345 350

(2) INFORMATION FOR SEQ ID NO:2000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..233

(D) OTHER INFORMATION: / Ceres Seq. ID 1571531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2000:

Met Lys Gln Pro Ile Tyr Val Tyr Tyr Gln Leu Glu Asn Phe Tyr Gln  
1 5 10 15  
Asn His Arg Arg Tyr Val Lys Ser Arg Ser Asp Ser Gln Leu Arg Ser  
20 25 30  
Val Lys Asp Glu Asn Gln Ile Asp Ala Cys Lys Pro Glu Asp Asp Phe  
35 40 45  
Gly Gly Gln Pro Ile Val Pro Cys Gly Leu Ile Ala Trp Ser Leu Phe  
50 55 60  
Asn Asp Thr Tyr Val Leu Ser Arg Asn Asn Gln Gly Leu Thr Val Asn  
65 70 75 80  
Lys Lys Gly Ile Ala Trp Lys Ser Asp Lys Glu His Lys Phe Gly Lys  
85 90 95  
Asn Val Phe Pro Lys Asn Phe Gln Lys Gly Asn Leu Thr Gly Gly Ala  
100 105 110  
Ser Leu Asp Pro Asn Lys Pro Leu Ser Asp Gln Glu Asp Leu Ile Val  
115 120 125  
Trp Met Arg Thr Ala Ala Leu Pro Thr Phe Arg Lys Leu Tyr Gly Lys  
130 135 140  
Ile Glu Ser Asp Leu Glu Lys Gly Glu Asn Ile Gln Val Thr Leu Gln  
145 150 155 160  
Asn Asn Tyr Asn Thr Tyr Ser Phe Ser Gly Lys Lys Lys Leu Val Leu  
165 170 175  
Ser Thr Thr Ser Trp Leu Gly Gly Lys Asn Asp Phe Leu Gly Ile Ala  
180 185 190  
Tyr Leu Thr Val Gly Gly Ile Cys Phe Val Leu Ala Leu Ala Phe Thr  
195 200 205  
Val Met Tyr Leu Val Lys Pro Arg Arg Leu Gly Asp Pro Thr Tyr Leu  
210 215 220  
Ser Trp Asn Arg Ile Pro Gly Gly Arg  
225 230

(2) INFORMATION FOR SEQ ID NO:2001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1458

(D) OTHER INFORMATION: / Ceres Seq. ID 1571543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2001:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aaaaattctcg aaatcggaaa atttacacag agaagcgcca tgacctaaaa atctcaaaac | 60  |
| ttccccaaca aaatggcg ttttactcaa cccatttctc ttacctacc ttgtacatta     | 120 |
| ccctttttc caaatctcac tttccactg aaataacccc atggcgagaga atcagaactg   | 180 |



|             |            |            |            |             |             |      |
|-------------|------------|------------|------------|-------------|-------------|------|
| tgcgaggatg  | acgagagcgg | cggcgaaacg | aaaagcgtcg | tccatggcgt  | tagacgaaaa  | 240  |
| cccagttagt  | aagaagagag | ttgttctcgg | agagcttccg | aatatgtcca  | atgtcgttgc  | 300  |
| tgtaccocat  | caagaagaag | agacccttaa | ggctaaaaa  | agtgttaata  | cotcgaaagag | 360  |
| gcagatgaag  | aaggctttga | tgattcctga | agctagcgta | ctaatacgat  | cgagatctgt  | 420  |
| tgatcctcag  | atgtgtgagc | cttttgctag | tgatatttgt | gcttatctcc  | gtgaaatgga  | 480  |
| gggggaagcg  | aaacatagac | cactacctga | ttatattgaa | aaggttcaga  | gtgattttaa  | 540  |
| tcacacacat  | agagcggttt | tgggtgattg | gttagtgagg | gttgctgagg  | agtacaagct  | 600  |
| tgtttcggat  | acgctttatc | tcactatctc | ctatgttgat | agattcttgt  | ctgtgaagcc  | 660  |
| tattaacagg  | cagaagcttc | agcttctggg | agtttctgca | atgcttattg  | cgtcgaaaaa  | 720  |
| tgaagagata  | ggctctccta | aagttgaaga | tttttgttac | attacgggata | atacattttac | 780  |
| taaaacaagg  | gtgggtgtcg | tggaggcgga | tatacttctt | gctctgcagt  | ttgaattagg  | 840  |
| aaqcccaaac  | atcaaaacat | tactaagacg | gtttacacgg | gttgacacaag | aagattttcaa | 900  |
| agactaccaa  | ttgcagatag | agttcctttg | ttgctatcta | tcagaattga  | gtatgttaga  | 960  |
| ttacacctgt  | gtgaagtagt | tgccatctct | tttgtctgct | tcagctgtat  | ttcttgcccg  | 1020 |
| gttcctatc   | cgtccaaaac | aacatcctgt | gaatcaaatg | ctagaagaat  | acacaaaagta | 1080 |
| caaaagcagt  | gatctacaag | tgtgcgtggg | tatcatacat | gacttgtatc  | taagcagaag  | 1140 |
| aggaacacct  | ctagaagctg | ttagaaataa | tacaaagcaa | cacaagtaga  | agtgcggtgc  | 1200 |
| gaccatgcct  | gtttcacccg | agctacacct | tgctttcttt | gaagatatta  | ccattagagg  | 1260 |
| aatggcgctg  | aagaagcttg | aagctttatg | attgggaagt | ttagttacct  | gaattttggg  | 1320 |
| ttgtatatat  | ctgttagaat | ggcagattag | tattgagtat | tatctctttt  | acgctatggt  | 1380 |
| caatgatttt  | tGctwacac  | tagttaAgaa | actttttttt | ttTgctTgac  | cattttttca  | 1440 |
| atggttttatt | agatttttt  |            |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..369
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2002:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Asn | Gln | Asn | Cys | Ala | Arg | Met | Thr | Arg | Ala | Ala | Ala | Lys |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Lys | Ala | Ser | Ser | Met | Ala | Leu | Asp | Glu | Asn | Pro | Val | Ser | Lys | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Val | Val | Leu | Gly | Glu | Leu | Pro | Asn | Met | Ser | Asn | Val | Val | Ala | Val |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Pro | Asn | Gln | Glu | Arg | Glu | Thr | Leu | Lys | Ala | Lys | Thr | Ser | Val | Asn | Thr |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Ser | Lys | Arg | Gln | Met | Lys | Lys | Ala | Leu | Met | Ile | Pro | Glu | Ala | Ser | Val |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     | 80  |
| Leu | Ile | Glu | Ser | Arg | Ser | Val | Asp | Pro | Gln | Met | Cys | Glu | Pro | Phe | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | Asp | Ile | Cys | Ala | Tyr | Leu | Arg | Glu | Met | Glu | Gly | Lys | Pro | Lys | His |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Pro | Leu | Pro | Asp | Tyr | Ile | Glu | Lys | Val | Gln | Ser | Asp | Leu | Thr | Pro |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| His | Met | Arg | Ala | Val | Leu | Val | Asp | Trp | Leu | Val | Glu | Val | Ala | Glu | Glu |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |
| Tyr | Lys | Leu | Val | Ser | Asp | Thr | Leu | Tyr | Leu | Thr | Ile | Ser | Tyr | Val | Asp |
|     |     |     | 145 |     |     |     |     | 150 |     |     |     | 155 |     |     | 160 |
| Arg | Phe | Leu | Ser | Val | Lys | Pro | Ile | Asn | Arg | Gln | Lys | Leu | Gln | Leu | Val |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Gly | Val | Ser | Ala | Met | Leu | Ile | Ala | Ser | Lys | Tyr | Glu | Glu | Ile | Gly | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Lys | Val | Glu | Asp | Phe | Cys | Tyr | Ile | Thr | Asp | Asn | Thr | Phe | Thr | Lys |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     | 205 |     |     |     |
| Gln | Glu | Val | Val | Ser | Met | Glu | Ala | Asp | Ile | Leu | Leu | Ala | Leu | Gln | Phe |

|                                                                     |     |     |
|---------------------------------------------------------------------|-----|-----|
| 210                                                                 | 215 | 220 |
| Glu Leu Gly Ser Pro Thr Ile Lys Thr Phe Leu Arg Arg Phe Thr Arg     |     |     |
| 225                                                                 | 230 | 235 |
| Val Ala Gln Glu Asp Phe Lys Asp Ser Gln Leu Gln Ile Glu Phe Leu     |     |     |
| 240                                                                 | 245 | 250 |
| Cys Cys Tyr Leu Ser Glu Leu Ser Met Leu Asp Tyr Thr Cys Val Lys     |     |     |
| 255                                                                 | 260 | 265 |
| Tyr Leu Pro Ser Ser Leu Leu Ser Ala Ser Ala Val Phe Leu Ala Arg Phe |     |     |
| 270                                                                 | 275 | 280 |
| Ile Ile Arg Pro Lys Gln His Pro Trp Asn Gln Met Leu Glu Glu Tyr     |     |     |
| 285                                                                 | 290 | 300 |
| Thr Lys Tyr Lys Ala Ala Asp Leu Gln Val Cys Val Gly Ile Ile His     |     |     |
| 310                                                                 | 315 | 320 |
| Asp Leu Tyr Leu Ser Arg Arg Gly Asn Thr Leu Glu Ala Val Arg Asn     |     |     |
| 325                                                                 | 330 | 335 |
| Lys Tyr Lys Gln His Lys Tyr Lys Cys Val Ala Thr Met Pro Val Ser     |     |     |
| 340                                                                 | 345 | 350 |
| Pro Glu Leu Pro Leu Ala Phe Phe Glu Asp Ile Thr Ile Arg Gly Met     |     |     |
| 355                                                                 | 360 | 365 |

Ala

(2) INFORMATION FOR SEQ ID NO:2003:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 360 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..360  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2003:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Thr Arg Ala Ala Lys Arg Lys Ala Ser Ser Met Ala Leu Asp     |     |
| 1                                                               | 5   |
| Glu Asn Pro Val Ser Lys Lys Arg Val Val Leu Gly Glu Leu Pro Asn |     |
| 20                                                              | 25  |
| Met Ser Asn Val Val Ala Val Pro Asn Gln Glu Arg Glu Thr Leu Lys |     |
| 35                                                              | 40  |
| Ala Lys Thr Ser Val Asn Thr Ser Lys Arg Gln Met Lys Lys Ala Leu |     |
| 50                                                              | 55  |
| Met Ile Pro Glu Ala Ser Val Leu Ile Glu Ser Arg Ser Val Asp Pro |     |
| 65                                                              | 70  |
| Gln Met Cys Glu Pro Phe Ala Ser Asp Ile Cys Ala Tyr Leu Arg Glu |     |
| 85                                                              | 90  |
| Met Glu Gly Lys Pro Lys His Arg Pro Leu Pro Asp Tyr Ile Glu Lys |     |
| 100                                                             | 105 |
| Val Gln Ser Asp Leu Thr Pro His Met Arg Ala Val Leu Val Asp Trp |     |
| 115                                                             | 120 |
| Leu Val Glu Val Ala Glu Glu Tyr Lys Leu Val Ser Asp Thr Leu Tyr |     |
| 130                                                             | 135 |
| Leu Thr Ile Ser Tyr Val Asp Arg Phe Leu Ser Val Lys Pro Ile Asn |     |
| 145                                                             | 150 |
| Arg Gln Lys Leu Gln Leu Val Gly Val Ser Ala Met Leu Ile Ala Ser |     |
| 165                                                             | 170 |
| Lys Tyr Glu Glu Ile Gly Pro Pro Lys Val Glu Asp Phe Cys Tyr Ile |     |
| 180                                                             | 185 |
| Thr Asp Asn Thr Phe Thr Lys Gln Glu Val Val Ser Met Glu Ala Asp |     |
| 195                                                             | 200 |
| Ile Leu Leu Ala Leu Gln Phe Glu Leu Gly Ser Pro Thr Ile Lys Thr |     |
| 210                                                             | 215 |
|                                                                 | 220 |

Phe Leu Arg Arg Phe Thr Arg Val Ala Gln Glu Asp Phe Lys Asp Ser  
225 230 235 240  
Gln Leu Gln Ile Glu Phe Leu Cys Cys Tyr Leu Ser Glu Leu Ser Met  
245 250 255  
Leu Asp Tyr Thr Cys Val Lys Tyr Leu Pro Ser Leu Leu Ser Ala Ser  
260 265 270  
Ala Val Phe Leu Ala Arg Phe Ile Ile Arg Pro Lys Gln His Pro Trp  
275 280 285  
Asn Gln Met Leu Glu Glu Tyr Thr Lys Tyr Lys Ala Ala Asp Leu Gln  
290 295 300  
Val Cys Val Gly Ile Ile His Asp Leu Tyr Leu Ser Arg Arg Gly Asn  
305 310 315 320  
Thr Leu Glu Ala Val Arg Asn Lys Tyr Lys Gln His Lys Tyr Cys  
325 330 335  
Val Ala Thr Met Pro Val Ser Pro Glu Leu Pro Leu Ala Phe Phe Glu  
340 345 350  
Asp Ile Thr Ile Arg Gly Met Ala  
355 360

(2) INFORMATION FOR SEQ ID NO:2004:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1571546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2004:

Met Ala Leu Asp Glu Asn Pro Val Ser Lys Lys Arg Val Val Leu Gly  
1 5 10 15  
Glu Leu Pro Asn Met Ser Asn Val Val Ala Val Pro Asn Gln Glu Arg  
20 25 30  
Glu Thr Leu Lys Ala Lys Thr Ser Val Asn Thr Ser Lys Arg Gln Met  
35 40 45  
Lys Lys Ala Leu Met Ile Pro Glu Ala Ser Val Leu Ile Glu Ser Arg  
50 55 60  
Ser Val Asp Pro Gln Met Cys Glu Pro Phe Ala Ser Asp Ile Cys Ala  
65 70 75 80  
Tyr Leu Arg Glu Met Glu Gly Lys Pro Lys His Arg Pro Leu Pro Asp  
85 90 95  
Tyr Ile Glu Lys Val Gln Ser Asp Leu Thr Pro His Met Arg Ala Val  
100 105 110  
Leu Val Asp Trp Leu Val Glu Val Ala Glu Glu Tyr Lys Leu Val Ser  
115 120 125  
Asp Thr Leu Tyr Leu Thr Ile Ser Tyr Val Asp Arg Phe Leu Ser Val  
130 135 140  
Lys Pro Ile Asn Arg Gln Lys Leu Gln Leu Val Gly Val Ser Ala Met  
145 150 155 160  
Leu Ile Ala Ser Lys Tyr Glu Glu Ile Gly Pro Pro Lys Val Glu Asp  
165 170 175  
Phe Cys Tyr Ile Thr Asp Asn Thr Phe Thr Lys Gln Glu Val Val Ser  
180 185 190  
Met Glu Ala Asp Ile Leu Leu Ala Leu Gln Phe Glu Leu Gly Ser Pro  
195 200 205  
Thr Ile Lys Thr Phe Leu Arg Arg Phe Thr Arg Val Ala Gln Glu Asp  
210 215 220  
Phe Lys Asp Ser Gln Leu Gln Ile Glu Phe Leu Cys Cys Tyr Leu Ser  
225 230 235 240  
Glu Leu Ser Met Leu Asp Tyr Thr Cys Val Lys Tyr Leu Pro Ser Leu

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 245 |     | 250 |     | 255 |     |     |     |     |     |     |     |     |     |     |
| Leu | Ser | Ala | Ser | Ala | Val | Phe | Leu | Ala | Arg | Phe | Ile | Ile | Arg | Pro | Lys |
|     | 260 |     | 265 |     | 270 |     |     |     |     |     |     |     |     |     |     |
| Gln | His | Pro | Trp | Asn | Gln | Met | Leu | Glu | Glu | Tyr | Thr | Lys | Tyr | Lys | Ala |
|     | 275 |     | 280 |     | 285 |     |     |     |     |     |     |     |     |     |     |
| Ala | Asp | Leu | Gln | Val | Cys | Val | Gly | Ile | Ile | His | Asp | Leu | Tyr | Leu | Ser |
|     | 290 |     | 295 |     | 300 |     |     |     |     |     |     |     |     |     |     |
| Arg | Arg | Gly | Asn | Thr | Leu | Glu | Ala | Val | Arg | Asn | Lys | Tyr | Lys | Gln | His |
|     | 305 |     | 310 |     | 315 |     |     |     |     |     |     |     |     |     |     |
| Lys | Tyr | Lys | Cys | Val | Ala | Thr | Met | Pro | Val | Ser | Pro | Glu | Leu | Pro | Leu |
|     | 320 |     | 325 |     | 330 |     |     |     |     |     |     |     |     |     |     |
| Ala | Phe | Phe | Glu | Asp | Ile | Thr | Ile | Arg | Gly | Met | Ala |     |     |     |     |
|     | 340 |     | 345 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1203
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2005:

|             |            |             |             |             |            |      |
|-------------|------------|-------------|-------------|-------------|------------|------|
| acaaaagcat  | cataagaaga | agaagaact   | acaatagtta  | atcaatcaaa  | gagaagtaag | 60   |
| agaaatggca  | gattctaact | gtggatgtgg  | ctctctctgc  | aaatgtgggtg | actctttcgg | 120  |
| tgtgataaatt | ggaaagcttg | tctttttcag  | caagaatttg  | ccttcaaaagt | atgaagattg | 180  |
| ggaggcaggt  | acaaaagctt | tgctcgacaa  | ggaaaatata  | atcgccatgg  | gatcgattgg | 240  |
| atcagctctat | agagcatctt | tcgaaggagg  | agtttccatt  | gcagtgaaga  | agcttgagac | 300  |
| cttaggaaga  | atcagaagcc | aagaagagtt  | tgagcaagaa  | attggcagcg  | ttggaggttt | 360  |
| gcaacatccg  | aatctgtctt | ctttccaagg  | ttaactcttt  | tcctcaacaa  | tgcagttgat | 420  |
| ctctctctgag | tttgtcccta | atggtagcct  | ctacgataat  | ctacacctaa  | gaattttccc | 480  |
| gggaaccacg  | tcaagctatg | ggaatactga  | tittgaattgg | cacagaagat  | ttcagattgc | 540  |
| tttaggaact  | gcaaaaagcg | tctctttctt  | tcacaatgac  | tgtaaaaccgg | cgattcttca | 600  |
| tctcaatggt  | aagtcaccca | acattcttct  | agacgaaagg  | tacgagccaa  | agctatcgga | 660  |
| ttatgggtta  | gaaaagtttc | tccgggttat  | ggacagcttt  | ggtttgacta  | agaagtcca  | 720  |
| caacgcgggt  | gggtacattg | ctccagagtt  | agctcagcag  | agtttgagag  | cgagtggaaa | 780  |
| atgcatgtgt  | tatagttacg | gtgtggttct  | tcttgagctg  | gttacaggta  | gaaaaccggt | 840  |
| ggagctccca  | tcggaaaacc | aagctctgat  | cttgagagac  | tatgtgaggg  | attttgttga | 900  |
| gactggttca  | gcttctgatt | gttttgacag  | TYTaagACgt  | tgagagagtt  | tgaagagaat | 960  |
| gagctgattc  | aagtcatgaa | tttaggactc  | ctttgtacgt  | ccgagaatcc  | actgaagaga | 1020 |
| ccgagcagtg  | ctgaggttgt | gcagggttct  | gaatcaatca  | gaaatggatt  | tgatcaatga | 1080 |
| tgaagctttt  | tccttttttt | tgagcaaaaga | ttgcatagga  | aatgtgcaga  | taagttttat | 1140 |
| ttttgggat   | tttccagttt | tagatttacg  | tttgtcaat   | gaaattgtta  | ctctggtttm | 1200 |

cac

(2) INFORMATION FOR SEQ ID NO:2006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..292
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2006:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asp | Ser | Asn | Cys | Gly | Cys | Gly | Ser | Ser | Cys | Lys | Cys | Gly | Asp |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |
| Ser | Phe | Gly | Val | Ile | Ile | Gly | Lys | Leu | Val | Leu | Phe | Ser | Lys | Asn | Leu |

(2) INFORMATION FOR SEQ ID NO:2007:

(A) LENGTH: 238 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..238

(D) OTHER INFORMATION: / Ceres Seq. ID 1571549

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:2007:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Ile | Gly | Ser | Val | Tyr | Arg | Ala | Ser | Phe | Glu | Gly | Gly | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ile | Gly | Ala | Val | Lys | Lys | Leu | Glu | Thr | Leu | Gly | Arg | Ile | Arg | Asn |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Glu | Glu | Phe | Glu | Gln | Glu | Ile | Gly | Arg | Leu | Gly | Gly | Leu | Gln | His | Pro |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Asn | Leu | Ser | Ser | Phe | Gln | Gly | Tyr | Tyr | Phe | Ser | Ser | Thr | Met | Gln | Leu |
|     |     |     |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |
| Ile | Leu | Ser | Glu | Phe | Val | Pro | Asn | Gly | Ser | Leu | Tyr | Asp | Asn | Leu | His |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Arg | Ile | Phe | Pro | Gly | Thr | Ser | Ser | Ser | Tyr | Gly | Asn | Thr | Asp | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Trp | His | Arg | Arg | Phe | Gln | Ile | Ala | Leu | Gly | Thr | Ala | Lys | Ala | Leu |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |

Ser Phe Leu His Asn Asp Cys Lys Pro Ala Ile Leu His Leu Asn Val  
115 120 125  
Lys Ser Thr Asn Ile Leu Leu Asp Glu Arg Tyr Glu Ala Lys Leu Ser  
130 135 140  
Asp Tyr Gly Leu Glu Lys Phe Leu Pro Val Met Asp Ser Phe Gly Leu  
145 150 155 160  
Thr Lys Lys Phe His Asn Ala Val Gly Tyr Ile Ala Pro Glu Leu Ala  
165 170 175  
Gln Gln Ser Leu Arg Ala Ser Glu Lys Cys Asp Val Tyr Ser Tyr Gly  
180 185 190  
Val Val Leu Leu Glu Leu Val Thr Gly Arg Lys Pro Val Glu Ser Pro  
195 200 205  
Ser Glu Asn Gln Val Leu Ile Leu Arg Asp Tyr Val Arg Asp Leu Leu  
210 215 220  
Glu Thr Gly Ser Ala Ser Asp Cys Phe Asp Ser Xaa Arg Arg  
225 230 235

(2) INFORMATION FOR SEQ ID NO:2008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..177
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2008:

Met Gln Leu Ile Leu Ser Glu Phe Val Pro Asn Gly Ser Leu Tyr Asp  
1 5 10 15  
Asn Leu His Leu Arg Ile Phe Pro Gly Thr Ser Ser Ser Tyr Gly Asn  
20 25 30  
Thr Asp Leu Asn Trp His Arg Arg Phe Gln Ile Ala Leu Gly Thr Ala  
35 40 45  
Lys Ala Leu Ser Phe Leu His Asn Asp Cys Lys Pro Ala Ile Leu His  
50 55 60  
Leu Asn Val Lys Ser Thr Asn Ile Leu Leu Asp Glu Arg Tyr Glu Ala  
65 70 75 80  
Lys Leu Ser Asp Tyr Gly Leu Glu Lys Phe Leu Pro Val Met Asp Ser  
85 90 95  
Phe Gly Leu Thr Lys Lys Phe His Asn Ala Val Gly Tyr Ile Ala Pro  
100 105 110  
Glu Leu Ala Gln Gln Ser Leu Arg Ala Ser Glu Lys Cys Asp Val Tyr  
115 120 125  
Ser Tyr Gly Val Val Leu Leu Glu Leu Val Thr Gly Arg Lys Pro Val  
130 135 140  
Glu Ser Pro Ser Glu Asn Gln Val Leu Ile Leu Arg Asp Tyr Val Arg  
145 150 155 160  
Asp Leu Leu Glu Thr Gly Ser Ala Ser Asp Cys Phe Asp Ser Xaa Arg  
165 170 175

Arg

(2) INFORMATION FOR SEQ ID NO:2009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..1154

(D) OTHER INFORMATION: / Ceres Seq. ID 1571559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2009:

|            |             |            |            |            |             |      |
|------------|-------------|------------|------------|------------|-------------|------|
| agccctcttc | ccaattattg  | atcaatttct | aaagaaaacc | ccttcctcta | ctagtctctc  | 60   |
| tcctatatat | acaaaatctt  | aagaaatctc | tctacttgtt | tcctctgtta | tcataatctc  | 120  |
| ttctctctat | ttctctcttc  | ttctctcttt | acctctgttt | tttttttcat | tcacagagac  | 180  |
| ccaggttgat | tgatttttgt  | attcagagat | atggggagag | gaaggattga | gattaaagaa  | 240  |
| attgagaata | tcaacagctg  | tcaagtcact | ttctctaaga | gacgaaaagg | tttgatcaag  | 300  |
| aagggtctaa | agcttttgat  | ttctctgtac | gccgagggtg | ctcttatcat | cttctccagc  | 360  |
| accggcaaga | tttacgatatt | ctccagcgct | tgatggagac | aaattctttc | tagatatgga  | 420  |
| tacactactg | cgctccactga | gcataaacc  | caagagagac | accaactctc | aatttgtgtc  | 480  |
| tcacatggaa | atgaagctgt  | gttgcgaaat | gatgattcta | tgaagggtga | acttgaaaga  | 540  |
| ttacagcttg | caattgagag  | acttaagggt | aaggagcttg | aaggtatgag | tttcccggtg  | 600  |
| cttattttct | ttgaaaacca  | gttgaacgag | agcttgcata | gtgtcaagga | tcaaaagaca  | 660  |
| caaatctctg | tcaaccagat  | tgagagatcc | aggatacagg | agaaaaaagc | attggaagaa  | 720  |
| aaccaaatct | tgccgcaaca  | ggttgagatg | ttggggagag | gttcaggacc | aaaagtgttg  | 780  |
| aatgaaaggg | ctcaagattc  | tagcccgaga | gccgatcccg | agagctcttc | actcagaagag | 840  |
| gatgagaatg | acaaacgagg  | gcaccattcc | gacactctct | tgcagttggg | gttgctgctg  | 900  |
| acggggtatt | gcacaaagag  | aaagaagccg | aagatcgaa  | tggtctcgca | taactctggg  | 960  |
| agtcgaatgg | cttctgtatg  | atggaatcga | ttatttttct | aattctgggt | gtttaggggt  | 1020 |
| ctctatgtgt | cttctgtgtt  | ctggctgttc | ttttgcttta | tttcaactca | agtagcattt  | 1080 |
| ttttaatgtt | taggtggaac  | atttttccat | aatcaagaag | ggatttgatc | aatcaataac  | 1140 |
| attagatttt | cytt        |            |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:2010:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1571560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2010:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Arg | Gly | Arg | Ile | Glu | Ile | Lys | Lys | Ile | Glu | Asn | Ile | Asn | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Arg | Gln | Val | Thr | Phe | Ser | Lys | Arg | Arg | Asn | Gly | Leu | Ile | Lys | Lys | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Glu | Leu | Ser | Ile | Leu | Cys | Asp | Ala | Glu | Val | Ala | Leu | Ile | Ile | Phe |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ser | Thr | Gly | Lys | Ile | Tyr | Asp | Phe | Ser | Ser | Val | Cys | Met | Glu | Gln |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ile | Leu | Ser | Arg | Tyr | Gly | Tyr | Thr | Thr | Ala | Ser | Thr | Glu | His | Lys | Gln |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |
| Gln | Arg | Glu | His | Gln | Leu | Leu | Ile | Cys | Ala | Ser | His | Gly | Asn | Glu | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Val | Leu | Arg | Asn | Asp | Asp | Ser | Met | Lys | Val | Glu | Leu | Glu | Arg | Leu | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Ala | Ile | Glu | Arg | Leu | Lys | Gly | Lys | Glu | Leu | Glu | Gly | Met | Ser | Phe |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Asp | Leu | Ile | Ser | Phe | Glu | Asn | Gln | Leu | Asn | Glu | Ser | Leu | His | Ser |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Val | Lys | Asp | Gln | Lys | Thr | Gln | Ile | Leu | Leu | Asn | Gln | Ile | Glu | Arg | Ser |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |
| Arg | Ile | Gln | Glu | Lys | Lys | Ala | Leu | Glu | Glu | Asn | Gln | Ile | Leu | Arg | Lys |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Gln | Val | Glu | Met | Leu | Gly | Arg | Gly | Ser | Gly | Pro | Lys | Val | Leu | Asn | Glu |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Arg | Pro | Gln | Asp | Ser | Ser | Pro | Glu | Ala | Asp | Pro | Glu | Ser | Ser | Ser | Ser |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Glu | Asp | Glu | Asn | Asp | Asn | Glu | Glu | His | His | Ser | Asp | Thr | Ser | Leu |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gln | Leu | Gly | Leu | Ser | Ser | Thr | Gly | Tyr | Cys | Thr | Lys | Arg | Lys | Lys | Pro |
| 225 |     |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Lys | Ile | Glu | Leu | Val | Cys | Asp | Asn | Ser | Gly | Ser | Gln | Val | Ala | Ser | Asp |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |

(2) INFORMATION FOR SEQ ID NO:2011:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..195

(D) OTHER INFORMATION: / Ceres Seq. ID 1571561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2011:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gln | Ile | Leu | Ser | Arg | Tyr | Gly | Tyr | Thr | Thr | Ala | Ser | Thr | Glu |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| His | Lys | Gln | Gln | Arg | Glu | His | Gln | Leu | Ile | Cys | Ala | Ser | His | Gly |     |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Asn | Glu | Ala | Val | Leu | Arg | Asn | Asp | Asp | Ser | Met | Lys | Val | Glu | Leu | Glu |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Arg | Leu | Gln | Leu | Ala | Ile | Glu | Arg | Leu | Lys | Gly | Lys | Glu | Leu | Glu | Gly |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Met | Ser | Phe | Pro | Asp | Leu | Ile | Ser | Phe | Glu | Asn | Gln | Leu | Asn | Glu | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | His | Ser | Val | Lys | Asp | Gln | Lys | Thr | Gln | Ile | Leu | Leu | Asn | Gln | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Arg | Ser | Arg | Ile | Gln | Glu | Lys | Lys | Ala | Leu | Glu | Glu | Asn | Gln | Ile |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Leu | Arg | Lys | Gln | Val | Glu | Met | Leu | Gly | Arg | Gly | Ser | Gly | Pro | Lys | Val |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Leu | Asn | Glu | Arg | Pro | Gln | Asp | Ser | Ser | Pro | Glu | Ala | Asp | Pro | Glu | Ser |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |
| Ser | Ser | Ser | Glu | Glu | Asp | Glu | Asn | Asp | Asn | Glu | Glu | His | His | Ser | Asp |
|     |     |     |     | 145 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Thr | Ser | Leu | Gln | Leu | Gly | Leu | Ser | Ser | Thr | Gly | Tyr | Cys | Thr | Lys | Arg |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Lys | Pro | Lys | Ile | Glu | Leu | Val | Cys | Asp | Asn | Ser | Gly | Ser | Gln | Val |
|     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |

Ala Ser Asp

195

(2) INFORMATION FOR SEQ ID NO:2012:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1571562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2012:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Val | Glu | Leu | Glu | Arg | Leu | Gln | Leu | Ala | Ile | Glu | Arg | Leu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Lys | Glu | Leu | Glu | Gly | Met | Ser | Phe | Pro | Asp | Leu | Ile | Ser | Phe | Glu |





|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Thr Ala Gly Ser Ser Ser Val Thr Ser Ser Ser Ser Leu Ile Gly Phe |     |     |     |
| 20                                                              |     | 25  | 30  |
| Pro Arg Phe Gln Thr Leu Arg Phe Lys Ser Arg Ser Val Tyr Ser Lys |     |     |     |
| 35                                                              | 40  | 45  |     |
| Ser Arg Ala Ser Ser Pro Val Ser Ala Leu Pro Ser Arg Ser Leu Glu |     |     |     |
| 50                                                              | 55  | 60  |     |
| Ala Leu Ile Phe Asp Cys Asp Gly Val Ile Leu Glu Ser Glu Asn Leu |     |     |     |
| 65                                                              | 70  | 75  | 80  |
| His Arg Gln Ala Tyr Asn Asp Ala Phe Ser His Phe Asp Val Arg Cys |     |     |     |
| 85                                                              | 90  | 95  |     |
| Pro Pro Ser Ser Ser Ala Ser Leu Asp Trp Ser Leu Glu Phe Tyr Asp |     |     |     |
| 100                                                             | 105 | 110 |     |
| Lys Phe Gln Asn Leu Val Gly Gly Lys Pro Lys Met Arg Trp Tyr     |     |     |     |
| 115                                                             | 120 | 125 |     |
| Phe Lys Glu Asn Gly Trp Pro Thr Ser Thr Ile Phe Asp Ser Pro Pro |     |     |     |
| 130                                                             | 135 | 140 |     |
| Gln Asn Asp Asp Asp Arg Ala Lys Leu Ile Asp Thr Leu Gln Asp Trp |     |     |     |
| 145                                                             | 150 | 155 | 160 |
| Lys Thr Asp Arg Tyr Lys Glu Ile Ile Lys Ser Gly Ser Val Glu Pro |     |     |     |
| 165                                                             | 170 | 175 |     |
| Arg Pro Gly Val Ile Arg Leu Met Asp Glu Ala Lys Ala Ala Gly Lys |     |     |     |
| 180                                                             | 185 | 190 |     |
| Lys Leu Ala Val Cys Ser Ala Ala Thr Lys Ser Ser Val Ile Leu Cys |     |     |     |
| 195                                                             | 200 | 205 |     |
| Leu Glu Asn Leu Leu Asp Ile Glu Arg Phe Gln Gly Leu Asp Cys Phe |     |     |     |
| 210                                                             | 215 | 220 |     |
| Leu Ala Gly Asp Asp Val Lys Glu Lys Lys Pro Asp Pro Ser Ile Tyr |     |     |     |
| 225                                                             | 230 | 235 | 240 |
| Ile Thr Ala Ala Glu Lys Leu Gly Val Ser Val Lys Asp Cys Leu Val |     |     |     |
| 245                                                             | 250 | 255 |     |
| Val Gly Asp Ser Val Ile Gly Leu Gln Ala Ala Thr Lys Ala Gly Met |     |     |     |
| 260                                                             | 265 | 270 |     |
| Ser Cys Val Ile Thr Tyr Thr Ser Thr Ser Asp Gln Asp Phe Asn     |     |     |     |
| 275                                                             | 280 | 285 |     |
| Asp Ala Ile Ala Val Tyr Pro Asp Leu Ser Asn Val Lys Leu Thr Asp |     |     |     |
| 290                                                             | 295 | 300 |     |
| Leu Glu Thr Leu Leu Glu Thr Ile Val Thr Ala Ala                 |     |     |     |
| 305                                                             | 310 | 315 |     |

(2) INFORMATION FOR SEQ ID NO:2015:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1571569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2015:

|                                                                 |    |    |    |
|-----------------------------------------------------------------|----|----|----|
| Met Arg Trp Tyr Phe Lys Glu Asn Gly Trp Pro Thr Ser Thr Ile Phe |    |    |    |
| 1                                                               | 5  | 10 | 15 |
| Asp Ser Pro Pro Gln Asn Asp Asp Asp Arg Ala Lys Leu Ile Asp Thr |    |    |    |
| 20                                                              | 25 | 30 |    |
| Leu Gln Asp Trp Lys Thr Asp Arg Tyr Lys Glu Ile Ile Lys Ser Gly |    |    |    |
| 35                                                              | 40 | 45 |    |
| Ser Val Glu Pro Arg Pro Gly Val Ile Arg Leu Met Asp Glu Ala Lys |    |    |    |
| 50                                                              | 55 | 60 |    |
| Ala Ala Gly Lys Lys Leu Ala Val Cys Ser Ala Ala Thr Lys Ser Ser |    |    |    |
| 65                                                              | 70 | 75 | 80 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Ile | Leu | Cys | Leu | Glu | Asn | Leu | Leu | Asp | Ile | Glu | Arg | Phe | Gln | Gly |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Leu | Asp | Cys | Phe | Leu | Ala | Gly | Asp | Asp | Val | Lys | Glu | Lys | Lys | Pro | Asp |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Pro | Ser | Ile | Tyr | Ile | Thr | Ala | Ala | Glu | Lys | Leu | Gly | Val | Ser | Val | Lys |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Asp | Cys | Leu | Val | Val | Gly | Asp | Ser | Val | Ile | Gly | Leu | Gln | Ala | Ala | Thr |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Lys | Ala | Gly | Met | Ser | Cys | Val | Ile | Thr | Tyr | Thr | Ser | Ser | Thr | Ser | Asp |  |
|     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Gln | Asp | Phe | Asn | Asp | Ala | Ile | Ala | Val | Tyr | Pro | Asp | Leu | Ser | Asn | Val |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Lys | Leu | Thr | Asp | Leu | Glu | Thr | Leu | Leu | Gln | Thr | Ile | Val | Thr | Ala | Ala |  |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1714
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2016:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| aaatataaaa  | aatggatgga  | tcaacgKgct  | gcgatcatcc  | ttaccctcat  | cgtaacctac  | 60   |
| attatatgggt | ttgtttctttt | acgtogttcg  | tataaaggctc | cacgtgtctgc | gcccttagtg  | 120  |
| ggcagttcttc | cagcactcat  | aacaaatgct  | caccgcgatgc | acgactctcat | cgccgataac  | 180  |
| ctcccgaatgt | ggcgccgtac  | gtaccaaaacg | tgcatattcc  | cgatcccgtt  | cttggtctaa  | 240  |
| aaacaaggctc | acgtgactgt  | cacgtgtgac  | ccaaagaatc  | tggagcatat  | cttgaagacc  | 300  |
| cggttcgata  | attaccccga  | gggtctctagc | tggcaatcag  | tcttcacaga  | tctgttagga  | 360  |
| gatgggatct  | ttaattcaga  | tgggtgacaca | tggcgggttc  | aacgtaagac  | cgctgcattg  | 420  |
| gagttgcacta | cacgtaccct  | tgcgcaagcc  | atggctcggt  | gggttgatcg  | agccatcaag  | 480  |
| aaccgtctcg  | tggcgattct  | tgaatcagct  | aggagtcgag  | ccgagccgat  | tgatcttcaa  | 540  |
| gatgttctttt | tacggctcac  | tttcgataac  | atttgcggct  | taacatttgg  | taaaagatcca | 600  |
| cggacactct  | cgccggagtt  | tcttgagaac  | ggattcgcgg  | tggcttttga  | tggagccacc  | 660  |
| gaagccactc  | ttcaacgggt  | tatcatgcct  | gagtttattt  | ggaagatcag  | aaaaatggctt | 720  |
| cggtctcggtt | tggaaagatga | tatgacgga   | agcatcagcc  | acgtggataa  | ttacttatca  | 780  |
| gagatcataa  | atacacgtaa  | gctcgaattg  | ctaggtcagc  | aacaagatgg  | atcccgcact  | 840  |
| gatgatctat  | tgtcacgggt  | catgaagaaa  | aaagaatcct  | actcggataa  | atatctttaa  | 900  |
| tacgtggcgt  | taaattttcat | cctagctgga  | cgtaaacagct | catcggttgc  | tatgagttgg  | 960  |
| ttcttctctgt | tgggttagtct | taaccccaga  | gtcgaagaaa  | aaatcataaa  | cgagatctcg  | 1020 |
| accattctga  | tcaagacacg  | tgacaccaat  | gtgtcgaagt  | ggaccgaaga  | gcggttgact  | 1080 |
| ttcgatgaaa  | ttgacagatt  | gggtctactta | aaagcggcat  | tgtccgaaac  | attgaggctga | 1140 |
| ttatcatcgct | taccagaaga  | tttcaaaattt | gtgttgccca  | acgatatttt  | acctgacggg  | 1200 |
| acattttgttc | catcgggcatc | aaacgtttaca | tattcgatat  | attcggttgg  | gcgatgaaa   | 1260 |
| ttcattttggg | gtgaaagatga | tctcgaattt  | aaaccggaaa  | gatggtttaga | gaaagccggg  | 1320 |
| gacgaaaaaat | gtaaaccaata | caaattctgta | gcgtttcaatg | ccggtccacg  | gattttgtcta | 1380 |
| ggcaaaagact | tggctttattt | cgagatgaaa  | tcaattactg  | cttcgatattt | gcctccggcat | 1440 |
| cggtctacgg  | tggctccggg  | acatcagagt  | gagcagaaga  | tgtcatttag  | gtgtgtcatg  | 1500 |
| aaagtgtgtgc | ttaaaaatgga | tgtgcataaa  | agggatttga  | cgttgcgggt  | ggagaaagtg  | 1560 |
| gttaatgaga  | tgaggaaaaa  | gtgagattat  | tgggaactaat | gatggttaac  | atgatgaagt  | 1620 |
| taaatgtgtc  | accggtttgg  | cataagcatt  | aatgtggagc  | atggttaatt  | agaaattgtg  | 1680 |
| ttgtgtgaag  | caaaaataaat | ttaaaaacata | cttt        |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2017:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 amino acids
- (B) TYPE: amino acid

[illegible]

(2) INFORMATION FOR SEQ ID NO:2018:

(A) LENGTH: 522 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

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{A} NAME/KEY: peptide
```

(B) LOCATION: 1..522

(D) OTHER INFORMATION: / Ceres Seq. ID 1571572

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2018:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Gln | Xaa | Ala | Ala | Ile | Ile | Leu | Thr | Leu | Ile | Val | Thr | Tyr | Ile |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Trp | Phe | Val | Ser | Leu | Arg | Arg | Ser | Tyr | Lys | Gly | Pro | Arg | Val | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Leu | Val | Gly | Ser | Leu | Pro | Ala | Leu | Ile | Thr | Asn | Ala | His | Arg | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Asp | Phe | Ile | Ala | Asp | Asn | Leu | Arg | Met | Cys | Gly | Gly | Thr | Tyr | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Thr | Cys | Ile | Phe | Pro | Ile | Pro | Phe | Leu | Ala | Lys | Lys | Gln | Gly | His | Val |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Val | Thr | Cys | Asp | Pro | Lys | Asn | Leu | Glu | His | Ile | Leu | Lys | Thr | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Phe | Asp | Asn | Tyr | Trp | Lys | Gly | Pro | Ser | Trp | Gln | Ser | Val | Phe | His | Asp |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Leu | Gly | Asp | Gly | Ile | Phe | Asn | Ser | Asp | Gly | Asp | Thr | Trp | Arg | Phe |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gln | Arg | Lys | Thr | Ala | Ala | Leu | Glu | Phe | Thr | Thr | Arg | Thr | Leu | Thr | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Ala | Met | Ala | Arg | Trp | Val | Asp | Arg | Ala | Ile | Lys | Asn | Arg | Leu | Val | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ile | Leu | Glu | Ser | Ala | Arg | Ser | Arg | Ala | Glu | Pro | Ile | Asp | Leu | Gln | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Leu | Leu | Arg | Leu | Thr | Phe | Asp | Asn | Ile | Cys | Gly | Leu | Thr | Phe | Gly |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Asp | Pro | Arg | Thr | Leu | Ser | Pro | Glu | Phe | Pro | Glu | Asn | Gly | Phe | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Ala | Phe | Asp | Gly | Ala | Thr | Glu | Ala | Thr | Leu | Gln | Arg | Phe | Ile | Met |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Pro | Glu | Phe | Ile | Trp | Lys | Ile | Arg | Lys | Trp | Leu | Arg | Leu | Gly | Leu | Glu |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Asp | Asp | Met | Ser | Arg | Ser | Ile | Ser | His | Val | Asp | Asn | Tyr | Leu | Ser | Glu |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Ile | Ile | Asn | Thr | Arg | Lys | Leu | Glu | Leu | Leu | Gly | Gln | Gln | Gln | Asp | Gly |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Arg | His | Asp | Asp | Leu | Leu | Ser | Arg | Phe | Met | Lys | Lys | Lys | Glu | Ser |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

Tyr Ser Asp Lys Tyr Leu Lys Tyr Val Ala Leu Asn Phe Ile Leu Ala  
290 295 300  
Gly Arg Asn Thr Ser Ser Val Ala Met Ser Trp Phe Phe Trp Leu Val  
305 310 315 320  
Ser Leu Asn Pro Arg Val Glu Glu Lys Ile Ile Asn Glu Ile Cys Thr  
325 330 335  
Ile Leu Ile Lys Thr Arg Asp Thr Asn Val Ser Lys Trp Thr Asp Glu  
340 345 350  
Pro Leu Thr Phe Asp Glu Ile Asp Gln Leu Val Tyr Leu Lys Ala Ala  
355 360 365  
Leu Ser Glu Thr Leu Arg Leu Tyr Pro Ser Val Pro Glu Asp Ser Lys  
370 375 380  
Phe Val Val Ala Asn Asp Val Leu Pro Asp Gly Thr Phe Val Pro Ser  
385 390 395 400  
Gly Ser Asn Val Thr Tyr Ser Ile Tyr Ser Val Gly Arg Met Lys Phe  
405 410 415  
Ile Trp Gly Glu Asp Cys Leu Glu Phe Lys Pro Glu Arg Trp Leu Glu  
420 425 430  
Glu Ser Arg Asp Glu Lys Cys Asn Gln Tyr Lys Phe Val Ala Phe Asn  
435 440 445  
Ala Gly Pro Arg Ile Cys Leu Gly Lys Asp Leu Ala Tyr Leu Gln Met  
450 455 460  
Lys Ser Ile Thr Ala Ser Ile Leu Leu Arg His Arg Leu Thr Val Ala  
465 470 475 480  
Pro Gly His Arg Val Glu Gln Lys Met Ser Leu Thr Leu Phe Met Lys  
485 490 495  
Phe Gly Leu Lys Met Asp Val His Lys Arg Asp Leu Thr Leu Pro Val  
500 505 510  
Glu Lys Val Val Asn Glu Met Arg Lys Lys  
515 520

(2) INFORMATION FOR SEQ ID NO:2019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..475
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2019:

Met His Asp Phe Ile Ala Asp Asn Leu Arg Met Cys Gly Thr Tyr  
1 5 10 15  
Gln Thr Cys Ile Phe Pro Ile Pro Phe Leu Ala Lys Lys Gln Gly His  
20 25 30  
Val Thr Val Thr Cys Asp Pro Lys Asn Leu Glu His Ile Leu Lys Thr  
35 40 45  
Arg Phe Asp Asn Tyr Pro Lys Gly Pro Ser Trp Gln Ser Val Phe His  
50 55 60  
Asp Leu Leu Gly Asp Gly Ile Phe Asn Ser Asp Gly Asp Thr Trp Arg  
65 70 75 80  
Phe Gln Arg Lys Thr Ala Ala Leu Glu Phe Thr Thr Arg Thr Arg  
85 90 95  
Gln Ala Met Ala Arg Trp Val Asp Arg Ala Ile Lys Asn Arg Leu Val  
100 105 110  
Pro Ile Leu Glu Ser Ala Arg Ser Arg Ala Glu Pro Ile Asp Leu Gln  
115 120 125  
Asp Val Leu Leu Arg Leu Thr Phe Asp Asn Ile Cys Gly Leu Thr Phe  
130 135 140  
Gly Lys Asp Pro Arg Thr Leu Ser Pro Glu Phe Pro Glu Asn Gly Phe

|                                                                 |     |     |  |     |  |     |
|-----------------------------------------------------------------|-----|-----|--|-----|--|-----|
| 145                                                             |     | 150 |  | 155 |  | 160 |
| Ala Val Ala Phe Asp Gly Ala Thr Glu Ala Thr Leu Gln Arg Phe Ile |     |     |  |     |  |     |
|                                                                 | 165 |     |  | 170 |  | 175 |
| Met Pro Glu Phe Ile Trp Lys Ile Arg Lys Trp Leu Arg Leu Gly Leu |     |     |  |     |  |     |
|                                                                 | 180 |     |  | 185 |  | 190 |
| Glu Asp Asp Met Ser Arg Ser Ile Ser His Val Asp Asn Tyr Leu Ser |     |     |  |     |  |     |
|                                                                 | 195 |     |  | 200 |  | 205 |
| Glu Ile Ile Asn Thr Arg Lys Leu Glu Leu Gly Gln Gln Gln Asp     |     |     |  |     |  |     |
|                                                                 | 210 |     |  | 215 |  | 220 |
| Gly Ser Arg His Asp Asp Leu Leu Ser Arg Phe Met Lys Lys Lys Glu |     |     |  |     |  |     |
|                                                                 | 225 |     |  | 230 |  | 235 |
| Ser Tyr Ser Asp Lys Tyr Leu Lys Tyr Val Ala Leu Asn Phe Ile Leu |     |     |  |     |  |     |
|                                                                 | 245 |     |  | 250 |  | 255 |
| Ala Gly Arg Asn Thr Ser Ser Val Ala Met Ser Trp Phe Phe Trp Leu |     |     |  |     |  |     |
|                                                                 | 260 |     |  | 265 |  | 270 |
| Val Ser Leu Asn Pro Arg Val Glu Glu Lys Ile Ile Asn Glu Ile Cys |     |     |  |     |  |     |
|                                                                 | 275 |     |  | 280 |  | 285 |
| Thr Ile Leu Ile Lys Thr Arg Asp Thr Asn Val Ser Lys Trp Thr Asp |     |     |  |     |  |     |
|                                                                 | 290 |     |  | 295 |  | 300 |
| Glu Pro Leu Thr Phe Asp Glu Ile Asp Gln Leu Val Tyr Leu Lys Ala |     |     |  |     |  |     |
|                                                                 | 305 |     |  | 310 |  | 315 |
| Ala Leu Ser Glu Thr Leu Arg Leu Tyr Pro Ser Val Pro Glu Asp Ser |     |     |  |     |  |     |
|                                                                 | 325 |     |  | 330 |  | 335 |
| Lys Phe Val Val Ala Asn Asp Val Leu Pro Asp Gly Thr Phe Val Pro |     |     |  |     |  |     |
|                                                                 | 340 |     |  | 345 |  | 350 |
| Ser Gly Ser Asn Val Thr Tyr Ser Ile Tyr Ser Val Gly Arg Met Lys |     |     |  |     |  |     |
|                                                                 | 355 |     |  | 360 |  | 365 |
| Phe Ile Trp Gly Glu Asp Cys Leu Glu Phe Lys Pro Glu Arg Trp Leu |     |     |  |     |  |     |
|                                                                 | 370 |     |  | 375 |  | 380 |
| Glu Glu Ser Arg Asp Glu Lys Cys Asn Gln Tyr Lys Phe Val Ala Phe |     |     |  |     |  |     |
|                                                                 | 385 |     |  | 390 |  | 395 |
| Asn Ala Gly Pro Arg Ile Cys Leu Gly Lys Asp Leu Ala Tyr Leu Gln |     |     |  |     |  |     |
|                                                                 | 405 |     |  | 410 |  | 415 |
| Met Lys Ser Ile Thr Ala Ser Ile Leu Leu Arg His Arg Leu Thr Val |     |     |  |     |  |     |
|                                                                 | 420 |     |  | 425 |  | 430 |
| Ala Pro Gly His Arg Val Glu Gln Lys Met Ser Leu Thr Leu Phe Met |     |     |  |     |  |     |
|                                                                 | 435 |     |  | 440 |  | 445 |
| Lys Phe Gly Leu Lys Met Asp Val His Lys Arg Asp Leu Thr Leu Pro |     |     |  |     |  |     |
|                                                                 | 450 |     |  | 455 |  | 460 |
| Val Glu Lys Val Val Asn Glu Met Arg Lys Lys                     |     |     |  |     |  |     |
|                                                                 | 465 |     |  | 470 |  | 475 |

(2) INFORMATION FOR SEQ ID NO:2020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1276

(D) OTHER INFORMATION: / Ceres Seq. ID 1571582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2020:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| aaaWgaagtt | cctcattcaa | aaaagatttc | tcagccatca | aaattctctt | tctcttcac   | 60  |
| caacaaaaaa | aaagcatacc | tctttttctt | ccatatagat | aagttaatta | agaaaacgaa  | 120 |
| ttatcaggtt | ttgtttcgcc | tgatctgagg | aagttcatct | atggatcagg | ctcagtgcc   | 180 |
| acaggagatt | gtagtgaagc | ccttggaaga | aatagtaaca | aacacatgcc | caaaagccaca | 240 |
| accgcaaccc | cttcaaacgc | agcagccacc | gtcgggtggg | ggagagagga | aggcaagacc  | 300 |
| agaaaagat  | caagctgtaa | actgtccgag | atgtaactca | accaacacaa | agttttgtta  | 360 |
| ctacaacaat | tatagtgtta | cgcagccaag | atacttctgc | aaaggttgta | gaaggtattg  | 420 |
| gaccgaaGgc | ggttcgotta | ggaacattcc | tgttggcggt | ggctcaagaa | agaacaagag  | 480 |

|            |             |             |            |            |            |      |
|------------|-------------|-------------|------------|------------|------------|------|
| atctcactct | ttttctctctg | atattagtaa  | caatcactcg | gattctacac | aaccagctac | 540  |
| aaagaagcat | ctctctgac   | atcaccacca  | cctcatgagc | atgtctcaac | aaggtttgac | 600  |
| cggtcaaaac | ctcaaatcc   | ttgagacgac  | ccacaagat  | ctcaatttag | gtttttcacc | 660  |
| acatgggatg | attaggacca  | acttcactga  | cctcatccac | aacattggca | acaacaccaa | 720  |
| caagagcaac | aacaataaca  | atccattgat  | tgttttctca | tgttctacca | tggtcacttc | 780  |
| ttctctggat | ctcataagaa  | acaatagtaa  | caatgggaat | tctcaaat   | cttccttcac | 840  |
| gggatttcca | gttcataatg  | aagatccagc  | atcaggaggg | ttttcaatgc | aagatcatta | 900  |
| caagccttgc | aacacaaaca  | ccacactgct  | aggggtttca | ttagatcatc | atcataataa | 960  |
| tggatttcat | ggaggggttc  | aagaggagga  | agaaggtgga | gaaggtgggt | atgatgtgaa | 1020 |
| tggaaggcac | ttgtttcctt  | ttgaggattt  | gaaattgcca | gtttcttctt | catcagcaac | 1080 |
| aattaatgtc | gacattaatg  | aaacatcagaa | gcgaggaagc | ggtagtgtgc | cagctgctac | 1140 |
| gtctgtgtgg | tattggactg  | ggatgttgag  | tggaggatca | tggtgtcata | taatttctcg | 1200 |
| gtttggttga | tgaagatagt  | actattagt   | gttaattatt | gctatttatt | taattaatca | 1260 |
| atatgttctt | aatttc      |             |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:2021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..342
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2021:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Thr | Ala | Gln | Trp | Pro | Gln | Glu | Ile | Val | Val | Lys | Pro | Leu | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Glu | Ile | Val | Thr | Asn | Thr | Cys | Pro | Lys | Pro | Gln | Pro | Gln | Pro | Leu | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Gln | Gln | Pro | Pro | Ser | Val | Gly | Gly | Glu | Arg | Lys | Ala | Arg | Pro | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Asp | Gln | Ala | Val | Asn | Cys | Pro | Arg | Cys | Asn | Ser | Thr | Asn | Thr | Lys |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Phe | Cys | Tyr | Tyr | Asn | Asn | Tyr | Ser | Leu | Thr | Gln | Pro | Arg | Tyr | Phe | Cys |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Gly | Cys | Arg | Arg | Tyr | Trp | Thr | Glu | Gly | Gly | Ser | Leu | Arg | Asn | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Pro | Val | Gly | Gly | Gly | Ser | Arg | Lys | Asn | Lys | Arg | Ser | His | Ser | Phe | Ser |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ser | Asp | Ile | Ser | Asn | Asn | His | Ser | Asp | Ser | Thr | Gln | Pro | Ala | Thr | Lys |
|     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Lys | His | Leu | Ser | Asp | His | His | His | Leu | Met | Ser | Met | Ser | Gln | Gln |     |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Leu | Thr | Gly | Gln | Asn | Pro | Lys | Phe | Leu | Glu | Thr | Thr | Gln | Gln | Asp |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Asn | Leu | Gly | Phe | Ser | Pro | His | Gly | Met | Ile | Arg | Thr | Asn | Phe | Thr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Asp | Leu | Ile | His | Asn | Ile | Gly | Asn | Asn | Thr | Asn | Lys | Ser | Asn | Asn | Asn |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Asn | Asn | Pro | Leu | Ile | Val | Ser | Ser | Cys | Ser | Thr | Met | Ala | Thr | Ser | Ser |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Asp | Leu | Ile | Arg | Asn | Asn | Ser | Asn | Asn | Gly | Asn | Ser | Ser | Asn | Ser |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Phe | Met | Gly | Phe | Pro | Val | His | Asn | Glu | Asp | Pro | Ala | Ser | Gly | Gly |
|     |     |     | 225 |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |
| Phe | Ser | Met | Gln | Asp | His | Tyr | Lys | Pro | Cys | Asn | Thr | Asn | Thr | Thr | Leu |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Gly | Phe | Ser | Leu | Asp | His | His | His | Asn | Asn | Gly | Phe | His | Gly | Gly |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Phe | Gln | Gly | Gly | Glu | Glu | Gly | Gly | Gly | Gly | Asp | Asp | Val | Asn | Gly |     |



(2) INFORMATION FOR SEO ID NO:2022:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1571584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2022:

(2) INFORMATION FOR SEQ ID NO:2023:

(A) LENGTH: 202 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..202

(D) OTHER INFORMATION: / Ceres Seq. ID 1571585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2023:

Met Ser Gln Gln Gly Leu Thr Gly Gln Asn Pro Lys Phe Leu Glu Thr  
1 5 10 15

```

Thr Gln Gln Asp Leu Asn Leu Gly Phe Ser Pro His Gly Met Ile Arg
 20 25 30
Thr Asn Phe Thr Asp Leu Ile His Asn Ile Gly Asn Asn Thr Asn Lys
 35 40 45
Ser Asn Asn Asn Asn Asn Pro Leu Ile Val Ser Ser Cys Ser Thr Met
 50 55 60
Ala Thr Ser Ser Leu Asp Leu Ile Arg Asn Asn Ser Asn Asn Gly Asn
 65 70 75 80
Ser Ser Asn Ser Ser Phe Met Gly Phe Pro Val His Asn Glu Asp Pro
 85 90 95
Ala Ser Gly Gly Phe Ser Met Gln Asp His Tyr Lys Pro Cys Asn Thr
 100 105 110
Asn Thr Thr Leu Leu Gly Phe Ser Leu Asp His His His Asn Asn Gly
 115 120 125
Phe His Gly Gly Phe Gln Gly Gly Glu Glu Gly Gly Glu Gly Asp
 130 135 140
Asp Val Asn Gly Arg His Leu Phe Pro Phe Glu Asp Leu Lys Leu Pro
 145 150 155 160
Val Ser Ser Ser Ser Ala Thr Ile Asn Val Asp Ile Asn Glu His Gln
 165 170 175
Lys Arg Gly Ser Gly Ser Asp Ala Ala Ala Thr Ser Gly Gly Tyr Trp
 180 185 190
Thr Gly Met Leu Ser Gly Gly Ser Trp Cys
 195 200

```

(2) INFORMATION FOR SEQ ID NO:2024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1709
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2024:

```

attttgtgca tttttctcaa gctgcgcgcg tttctcactc ttttttatct ctcaaatgtg 60
accttctctcg ttgttctttc gcacgcgcctca ggagcagaag cttcaatctt tgataaatgc 120
gaggaaacaag gggttggtcg agcaagatct taaaaaattg gatgtaactg gtctacatcc 180
tctgtctctcc gaggtcattt ctccgccaggc cactattaat ataggaacca ttggtcatgt 240
cgctcatcgga aagtcacactg ttgtttaaagc tatttctggt gtccagactg tccgttttaa 300
aaatgaattg gagcgttaaca ttaccattaa gcttggtgat gcaaacgccca agatttaca 360
atgtgaggat gagaattgcc ctagaccaat gtgctacaag gccacggaa gtggaaggaa 420
agacactccc aattgtgatg tccccggatt tgaaaactcc aagatgaaac tattgaggca 480
gtgtctcattc gttgattgcc ogggtcacga tattctcatg gcMacaatgc ttaatggagc 540
agccatcatg gatgggtgcac tacttttaac cgctgcacaa gaaacttgct cacaaccaca 600
aacgtctgaa catcttgctg ccgttgagat tatgcaactt aagcatatca tcatccttca 660
gaacaagatt gatcttattc aagagaatgt tgccattaat cagcacgagg caattcagaa 720
atttataatg aaactgtgtg ctgatgctgc tccgatcgtc cctgtctcag cacaactgaa 780
atacaacatt gatgtggtgt gcgagtacat tgtcaagaag atccaattcc ctgagaggaa 840
ttttgtgtca cccccaaata tgatagtgat tcggtctttt gatgtcaaca aacctgggta 900
tgaggttgat gagatcaaa gttggagtgc aggttgaaat atctacggg gtgttttag 960
agtcacaacca ttaatcgaaa tccgacctgt tatcgttacc aaagacgagc gtggcaactc 1020
aaaatgcact ccaatttact ctgcctcatc ttcaacttac cggaagagaa acgagcttca 1080
gtttgtgtgt cctgaaggct taataggagt tggaaacaaca atggacccaa ctctcaactc 1140
tcgacatcga ttagtgtgtc aagtcctgtg tgaaatcggt tcaacttctg atgtattatg 1200
tgaactcgag gtgaacttct ttctctcagc acgtttgtgt ggaagtggaa caaagggatc 1260
agagaaacaa gggaaagtgt caaagctaac gaaagagagc attctgatgc tcaactatgt 1320
ttcgatgtcc actggagcca agtttgtagg agtttaaagt gatctgccta acgttcaact 1380
gactgcgcct gtttgtacca gcaaaaggaga gaaagtggct ctaagcagac gtgtggaaaa 1440
gcattggcgt ttgattgtgt ggggtcagat tcaagctgga accaccatcg aagtgcctcc 1500

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ttcacctttc taagctatgt gttatttttg tcttttttgt ttgtgtttct gaaaaaaga 1560  
ttgttaaacc cctcaaaaag ataataaac tctttttctc gttggggagt ttggagagt 1620  
tcgtctttgc ggattaaaca tcttcaaca gtacctgatt tgttattgtt actagtttgc 1680  
tctttgttat tgtaactagt ttgctcttt

(2) INFORMATION FOR SEQ ID NO:2025:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..465

(D) OTHER INFORMATION: / Ceres Seq. ID 1571587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2025:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Arg | Asn | Lys | Gly | Leu | Ala | Glu | Gln | Asp | Leu | Lys | Lys | Leu | Asp |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Thr | Val | Leu | His | Pro | Leu | Ser | Pro | Glu | Val | Ile | Ser | Arg | Gln | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ile | Asn | Ile | Gly | Thr | Ile | Gly | His | Val | Ala | His | Gly | Lys | Ser | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Val | Lys | Ala | Ile | Ser | Gly | Val | Gln | Thr | Val | Arg | Phe | Lys | Asn | Glu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Glu | Arg | Asn | Ile | Thr | Ile | Lys | Leu | Gly | Tyr | Ala | Asn | Ala | Lys | Ile |
|     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Tyr | Lys | Cys | Glu | Asp | Glu | Lys | Cys | Pro | Arg | Pro | Met | Cys | Tyr | Lys | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |     |
| Tyr | Gly | Ser | Gly | Lys | Glu | Asp | Thr | Pro | Asn | Cys | Asp | Val | Pro | Gly | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Glu | Asn | Ser | Lys | Met | Lys | Leu | Leu | Arg | His | Val | Ser | Phe | Val | Asp | Cys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Gly | His | Asp | Ile | Leu | Met | Xaa | Thr | Met | Leu | Asn | Gly | Ala | Ala | Ile |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Met | Asp | Gly | Ala | Leu | Leu | Leu | Ile | Ala | Ala | Asn | Glu | Thr | Cys | Pro | Gln |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Pro | Gln | Thr | Ser | Glu | His | Leu | Ala | Ala | Val | Glu | Ile | Met | Gln | Leu | Lys |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |
| His | Ile | Ile | Ile | Leu | Gln | Asn | Lys | Ile | Asp | Leu | Ile | Gln | Glu | Asn | Val |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Ala | Ile | Asn | Gln | His | Glu | Ala | Ile | Gln | Lys | Phe | Ile | Met | Asn | Thr | Val |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Asp | Ala | Ala | Pro | Ile | Val | Pro | Val | Ser | Ala | Gln | Leu | Lys | Tyr | Asn |
|     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Ile | Asp | Val | Val | Cys | Glu | Tyr | Ile | Val | Lys | Lys | Ile | Pro | Ile | Pro | Glu |
|     |     |     | 225 |     |     | 230 |     |     |     | 235 |     |     |     | 240 |     |
| Arg | Asn | Phe | Val | Ser | Pro | Pro | Asn | Met | Ile | Val | Ile | Arg | Ser | Phe | Asp |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Val | Asn | Lys | Pro | Gly | Tyr | Glu | Val | Asp | Glu | Ile | Lys | Gly | Gly | Val | Ala |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Gly | Gly | Ser | Ile | Leu | Arg | Gly | Val | Leu | Arg | Val | Asn | Gln | Leu | Ile | Glu |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Arg | Pro | Gly | Ile | Val | Thr | Lys | Asp | Glu | Arg | Gly | Asn | Ser | Lys | Cys |
|     |     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Thr | Pro | Ile | Tyr | Ser | Arg | Ile | Ile | Ser | Leu | Tyr | Ala | Glu | Gln | Asn | Glu |
|     |     |     | 305 |     |     |     | 310 |     |     |     | 315 |     |     | 320 |     |
| Leu | Gln | Phe | Ala | Val | Pro | Glu | Gly | Leu | Ile | Gly | Val | Gly | Thr | Thr | Met |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     | 335 |     |     |
| Asp | Pro | Thr | Leu | Thr | Arg | Ala | Asp | Arg | Leu | Val | Gly | Gln | Val | Leu | Gly |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Glu | Ile | Gly | Ser | Leu | Pro | Asp | Val | Phe | Val | Glu | Leu | Glu | Val | Asn | Phe |

Phe  
465

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

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 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

```

(A) NAME/KEY: peptide

(B) LOCATION: 1..374

(D) OTHER INFORMATION: / Ceres Seq. ID 1571588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2026:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Tyr | Lys | Ala | Tyr | Gly | Ser | Gly | Lys | Glu | Asp | Thr | Pro | Asn | Cys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asp | Val | Pro | Gly | Phe | Glu | Asn | Ser | Lys | Met | Lys | Leu | Leu | Arg | His | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Phe | Val | Asp | Cys | Pro | Gly | His | Asp | Ile | Leu | Met | Xaa | Thr | Met | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Gly | Ala | Ala | Ile | Met | Asp | Gly | Ala | Leu | Leu | Leu | Ile | Ala | Ala | Asn |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Thr | Cys | Pro | Gln | Pro | Gln | Thr | Ser | Glu | His | Leu | Ala | Ala | Val | Glu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Met | Gln | Leu | Lys | His | Ile | Ile | Ile | Leu | Gln | Asn | Lys | Ile | Asp | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Gln | Glu | Asn | Val | Ala | Ile | Asn | Gln | His | Glu | Ala | Ile | Gln | Lys | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Met | Asn | Thr | Val | Ala | Asp | Ala | Ala | Pro | Ile | Val | Pro | Val | Ser | Ala |
|     |     |     | 115 |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gln | Leu | Lys | Tyr | Asn | Ile | Asp | Val | Val | Cys | Glu | Tyr | Ile | Val | Lys | Lys |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Pro | Ile | Pro | Glu | Arg | Asn | Phe | Val | Ser | Pro | Pro | Asn | Met | Ile | Val |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Ile | Arg | Ser | Phe | Asp | Val | Asn | Lys | Pro | Gly | Tyr | Glu | Val | Asp | Glu | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Lys | Gly | Gly | Val | Ala | Gly | Gly | Ser | Ile | Leu | Arg | Gly | Val | Leu | Arg | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asn | Gln | Leu | Ile | Glu | Ile | Arg | Pro | Gly | Ile | Val | Thr | Lys | Asp | Glu | Arg |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Asn | Ser | Lys | Cys | Thr | Pro | Ile | Tyr | Ser | Arg | Ile | Ile | Ser | Leu | Tyr |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Glu | Gln | Asn | Glu | Leu | Gln | Phe | Ala | Val | Pro | Glu | Gly | Ile | Ile | Gly |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |     |
| Val | Gly | Thr | Thr | Met | Asp | Pro | Thr | Leu | Thr | Arg | Ala | Asp | Arg | Leu | Val |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Gly | Gln | Val | Leu | Gly | Glu | Ile | Gly | Ser | Leu | Pro | Asp | Val | Phe | Val | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |

Leu Glu Val Asn Phe Phe Leu Leu Arg Arg Leu Leu Gly Val Arg Thr  
275 280 285  
Lys Gly Ser Glu Lys Gln Gly Lys Val Ser Lys Leu Thr Lys Gly Glu  
290 295 300  
Ile Leu Met Leu Asn Ile Gly Ser Met Ser Thr Gly Ala Lys Val Val  
305 310 315  
Gly Val Lys Val Asp Leu Ala Lys Leu Gln Leu Thr Ala Pro Val Cys  
325 330 335  
Thr Ser Lys Gly Glu Lys Val Ala Leu Ser Arg Arg Val Glu Lys His  
340 345 350  
Trp Arg Leu Ile Gly Trp Gly Gln Ile Gln Ala Gly Thr Thr Ile Glu  
355 360 365  
Val Pro Pro Ser Pro Phe  
370

(2) INFORMATION FOR SEQ ID NO:2027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..349
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2027:

Met Lys Leu Leu Arg His Val Ser Phe Val Asp Cys Pro Gly His Asp  
1 5 10 15  
Ile Leu Met Xaa Thr Met Leu Asn Gly Ala Ala Ile Met Asp Gly Ala  
20 25 30  
Leu Leu Leu Ile Ala Ala Asn Glu Thr Cys Pro Gln Pro Gln Thr Ser  
35 40 45  
Glu His Leu Ala Ala Val Glu Ile Met Gln Leu Lys His Ile Ile Ile  
50 55 60  
Leu Gln Asn Lys Ile Asp Leu Ile Gln Glu Asn Val Ala Ile Asn Gln  
65 70 75 80  
His Glu Ala Ile Gln Lys Phe Ile Met Asn Thr Val Ala Asp Ala Ala  
85 90 95  
Pro Ile Val Pro Val Ser Ala Gln Leu Lys Tyr Asn Ile Asp Val Val  
100 105 110  
Cys Glu Tyr Ile Val Lys Lys Ile Pro Ile Pro Glu Arg Asn Phe Val  
115 120 125  
Ser Pro Pro Asn Met Ile Val Ile Arg Ser Phe Asp Val Asn Lys Pro  
130 135 140  
Gly Tyr Glu Val Asp Glu Ile Lys Gly Gly Val Ala Gly Gly Ser Ile  
145 150 155  
Leu Arg Gly Val Leu Arg Val Asn Gln Leu Ile Glu Ile Arg Pro Gly  
160 165 170 175  
Ile Val Thr Lys Asp Glu Arg Gly Asn Ser Lys Cys Thr Pro Ile Tyr  
180 185 190  
Ser Arg Ile Ile Ser Leu Tyr Ala Glu Gln Asn Glu Leu Gln Phe Ala  
195 200 205  
Val Pro Glu Gly Leu Ile Gly Val Gly Thr Thr Met Asp Pro Thr Leu  
210 215 220  
Thr Arg Ala Asp Arg Glu Val Gly Gln Val Leu Gly Glu Ile Gly Ser  
225 230 235 240  
Leu Pro Asp Val Phe Val Glu Leu Glu Val Asn Phe Phe Leu Leu Arg  
245 250 255  
Arg Leu Leu Gly Val Arg Thr Lys Gly Ser Glu Lys Gln Gly Lys Val  
260 265 270  
Ser Lys Leu Thr Lys Gly Glu Ile Leu Met Leu Asn Ile Gly Ser Met

(2) INFORMATION FOR SEO ID NO:2028:

(A) LENGTH: 1468 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1571612

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| atctttaca   | aacgatttc   | tttttgcgga  | atcttgagctc | agcataacctg | ctaccacttc  | 60   |
| cagagttcaa  | tcagctcttcg | ctcctgttAa  | acgttttCcc  | ttcttgata   | tcaaacaggtc | 120  |
| ctccactcgt  | atcattccacg | ctctccaaata | attttgcgat  | ctctctcgtt  | gttccaattt  | 180  |
| gattctacta  | gtgactcgtg  | atttaattta  | gggtttttgaa | agatgtgcagc | tttgaaaaaat | 240  |
| tacggtctta  | tctccattga  | tttctgcctc  | catctttctc  | gatacaatac  | attgcagagc  | 300  |
| tataagatga  | atgcaaaatg  | ggtctctcca  | atagacgtct  | tttgactaaa  | cttccactct  | 360  |
| ccatgctgcga | gtctcggagg  | taaaaaacag  | acaaacacag  | acgacataag  | ctcccttaga  | 420  |
| gtgatccacg  | ccattaagac  | acgctattga  | ctcgtatgga  | gtctgacact  | ccaagctata  | 480  |
| gactgactat  | tcaacacgca  | cagatataaa  | ggtctcgaa   | gtgtgatgtg  | tgtgtgcatac | 540  |
| aactgtggaag | gcgaattatg  | gagctgggat  | gagcacataa  | tgcctatagt  | ccactactgt  | 600  |
| attgttgttt  | ggggaaggat  | caaaagtcat  | ggaaacactg  | gaagtaactc  | gcataggaaa  | 660  |
| gctattcatg  | ccactgagca  | aggatttcgc  | atggggaatc  | acggggcact  | gcacattaac  | 720  |
| ctctactatg  | gaaaaaacat  | cattgaaagc  | attgaatgcg  | attttcaaac  | ctgtcttcac  | 780  |
| atgggaccca  | ctattatata  | caacgtgcga  | ggtcgaaagt  | gtcaggataa  | acctccccag  | 840  |
| gttatcttga  | aaactctctc  | tgaaacctaa  | attgctgggg  | ttaaggaaatg | cgttggtgat  | 900  |
| aacccagttg  | aagagtatac  | tgagaaggga  | attgtcgttt  | ggagtggaaa  | tgatgatcat  | 960  |
| tgcattcgtt  | ctatagtgga  | tcaacgtgcc  | acgagtgga   | tatcggttac  | tagcaattta  | 1020 |
| gtctcggggt  | tgatgaggaa  | gtttatgttt  | gaaggtagaa  | ctacgcgtt   | gaacgcaaa   | 1080 |
| ctctctcctt  | taatggatgt  | gctattccaa  | gaaccgaatc  | ctatcgtgtg  | aaacactcgt  | 1140 |
| tttgtcactt  | taggagtgtc  | tgaggcgggt  | tttcgtttac  | ccattgtgoc  | attgcctctc  | 1200 |
| tcacaaagga  | ttgagttcgt  | taaacctggt  | aaggaatact  | gaagggagca  | ttttgtagga  | 1260 |
| gacagagatg  | ttcaggtatg  | tgtatgatgt  | gactctctct  | taatcgctga  | atatttagta  | 1320 |
| ctctctccctg | aagatttgtt  | gtgtttatac  | tttcttcgtt  | caagtgttag  | ttatttagct  | 1380 |
| gtatdaaaac  | tcaacatgat  | atcaaaagct  | cttaattttg  | tattgtttgt  | ctctgtactt  | 1440 |

(A) LENGTH: 364 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1571613

Met Ser Ala Leu Lys Asn Tyr Gly Leu Ile Ser Ile Asp Ser Ala Leu  
1 5 10 15  
His Phe Pro Arg Ser Asn Gln Leu Gln Ser Tyr Lys Arg Asn Ala Lys

33

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Asn Gly Ala Glu Gly Val Ile Val Gly Gly Thr Thr Gly Glu Gly Gln
 50 55 60
Leu Met Ser Trp Asp Glu His Ile Met Leu Ile Gly His Thr Val Asn
 65 70 75 80
Cys Phe Gly Gly Arg Ile Lys Val Ile Gly Asn Thr Gly Ser Asn Ser
 85 90 95
Thr Arg Glu Ala Ile His Ala Thr Glu Gln Gly Phe Ala Met Gly Met
100 105 110
His Gly Ala Leu His Ile Asn Pro Tyr Tyr Gly Lys Thr Ser Ile Glu
115 120 125
Gly Met Asn Ala His Phe Gln Thr Val Leu His Met Gly Pro Thr Ile
130 135 140
Ile Tyr Asn Val Pro Gly Arg Thr Cys Gln Asp Ile Pro Pro Gln Val
145 150 155 160
Ile Phe Lys Leu Ser Gln Asn Pro Asn Met Ala Gly Val Lys Glu Cys
165 170 175
Val Gly Asn Asn Arg Val Glu Glu Tyr Thr Glu Lys Gly Ile Val Val
180 185 190
Trp Ser Gly Asn Asp Asp Gln Cys His Asp Ser Arg Trp Asp His Gly
195 200 205
Ala Thr Gly Val Ile Ser Val Thr Ser Asn Leu Val Pro Gly Leu Met
210 215 220
Arg Lys Leu Met Phe Glu Gly Arg Asn Ser Ala Leu Asn Ala Lys Leu
225 230 235 240
Leu Pro Leu Met Asp Trp Leu Phe Gln Glu Pro Asn Pro Ile Gly Val
245 250 255
Asn Thr Ala Leu Ala Gln Leu Gly Val Ala Arg Pro Val Phe Arg Leu
260 265 270
Pro Tyr Val Pro Leu Pro Leu Ser Lys Arg Ile Glu Phe Val Lys Leu
275 280 285
Val Lys Glu Ile Gly Arg Glu His Phe Val Gly Asp Arg Asp Val Gln
290 295 300
Val Leu Asp Asp Asp Asp Phe Ile Leu Ile Gly Arg Tyr
305 310 315

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(2) INFORMATION FOR SEQ ID NO:2031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..252

(D) OTHER INFORMATION: / Ceres Seq. ID 1571615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2031:

```

Met Ser Trp Asp Glu His Ile Met Leu Ile Gly His Thr Val Asn Cys
 1 5 10 15
Phe Gly Gly Arg Ile Lys Val Ile Gly Asn Thr Gly Ser Asn Ser Thr
20 25 30
Arg Glu Ala Ile His Ala Thr Glu Gln Gly Phe Ala Met Gly Met His
35 40 45
Gly Ala Leu His Ile Asn Pro Tyr Tyr Gly Lys Thr Ser Ile Glu Gly
50 55 60
Met Asn Ala His Phe Gln Thr Val Leu His Met Gly Pro Thr Ile Ile
65 70 75 80
Tyr Asn Val Pro Gly Arg Thr Cys Gln Asp Ile Pro Pro Gln Val Ile
85 90 95
Phe Lys Leu Ser Gln Asn Pro Asn Met Ala Gly Val Lys Glu Cys Val
100 105 110
Gly Asn Asn Arg Val Glu Glu Tyr Thr Glu Lys Gly Ile Val Val Trp

```



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 115                                                             | 120 | 125 |
| Ser Gly Asn Asp Asp Gln Cys His Asp Ser Arg Trp Asp His Gly Ala |     |     |
| 130                                                             | 135 | 140 |
| Thr Gly Val Ile Ser Val Thr Ser Asn Leu Val Pro Gly Leu Met Arg |     |     |
| 145                                                             | 150 | 155 |
| Lys Leu Met Phe Glu Gly Arg Asn Ser Ala Leu Asn Ala Lys Leu Leu |     |     |
| 165                                                             | 170 | 175 |
| Pro Leu Met Asp Trp Leu Phe Gln Glu Pro Asn Pro Ile Gly Val Asn |     |     |
| 180                                                             | 185 | 190 |
| Thr Ala Leu Ala Gln Leu Gly Val Ala Arg Pro Val Phe Arg Leu Pro |     |     |
| 195                                                             | 200 | 205 |
| Tyr Val Pro Leu Pro Leu Ser Lys Arg Ile Glu Phe Val Lys Leu Val |     |     |
| 210                                                             | 215 | 220 |
| Lys Glu Ile Gly Arg Glu His Phe Val Gly Asp Arg Asp Val Gln Val |     |     |
| 225                                                             | 230 | 235 |
| Leu Asp Asp Asp Asp Phe Ile Leu Ile Gly Arg Tyr                 |     |     |
| 245                                                             | 250 |     |

(2) INFORMATION FOR SEQ ID NO:2032:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1786 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1786

(D) OTHER INFORMATION: / Ceres Seq. ID 1571616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2032:

|             |             |            |             |      |
|-------------|-------------|------------|-------------|------|
| acattcaactg | tcactactct  | ctctctctct | ctaattctct  | 60   |
| aggaacagag  | taaaagactt  | tggtcagct  | ctctctctct  | 120  |
| atggctttta  | gcaatgatgt  | gtttactctt | ctctctctct  | 180  |
| cgacaacatc  | tcttctctcc  | ctagatccga | cgaaaccgaa  | 240  |
| cgaatccaga  | tgaagttagc  | gacgAagttc | tcgctctgac  | 300  |
| ataccgagag  | gaggaaaacta | ggttacttta | cttgccggaac | 360  |
| gtttggcgat  | tgacccccat  | tgccacaaga | accgtaaaac  | 420  |
| gatttggaa   | aaacgcgatc  | gggtggtcgt | atggacgatt  | 480  |
| gagacgacaa  | tcgggttaac  | cctagaccgg | ggactttacg  | 540  |
| ccgaccacta  | tggaatcgtt  | tcaaacgtga | catgttgatt  | 600  |
| cggttaacgt  | tcaaaaacga  | tcgatggacg | tgccgcaaac  | 660  |
| tgcatcaacg  | attcagtttg  | tgacgaatgt | gatcgttcac  | 720  |
| taaacccaat  | ggtaacgcta  | tggtgagaag | ctcagagacg  | 780  |
| ggcagatggt  | gacgcgatgt  | gcactctttg | atcgagtcac  | 840  |
| gtttgtccat  | tgccgtgatg  | ggcttgttga | cgacgtcatg  | 900  |
| ctctaaacac  | cacttaactc  | accataacga | ggttatgttg  | 960  |
| catgagggag  | aaagctatgc  | aagtgtaacc | tgcttaacat  | 1020 |
| ctaaagaatg  | ccgaggtgtg  | gacacgggta | cttccatggt  | 1080 |
| ctgggaaatg  | tacgcaatag  | tggttagcgc | aaacccgaca  | 1140 |
| ctatgcgcgc  | ccaaaaaac   | cttttgctaa | agaggtgacg  | 1200 |
| tagtcatttg  | aaaggatgga  | attggagatc | ggaaggagat  | 1260 |
| cttcaactct  | tcagagcgcg  | ccgcgtctcg | cagCtagcga  | 1320 |
| gaaatctctg  | tcatttggtg  | gacacattac | ttccgacgtc  | 1380 |
| aggaactcga  | gtttctctat  | agttactacc | ccaccaccac  | 1440 |
| tatatctaga  | caaaaagtga  | aatttacaca | catttgtcat  | 1500 |
| ttttttttgc  | ttttcggtgt  | gtgtgtttgt | gtcgtatttt  | 1560 |
| cttcaaccgc  | aagttaacac  | aagaaaaggg | aaaaaagaca  | 1620 |
| aatcccgcaa  | gtgtgtgtgt  | ttgtttgggt | ctatctgac   | 1680 |
| gtgctcgtgc  | ttctatccag  | agaaacaaga | atattatctc  | 1740 |
| aatttttgag  | gtttataaat  | taatataggg | ttataataat  |      |

(2) INFORMATION FOR SEQ ID NO:2033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..276  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571617  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2033:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ile | Gln | Leu | Lys | Gln | Glu | Leu | Ile | Val | Asn | Ser | Phe | Lys | Thr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Asp | Gly | Arg | Gly | Ala | Asn | Val | His | Ile | Ala | Asn | Gly | Gly | Cys | Ile |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Thr | Ile | Gln | Phe | Val | Thr | Asn | Val | Ile | Val | His | Gly | Leu | His | Ile | His |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Cys | Lys | Pro | Thr | Gly | Asn | Ala | Met | Val | Arg | Ser | Ser | Glu | Thr | His |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Gly | Trp | Arg | Thr | Met | Ala | Asp | Gly | Asp | Ala | Ile | Ser | Ile | Phe | Gly |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Ser | Ser | His | Val | Trp | Ile | Asp | His | Asn | Ser | Leu | Ser | His | Cys | Ala | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Leu | Val | Asp | Ala | Val | Met | Gly | Ser | Thr | Ala | Ile | Thr | Ile | Ser | Asn |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Asn | His | Leu | Thr | His | His | Asn | Glu | Val | Met | Leu | Leu | Gly | His | Ser | Asp |
|     |     |     | 115 |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ser | Tyr | Met | Arg | Asp | Lys | Ala | Met | Gln | Val | Thr | Ile | Ala | Tyr | Asn | His |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Gly | Val | Gly | Leu | Ile | Gln | Arg | Met | Pro | Arg | Cys | Arg | His | Gly | Tyr |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Phe | His | Val | Val | Asn | Asn | Asp | Tyr | Thr | His | Trp | Glu | Met | Tyr | Ala | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Gly | Gly | Ser | Ala | Asn | Pro | Thr | Ile | Asn | Ser | Gln | Gly | Asn | Arg | Tyr | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Pro | Lys | Asn | Pro | Phe | Ala | Lys | Glu | Val | Thr | Lys | Arg | Val | Asp | Thr |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Ala | Ser | His | Trp | Lys | Gly | Trp | Asn | Trp | Arg | Ser | Glu | Gly | Asp | Leu |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Gln | Asn | Gly | Ala | Tyr | Phe | Thr | Ser | Ser | Gly | Ala | Ala | Ala | Ser | Gly |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Ser | Tyr | Ala | Arg | Ala | Ser | Ser | Leu | Ser | Ala | Lys | Ser | Ser | Ser | Leu | Val |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Gly | His | Ile | Thr | Ser | Asp | Ala | Gly | Ala | Leu | Pro | Cys | Arg | Arg | Gly | Arg |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Gln | Cys | Ser | Ser |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 275 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2034:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 220 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..220  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2034:  
Met Val Arg Ser Ser Glu Thr His Phe Gly Trp Arg Thr Met Ala Asp  
1 5 10 15  
Gly Asp Ala Ile Ser Ile Phe Gly Ser Ser His Val Trp Ile Asp His

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 20                                                              | 25  | 30  |
| Asn Ser Leu Ser His Cys Ala Asp Gly Leu Val Asp Ala Val Met Gly |     |     |
| 35                                                              | 40  | 45  |
| Ser Thr Ala Ile Thr Ile Ser Asn Asn His Leu Thr His His Asn Glu |     |     |
| 50                                                              | 55  | 60  |
| Val Met Leu Leu Gly His Ser Asp Ser Tyr Met Arg Asp Lys Ala Met |     |     |
| 65                                                              | 70  | 75  |
| Gln Val Thr Ile Ala Tyr Asn His Phe Gly Val Gly Leu Ile Gln Arg |     |     |
| 85                                                              | 90  | 95  |
| Met Pro Arg Cys Arg His Gly Tyr Phe His Val Val Asn Asn Asp Tyr |     |     |
| 100                                                             | 105 | 110 |
| Thr His Trp Glu Met Tyr Ala Ile Gly Gly Ser Ala Asn Pro Thr Ile |     |     |
| 115                                                             | 120 | 125 |
| Asn Ser Gln Gly Asn Arg Tyr Ala Ala Pro Lys Asn Pro Phe Ala Lys |     |     |
| 130                                                             | 135 | 140 |
| Glu Val Thr Lys Arg Val Asp Thr Pro Ala Ser His Trp Lys Gly Trp |     |     |
| 145                                                             | 150 | 155 |
| Asn Trp Arg Ser Glu Gly Asp Leu Leu Gln Asn Gly Ala Tyr Phe Thr |     |     |
| 165                                                             | 170 | 175 |
| Ser Ser Gly Ala Ala Ala Ser Gly Ser Tyr Ala Arg Ala Ser Ser Leu |     |     |
| 180                                                             | 185 | 190 |
| Ser Ala Lys Ser Ser Ser Leu Val Gly His Ile Thr Ser Asp Ala Gly |     |     |
| 195                                                             | 200 | 205 |
| Ala Leu Pro Cys Arg Arg Gly Arg Gln Cys Ser Ser                 |     |     |
| 210                                                             | 215 | 220 |

(2) INFORMATION FOR SEQ ID NO:2035:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..207

(D) OTHER INFORMATION: / Ceres Seq. ID 1571619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2035:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Ala Asp Gly Asp Ala Ile Ser Ile Phe Gly Ser Ser His Val Trp |     |
| 1                                                               | 5   |
| Ile Asp His Asn Ser Leu Ser His Cys Ala Asp Gly Leu Val Asp Ala |     |
| 20                                                              | 25  |
| Val Met Gly Ser Thr Ala Ile Thr Ile Ser Asn Asn His Leu Thr His |     |
| 35                                                              | 40  |
| His Asn Glu Val Met Leu Leu Gly His Ser Asp Ser Tyr Met Arg Asp |     |
| 50                                                              | 55  |
| Lys Ala Met Gln Val Thr Ile Ala Tyr Asn His Phe Gly Val Gly Leu |     |
| 65                                                              | 70  |
| Ile Gln Arg Met Pro Arg Cys Arg His Gly Tyr Phe His Val Val Asn |     |
| 85                                                              | 90  |
| Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile Gly Gly Ser Ala Asn |     |
| 100                                                             | 105 |
| Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr Ala Ala Pro Lys Asn Pro |     |
| 115                                                             | 120 |
| Phe Ala Lys Glu Val Thr Lys Arg Val Asp Thr Pro Ala Ser His Trp |     |
| 130                                                             | 135 |
| Lys Gly Trp Asn Trp Arg Ser Glu Gly Asp Leu Leu Gln Asn Gly Ala |     |
| 145                                                             | 150 |
| Tyr Phe Thr Ser Ser Gly Ala Ala Ala Ser Gly Ser Tyr Ala Ala     |     |
| 165                                                             | 170 |
| Ser Ser Leu Ser Ala Lys Ser Ser Ser Leu Val Gly His Ile Thr Ser |     |
| 180                                                             | 185 |
|                                                                 | 190 |

Asp Ala Gly Ala Leu Pro Cys Arg Arg Gly Arg Gln Cys Ser Ser  
195 200 205

(2) INFORMATION FOR SEQ ID NO:2036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1176
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2036:

|             |            |             |             |             |             |      |
|-------------|------------|-------------|-------------|-------------|-------------|------|
| atactgtogt  | ctccctggat | tctatcttct  | cgatttttgt  | gattcgaaca  | cgattttacc  | 60   |
| tatcccttgag | cgatctcgat | ccccactttt  | tgagttgatt  | ttatttcagg  | agttttccaaa | 120  |
| aaatctgttg  | ttaagtgggt | aatcggaaaa  | tgctgcagtc  | ttccgtcgat  | ataccgcaaa  | 180  |
| aagggtgggtt | tagcttcgat | ctgtgcacaaa | ggaatgatat  | gctgacacag  | aagggtcttta | 240  |
| aagcgccgtc  | gtttctcaag | actgggaacga | ctatcgttgg  | attgatattt  | aaggatgggtg | 300  |
| taatacttgg  | ggctgataca | cgggcaactg  | aaggggcctat | tgtggctgat  | aagaactgtg  | 360  |
| agaagattca  | ctacatggca | ccaaacattt  | actgttggtg  | tgcaaggaacc | gctgctgaca  | 420  |
| ctgaagcagt  | aactgatgat | gtcagctcac  | agctgcgggt  | gcatagatac  | cgagctggccc | 480  |
| gagattctcg  | agctggtact | gcattgaccc  | ttctcaaaaa  | acHtcttttc  | agctaccaag  | 540  |
| gccatgtctc  | agctgctctt | gtgcttgggt  | gagttgatat  | taccggggcct | catctttcaca | 600  |
| cgatataccc  | acacgggtct | actgacactc  | taccatttgc  | tacaatgggt  | ctggtgtccc  | 660  |
| ttgctgcocat | gtcagtgttt | gaagcaaaat  | ataaagaagg  | tctaaactaga | gatgaaggaa  | 720  |
| tcaagtgtgt  | tgctgaagcc | atatgtctct  | gtatattcaa  | cgaccttggt  | agtggtagca  | 780  |
| atgtgggat   | ctgtgtgatc | actaaagggc  | acaaggaata  | cttgaggaat  | tacatgggaac | 840  |
| caaaccccaa  | aacctatgtt | agcagcaaa   | gctattcatt  | caccaagaaa  | accagaggttc | 900  |
| tactaccaca  | aattaccaca | ttattggagc  | gagtcgaaat  | tgtagaagtg  | gctggtgaag  | 960  |
| ctatggagga  | atgaatcttg | tgtagagagc  | agatactaa   | agtgaaacca  | ttgtctatcc  | 1020 |
| tcacatgaca  | gtcatgttta | cgttttctac  | ttgttccaat  | atgaacgact  | aaaatcgaa   | 1080 |
| cgtagttgcc  | tcacatttgt | ctttaaattt  | ggcttgaact  | tggtattaat  | gagtatggat  | 1140 |
| attgtgggtt  | tgaaatttag | ctctcacata  | attttc      |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..274
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2037:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gln | Ser | Ser | Val | Asp | Ile | Pro | Pro | Lys | Gly | Gly | Phe | Ser | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Asp | Leu | Cys | Lys | Arg | Asn | Asp | Met | Leu | Thr | Gln | Lys | Gly | Leu | Lys | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ser | Phe | Leu | Lys | Thr | Gly | Thr | Thr | Ile | Val | Gly | Leu | Ile | Phe | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Gly | Val | Ile | Leu | Gly | Ala | Asp | Thr | Arg | Ala | Thr | Glu | Gly | Pro | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Ala | Asp | Lys | Asn | Cys | Glu | Lys | Ile | His | Tyr | Met | Ala | Pro | Asn | Ile |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Tyr | Cys | Cys | Gly | Ala | Gly | Thr | Ala | Ala | Asp | Thr | Glu | Ala | Val | Thr | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Met | Val | Ser | Ser | Gln | Leu | Arg | Leu | His | Arg | Tyr | Gln | Thr | Gly | Arg | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Arg | Val | Val | Thr | Ala | Leu | Thr | Leu | Lys | Lys | Xaa | Leu | Phe | Ser |     |

(2) INFORMATION FOR SEO ID NO:2038:

(A) LENGTH: 251 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2038:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Thr | Gln | Lys | Gly | Leu | Lys | Ala | Pro | Ser | Phe | Leu | Lys | Thr | Gly |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Thr | Thr | Ile | Val | Gly | Leu | Ile | Phe | Lys | Asp | Gly | Val | Ile | Leu | Gly | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Thr | Arg | Ala | Thr | Glu | Gly | Pro | Ile | Val | Ala | Asp | Lys | Asn | Cys | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Ile | His | Tyr | Met | Ala | Pro | Asn | Ile | Tyr | Cys | Cys | Gly | Ala | Gly | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Ala | Asp | Thr | Glu | Ala | Val | Thr | Asp | Met | Val | Ser | Ser | Gln | Leu | Arg |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | His | Arg | Tyr | Gln | Thr | Gly | Arg | Asp | Ser | Arg | Val | Val | Thr | Ala | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Leu | Leu | Lys | Lys | Xaa | Leu | Phe | Ser | Tyr | Gln | Gly | His | Val | Ser | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Leu | Val | Leu | Gly | Gly | Val | Asp | Ile | Thr | Gly | Pro | His | Leu | His | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Tyr | Pro | His | Gly | Ser | Thr | Asp | Thr | Leu | Pro | Phe | Ala | Thr | Met | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Gly | Ser | Leu | Ala | Ala | Met | Ser | Val | Phe | Glu | Ala | Lys | Tyr | Lys | Glu |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Leu | Thr | Arg | Asp | Glu | Gly | Ile | Lys | Leu | Val | Ala | Glu | Ala | Ile | Cys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Gly | Ile | Phe | Pro | Asn | Asp | Leu | Gly | Ser | Gly | Ser | Asn | Val | Asp | Ile |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |
| Val | Ile | Thr | Lys | Gly | His | Lys | Glu | Tyr | Leu | Arg | Asn | Tyr | Met | Glu | Pro |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | Pro | Arg | Thr | Tyr | Val | Ser | Ser | Lys | Gly | Tyr | Ser | Phe | Thr | Lys | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |

Thr Glu Val Leu Leu Thr Lys Ile Thr Pro Leu Leu Glu Arg Val Glu  
225 230 235 240  
Ile Val Glu Val Ala Gly Glu Ala Met Glu Glu  
245 250

(2) INFORMATION FOR SEQ ID NO:2039:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..199
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2039:

Met Ala Pro Asn Ile Tyr Cys Cys Gly Ala Gly Thr Ala Ala Asp Thr  
1 5 10 15  
Glu Ala Val Thr Asp Met Val Ser Ser Gln Leu Arg Leu His Arg Tyr  
20 25 30  
Gln Thr Gly Arg Asp Ser Arg Val Val Thr Ala Leu Thr Leu Leu Lys  
35 40 45  
Lys Xaa Leu Phe Ser Tyr Gln Gly His Val Ser Ala Ala Leu Val Leu  
50 55 60  
Gly Gly Val Asp Ile Thr Gly Pro His Leu His Thr Ile Tyr Pro His  
65 70 75 80  
Gly Ser Thr Asp Thr Leu Pro Phe Ala Thr Met Gly Ser Gly Ser Leu  
85 90 95  
Ala Ala Met Ser Val Phe Glu Ala Lys Tyr Lys Glu Gly Leu Thr Arg  
100 105 110  
Asp Glu Gly Ile Lys Leu Val Ala Glu Ala Ile Cys Ser Gly Ile Phe  
115 120 125  
Asn Asp Leu Gly Ser Gly Ser Asn Val Asp Ile Cys Val Ile Thr Lys  
130 135 140  
Gly His Lys Glu Tyr Leu Arg Asn Tyr Met Glu Pro Asn Pro Arg Thr  
145 150 155 160  
Tyr Val Ser Ser Lys Gly Tyr Ser Phe Thr Lys Lys Thr Glu Val Leu  
165 170 175  
Leu Thr Lys Ile Thr Pro Leu Leu Glu Arg Val Glu Ile Val Glu Val  
180 185 190  
Ala Gly Glu Ala Met Glu Glu  
195

(2) INFORMATION FOR SEQ ID NO:2040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1437
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2040:

aaaaacttca aattaaaagc ttctgtgtctt cataaaacc taatctcgcg acttcgtctc 60  
tatccccaaa aacccttttc tctcttccct ctgtgtgtg acgagaaaaa aaagatgact 120  
aagaacagta accacgacga gaatgagttc acgacttttg aaccaaatac gaacacgaag 180  
atacgtcttg aaagatgctga tgaagacgaa gttgctgaag ggtctgtgtg tcgccggcga 240  
gaaactcccc aaagatgagtc catgtttcgc gccggagaga gcgccgacac gcctgaagta 300  
actgatgata ccaccagatgc cgattactac ttcgattctt actctcactt tggaaatcat 360  
gaagagatgt tgaaggatgt tgtgagaaca aagacttata agaattgtat ttatcagaac 420

|             |             |            |            |            |             |      |
|-------------|-------------|------------|------------|------------|-------------|------|
| aagtttctta  | tcaaggacaa  | aattgttctt | gatgttggag | ctggaaccgg | aattttgtct  | 480  |
| ctgttctgtg  | ccaaggcagg  | agctgctcat | gtctacgctg | ttgagtgttc | tcaaatggct  | 540  |
| gacatggtca  | aggagattgt  | taaagctaat | ggattttctg | atgttattac | ggatttgaaa  | 600  |
| gggaagattg  | aggagataga  | gcttcccatc | cctaaagtgg | atgtgattat | atcggaatgg  | 660  |
| atgggttact  | ttttgttgtt  | tgaataatgt | ttggacagtg | tcttgtatgc | tcgtgataaa  | 720  |
| tggtctgttg  | aagtgaggat  | tgtgtaccac | gacaaagcct | ctctgcactc | tacagccata  | 780  |
| gaggattcag  | agtacaaaag  | agacaaaatc | gaattttgga | acagtggtga | tggttttgac  | 840  |
| atgtcatgta  | ttaagaaaaa  | agctatgatg | gaaccacttg | ttgacacagt | cgaccacaaac | 900  |
| caaatctgtc  | ccgatagtac  | gcttctaaag | acgatggata | tctcaaatgt | gtcctctggg  | 960  |
| gatgtctctc  | tcaacagctcc | ctttaagctt | gttgacacac | gcaatgacta | catccaagcc  | 1020 |
| ctttagtccct | actttgatgt  | atcgtttacc | atgtgccaca | agctgctggg | cttctcaaca  | 1080 |
| ggaccgaaat  | cccagctcac  | acactggaaa | caaacagttc | tgtatctaga | agatgtgtta  | 1140 |
| accatatgtg  | agggtgagac  | aatacctgga | actatgtccg | tttctctcaa | caagaagaat  | 1200 |
| cctcgagaca  | ttgacataaa  | gctaagctat | tctttgaatg | gccagcattg | caagatctca  | 1260 |
| aggaccacaac | actacaaaat  | gcgttaaagt | tctctcataa | gaagcagaac | ttcagaagat  | 1320 |
| acaattctca  | tattgtgatt  | tagtttttat | atctctcttt | tctccagatt | acaactttcc  | 1380 |
| atattgttca  | cattgcacaa  | tttgcctcat | ctcaagttaa | attaatgatt | ttgtctcc    |      |

(2) INFORMATION FOR SEQ ID NO:2041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..390

(D) OTHER INFORMATION: / Ceres Seq. ID 1571643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2041:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Lys | Asn | Ser | Asn | His | Asp | Glu | Asn | Glu | Phe | Ile | Ser | Phe | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Asn | Gln | Asn | Thr | Lys | Ile | Arg | Phe | Glu | Asp | Ala | Asp | Glu | Asp | Glu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Val | Ala | Glu | Gly | Ser | Gly | Val | Ala | Gly | Glu | Glu | Thr | Pro | Gln | Asp | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Met | Phe | Asp | Ala | Gly | Glu | Ser | Ala | Asp | Thr | Ala | Glu | Val | Thr | Asp |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Thr | Thr | Ser | Ala | Asp | Tyr | Tyr | Phe | Asp | Ser | Tyr | Ser | His | Phe | Gly |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     |     | 80  |     |
| Ile | His | Glu | Glu | Met | Leu | Lys | Asp | Val | Val | Arg | Thr | Lys | Thr | Tyr | Gln |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asn | Val | Ile | Tyr | Gln | Asn | Lys | Phe | Leu | Ile | Lys | Asp | Lys | Ile | Val | Leu |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Asp | Val | Gly | Ala | Gly | Thr | Gly | Ile | Leu | Ser | Leu | Phe | Cys | Ala | Lys | Ala |
|     |     |     | 115 |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Ala | Ala | His | Val | Tyr | Ala | Val | Glu | Cys | Ser | Gln | Met | Ala | Asp | Met |
|     |     |     | 130 |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Ala | Lys | Glu | Ile | Val | Lys | Ala | Asn | Gly | Phe | Ser | Asp | Val | Ile | Thr | Val |
|     |     |     | 145 |     |     | 150 |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Lys | Gly | Lys | Ile | Glu | Glu | Ile | Glu | Leu | Pro | Thr | Pro | Lys | Val | Asp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Val | Ile | Ile | Ser | Glu | Trp | Met | Gly | Tyr | Phe | Leu | Leu | Phe | Glu | Asn | Met |
|     |     |     | 180 |     |     | 185 |     |     |     |     |     | 190 |     |     |     |
| Leu | Asp | Ser | Val | Leu | Tyr | Ala | Arg | Asp | Lys | Trp | Leu | Val | Glu | Gly | Gly |
|     |     |     | 195 |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Val | Val | Leu | Pro | Asp | Lys | Ala | Ser | Leu | His | Leu | Thr | Ala | Ile | Glu | Asp |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Glu | Tyr | Lys | Glu | Asp | Lys | Ile | Glu | Phe | Trp | Asn | Ser | Val | Tyr | Gly |
|     |     |     | 225 |     |     | 230 |     |     | 235 |     |     |     |     | 240 |     |
| Phe | Asp | Met | Ser | Cys | Ile | Lys | Lys | Lys | Ala | Met | Met | Glu | Pro | Leu | Val |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Thr | Val | Asp | Gln | Asn | Gln | Ile | Val | Thr | Asp | Ser | Arg | Leu | Leu | Lys |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Met | Asp | Ile | Ser | Lys | Met | Ser | Ser | Gly | Asp | Ala | Ser | Phe | Thr | Ala |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Pro | Phe | Lys | Leu | Val | Ala | Gln | Arg | Asn | Asp | Tyr | Ile | His | Ala | Leu | Val |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ala | Tyr | Phe | Asp | Val | Ser | Phe | Thr | Met | Cys | His | Lys | Leu | Leu | Gly | Phe |
|     |     | 305 |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |     |
| Ser | Thr | Gly | Pro | Lys | Ser | Arg | Ala | Thr | His | Trp | Lys | Gln | Thr | Val | Leu |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Tyr | Leu | Glu | Asp | Val | Leu | Thr | Ile | Cys | Glu | Gly | Glu | Thr | Ile | Thr | Gly |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     | 350 |     |     |     |
| Thr | Met | Ser | Val | Ser | Pro | Asn | Lys | Lys | Asn | Pro | Arg | Asp | Ile | Asp | Ile |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Lys | Leu | Ser | Tyr | Ser | Leu | Asn | Gly | Gln | His | Cys | Lys | Ile | Ser | Arg | Thr |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Gln | His | Tyr | Lys | Met | Arg |     |     |     |     |     |     |     |     |     |     |
|     |     | 385 |     |     | 390 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2042:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..341

(D) OTHER INFORMATION: / Ceres Seq. ID 1571644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2042:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Asp | Ala | Gly | Glu | Ser | Ala | Asp | Thr | Ala | Glu | Val | Thr | Asp | Asp |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Thr | Ser | Ala | Asp | Tyr | Tyr | Phe | Asp | Ser | Tyr | Ser | His | Phe | Gly | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| His | Glu | Glu | Met | Leu | Lys | Asp | Val | Val | Arg | Thr | Lys | Thr | Tyr | Gln | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Ile | Tyr | Gln | Asn | Lys | Phe | Leu | Ile | Lys | Asp | Lys | Ile | Val | Leu | Asp |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Gly | Ala | Gly | Thr | Gly | Ile | Leu | Ser | Leu | Phe | Cys | Ala | Lys | Ala | Gly |
|     |     |     | 65  |     | 70  |     |     | 75  |     |     |     |     |     | 80  |     |
| Ala | Ala | His | Val | Tyr | Ala | Val | Glu | Cys | Ser | Gln | Met | Ala | Asp | Met | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Glu | Ile | Val | Lys | Ala | Asn | Gly | Phe | Ser | Asp | Val | Ile | Thr | Val | Leu |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Lys | Gly | Lys | Ile | Glu | Glu | Ile | Glu | Leu | Pro | Thr | Pro | Lys | Val | Asp | Val |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Ile | Ser | Glu | Trp | Met | Gly | Tyr | Phe | Leu | Leu | Phe | Glu | Asn | Met | Leu |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Ser | Val | Leu | Tyr | Ala | Arg | Asp | Lys | Trp | Leu | Val | Glu | Gly | Gly | Val |
|     |     |     | 145 |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Val | Leu | Pro | Asp | Lys | Ala | Ser | Leu | His | Leu | Thr | Ala | Ile | Glu | Asp | Ser |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Glu | Tyr | Lys | Glu | Asp | Lys | Ile | Glu | Phe | Trp | Asn | Ser | Val | Tyr | Gly | Phe |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Asp | Met | Ser | Cys | Ile | Lys | Lys | Lys | Ala | Met | Met | Glu | Pro | Leu | Val | Asp |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Val | Asp | Gln | Asn | Gln | Ile | Val | Thr | Asp | Ser | Arg | Leu | Leu | Lys | Thr |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Met | Asp | Ile | Ser | Lys | Met | Ser | Ser | Gly | Asp | Ala | Ser | Phe | Thr | Ala | Pro |
|     |     |     | 225 |     |     | 230 |     |     | 235 |     |     |     |     | 240 |     |
| Phe | Lys | Leu | Val | Ala | Gln | Arg | Asn | Asp | Tyr | Ile | His | Ala | Leu | Val | Ala |



(2) INFORMATION FOR SEO ID NO:2043:

(A) LENGTH: 306 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..306

(D) OTHER INFORMATION: / Ceres Seq. ID 1571645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2043:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Lys | Asp | Val | Val | Arg | Thr | Lys | Thr | Tyr | Gln | Asn | Val | Ile | Tyr |
| 1   | Gln | Asn | Lys | Phe | Leu | Ile | Lys | Asp | Lys | Ile | Val | Leu | Asp | Val | Gly |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     | Ala |
| Gly | Thr | Gly | Ile | Leu | Ser | Leu | Phe | Cys | Ala | Lys | Ala | Gly | Ala | Ala | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Tyr | Ala | Val | Glu | Cys | Ser | Gln | Met | Ala | Asp | Met | Ala | Lys | Glu | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Lys | Ala | Asn | Gly | Phe | Ser | Asp | Val | Ile | Thr | Val | Leu | Lys | Gly | Lys |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Glu | Glu | Ile | Glu | Leu | Pro | Thr | Pro | Lys | Val | Asp | Val | Ile | Ile | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Trp | Met | Gly | Tyr | Phe | Leu | Leu | Phe | Glu | Asn | Met | Leu | Asp | Ser | Val |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Leu | Tyr | Ala | Arg | Asp | Lys | Trp | Leu | Val | Glu | Gly | Gly | Val | Val | Leu | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Lys | Ala | Ser | Leu | His | Leu | Thr | Ala | Ile | Glu | Asp | Ser | Glu | Tyr | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Asp | Lys | Ile | Glu | Phe | Trp | Asn | Ser | Val | Tyr | Gly | Phe | Asp | Met | Ser |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Cys | Ile | Lys | Lys | Lys | Ala | Met | Met | Glu | Pro | Leu | Val | Asp | Thr | Val | Asp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | Asn | Gln | Ile | Val | Thr | Asp | Ser | Arg | Leu | Leu | Lys | Thr | Met | Asp | Ile |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Lys | Met | Ser | Ser | Gly | Asp | Ala | Ser | Phe | Thr | Ala | Pro | Phe | Lys | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Ala | Gln | Arg | Asn | Asp | Tyr | Ile | His | Ala | Leu | Val | Ala | Tyr | Phe | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Ser | Phe | Thr | Met | Cys | His | Lys | Leu | Leu | Gly | Phe | Ser | Thr | Gly | Pro |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Lys | Ser | Arg | Ala | Thr | His | Trp | Lys | Gln | Thr | Val | Leu | Tyr | Leu | Glu | Asp |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Leu | Thr | Ile | Cys | Glu | Gly | Glu | Thr | Ile | Thr | Gly | Thr | Met | Ser | Val |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Pro | Asn | Lys | Lys | Asn | Pro | Arg | Asp | Ile | Asp | Ile | Lys | Leu | Ser | Tyr |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

Ser Leu Asn Gly Gln His Cys Lys Ile Ser Arg Thr Gln His Tyr Lys  
290 295 300  
Met Arg  
305

(2) INFORMATION FOR SEQ ID NO:2044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..723
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2044:

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| agtcgtctag | ggtttgtttt  | tgtttttt   | tccgattgtt | cagaggaatt  | gcgaattaag | 60  |
| ataaagatga | ggccagtggt  | cgtcggaat  | tccgagtatg | aaactcgcca  | gtcggatctg | 120 |
| gaacgggtgt | tcgacaagta  | tgggagagtc | gaccgagtg  | acatgaaatc  | tggatagtct | 180 |
| tttgtgtact | ttgagtagta  | acgtgatgct | gaagacgcta | ttcgcaaaat  | cgacaatttt | 240 |
| cttttttgat | atgagaaaacg | caggttatca | gttgaatggg | caaaagggtga | acgtggcagg | 300 |
| ctctgtgtgt | acgcgaaaacg | cccttcaa   | ctgaagccta | caaaagacact | gtttgtcatt | 360 |
| aactttgacc | ccattagac   | aaaagagcac | gacattgaaa | aacactttga  | gccctatggt | 420 |
| aaggtcacc  | cgatcgat    | cagacgcaac | ttctcattg  | ttcagttga   | aacacaagag | 480 |
| gatgctacaa | aagcccttga  | agctactcaa | agaagcaaaa | tattggatag  | gggtgtttcc | 540 |
| gtggagtagt | cggtgaaaga  | gacgatgac  | agaagatgac | gaaatggtgg  | tcgtagcccg | 600 |
| agaaggtctc | ttagtcctgt  | gtatcgtagG | cgctcatgta | tgatgtactg  | tcgttatttt | 660 |
| aaagaaaatt | tggcaccttt  | tgtataaaca | gaatttccta | tacctcgacg  | tttgtgttta | 720 |
| cgt        |             |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..228
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2045:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Arg | Leu | Gly | Phe | Val | Phe | Arg | Phe | Phe | Ser | Asp | Cys | Ser | Glu | Glu |
| 1   |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Arg | Ile | Lys | Ile | Lys | Met | Arg | Pro | Val | Phe | Val | Gly | Asn | Phe | Glu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Glu | Thr | Arg | Gln | Ser | Asp | Leu | Glu | Arg | Leu | Phe | Asp | Lys | Tyr | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Val | Asp | Arg | Val | Asp | Met | Lys | Ser | Gly | Tyr | Ala | Phe | Val | Tyr | Phe |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Asp | Glu | Arg | Asp | Ala | Glu | Asp | Ala | Ile | Arg | Lys | Leu | Asp | Asn | Phe |
|     |     | 65  |     |     | 70  |     |     | 75  |     |     |     |     |     | 80  |     |
| Pro | Phe | Gly | Tyr | Glu | Lys | Arg | Arg | Leu | Ser | Val | Glu | Trp | Ala | Lys | Gly |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Arg | Gly | Arg | Pro | Arg | Gly | Asp | Ala | Lys | Ala | Pro | Ser | Asn | Leu | Lys |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Thr | Lys | Thr | Leu | Phe | Val | Ile | Asn | Phe | Asp | Pro | Ile | Arg | Thr | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Glu | His | Asp | Ile | Glu | Lys | His | Phe | Glu | Pro | Tyr | Gly | Lys | Val | Thr | Asn |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Arg | Ile | Arg | Arg | Asn | Phe | Ser | Phe | Val | Gln | Phe | Glu | Thr | Gln | Glu |
|     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |

Asp Ala Thr Lys Ala Leu Glu Ala Thr Gln Arg Ser Lys Ile Leu Asp  
165 170 175  
Arg Val Val Ser Val Glu Tyr Ala Leu Lys Asp Asp Asp Glu Arg Asp  
180 185 190  
Asp Arg Asn Gly Gly Arg Ser Pro Arg Arg Ser Leu Ser Pro Val Tyr  
195 200 205  
Arg Arg Arg His Val Met Met Tyr Cys Arg Tyr Phe Lys Glu Asn Leu  
210 215 220  
Ala Pro Phe Val  
225

(2) INFORMATION FOR SEQ ID NO:2046:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1571671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2046:

Met Arg Pro Val Phe Val Gly Asn Phe Glu Tyr Glu Thr Arg Gln Ser  
1 5 10 15  
Asp Leu Glu Arg Leu Phe Asp Lys Tyr Gly Arg Val Asp Arg Val Asp  
20 25 30  
Met Lys Ser Gly Tyr Ala Phe Val Tyr Phe Glu Asp Glu Arg Asp Ala  
35 40 45  
Glu Asp Ala Ile Arg Lys Leu Asp Asn Phe Pro Phe Gly Tyr Glu Lys  
50 55 60  
Arg Arg Leu Ser Val Glu Trp Ala Lys Gly Glu Arg Gly Arg Pro Arg  
65 70 75 80  
Gly Asp Ala Lys Ala Pro Ser Asn Leu Lys Pro Thr Lys Thr Leu Phe  
85 90 95  
Val Ile Asn Phe Asp Pro Ile Arg Thr Lys Glu His Asp Ile Glu Lys  
100 105 110  
His Phe Glu Pro Tyr Gly Lys Val Thr Asn Val Arg Ile Arg Arg Asn  
115 120 125  
Phe Ser Phe Val Gln Phe Glu Thr Gln Glu Asp Ala Thr Lys Ala Leu  
130 135 140  
Glu Ala Thr Gln Arg Ser Lys Ile Leu Asp Arg Val Val Ser Val Glu  
145 150 155 160  
Tyr Ala Leu Lys Asp Asp Asp Glu Arg Asp Arg Asn Gly Gly Arg  
165 170 175  
Ser Pro Arg Arg Ser Leu Ser Pro Val Tyr Arg Arg Arg His Val Met  
180 185 190  
Met Tyr Cys Arg Tyr Phe Lys Glu Asn Leu Ala Pro Phe Val  
195 200 205

(2) INFORMATION FOR SEQ ID NO:2047:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..174

(D) OTHER INFORMATION: / Ceres Seq. ID 1571672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2047:

Met Lys Ser Gly Tyr Ala Phe Val Tyr Phe Glu Asp Glu Arg Asp Ala

|             |                     |                 |                     |
|-------------|---------------------|-----------------|---------------------|
| 1           | 5                   | 10              | 15                  |
| Glu Asp Ala | Ile Arg Lys Leu Asp | Asn Phe Pro     | Phe Gly Tyr Glu Lys |
|             | 20                  | 25              | 30                  |
| Arg Arg Leu | Ser Val Glu Trp     | Ala Lys Gly Glu | Arg Gly Arg Pro Arg |
|             | 35                  | 40              | 45                  |
| Gly Asp Ala | Lys Ala Pro Ser     | Asn Leu Lys Pro | Thr Lys Thr Leu Phe |
|             | 50                  | 55              | 60                  |
| Val Ile Asn | Phe Asp Pro Ile     | Arg Thr Lys Glu | His Asp Ile Glu Lys |
|             | 65                  | 70              | 75                  |
| His Phe Glu | Pro Tyr Gly Lys     | Val Thr Asn Val | Arg Ile Arg Arg Asn |
|             | 85                  | 90              | 95                  |
| Phe Ser Phe | Val Gln Phe Glu Thr | Gln Glu Asp Ala | Thr Lys Ala Leu     |
|             | 100                 | 105             | 110                 |
| Glu Ala Thr | Gln Arg Ser Lys     | Ile Leu Asp Arg | Val Val Ser Val Glu |
|             | 115                 | 120             | 125                 |
| Tyr Ala Leu | Lys Asp Asp Asn     | Glu Arg Asp Asp | Arg Asn Gly Gly Arg |
|             | 130                 | 135             | 140                 |
| Ser Pro Arg | Arg Ser Leu Ser     | Pro Val Tyr Arg | Arg Arg His Val Met |
|             | 145                 | 150             | 155                 |
| Met Tyr Cys | Arg Tyr Phe Lys     | Glu Asn Leu Ala | Pro Phe Val         |
|             | 165                 | 170             |                     |

(2) INFORMATION FOR SEQ ID NO:2048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..967

(D) OTHER INFORMATION: / Ceres Seq. ID 1571677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2048:

|             |             |             |             |            |             |     |
|-------------|-------------|-------------|-------------|------------|-------------|-----|
| actcatttta  | ctgttaagca  | aacacaagat  | aagaagaasac | aaacaatggc | gatttctttc  | 60  |
| attttagatat | tttcctcgat  | tcttagcttc  | tggatttttg  | tgaaggatt  | tgaaatggcg  | 120 |
| gtgtcgcttt  | tatcgaaatt  | acgggtgtata | acagtagatg  | ttactgttac | acttataagt  | 180 |
| tacaaaggag  | agcttgggtga | ttactattgt  | atggctgcta  | aagccattgg | tttgccttgt  | 240 |
| ctgtattata  | aacgagttca  | tgaaggtttt  | aaactagctt  | atacagatat | ggcacaaaaa  | 300 |
| tatccttggtt | tcggtttcca  | tgccaaaatg  | ccaaacattg  | tttgggtgaa | aacttgtgtg  | 360 |
| agagattcat  | ttgtcaagcg  | aggatatgag  | tatgatgagg  | agacatttga | gaagatattt  | 420 |
| aggagaatct  | attcgacgtt  | tggttctgct  | gcaccttact  | ctgbgtttca | agattctcaa  | 480 |
| cggtttttaa  | gatggggcacg | caggaaaagt  | cttatagctg  | gacttgttag | caatgccgaa  | 540 |
| taccgatatc  | aagaagtatt  | ttacacctCc  | ttcggtttga  | gcaaggcaga | gtgggatttt  | 600 |
| gggtgtattct | ctggaattga  | agggatagag  | aaaccagatc  | cgaggatttt | tacGctgcgcg | 660 |
| ctagagagag  | ccgggaataa  | tattgcgcct  | gaagagggtt  | tgcataattg | agacagcatg  | 720 |
| cgcaagattt  | atgttccagc  | aaagagtatt  | gggatgcagt  | ctttgttggt | tgaagggttt  | 780 |
| aagacggaag  | ctgtctaaga  | ctgtagataa  | gctggagcca  | ttgtgcttcc | agatttgggt  | 840 |
| gctgttcaac  | aacttttggg  | gtctgataag  | ttgaaatgtt  | agaaaacaga | ccctctcttaa | 900 |
| gtatgaaatc  | taattgtatt  | tagtattgca  | catttgagta  | aaataagttt | caacgcgttc  | 960 |
| tttggtt     |             |             |             |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..255

(D) OTHER INFORMATION: / Ceres Seq. ID 1571678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2049:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Val | Ser | Leu | Leu | Ser | Lys | Leu | Arg | Cys | Ile | Thr | Val | Asp | Val |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Thr | Gly | Thr | Leu | Ile | Ala | Tyr | Lys | Gly | Glu | Leu | Gly | Asp | Tyr | Tyr | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Ala | Ala | Lys | Ala | Ile | Gly | Leu | Pro | Cys | Pro | Asp | Tyr | Lys | Arg | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Glu | Gly | Phe | Lys | Leu | Ala | Tyr | Thr | Asp | Met | Ala | Gln | Lys | Tyr | Pro |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Phe | Gly | Phe | His | Ala | Lys | Met | Pro | Asn | Ile | Val | Trp | Trp | Lys | Thr |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Cys | Val | Arg | Asp | Ser | Phe | Val | Lys | Ala | Gly | Tyr | Glu | Tyr | Asp | Glu | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Phe | Glu | Lys | Ile | Phe | Arg | Arg | Ile | Tyr | Ser | Thr | Phe | Gly | Ser | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Pro | Tyr | Ser | Xaa | Phe | Gln | Asp | Ser | Gln | Pro | Phe | Leu | Arg | Trp | Ala |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Arg | Lys | Gly | Leu | Ile | Val | Gly | Leu | Val | Ser | Asn | Ala | Glu | Tyr | Arg |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Tyr | Gln | Glu | Val | Ile | Leu | Pro | Ser | Phe | Gly | Leu | Ser | Lys | Ala | Glu | Trp |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Asp | Phe | Gly | Val | Phe | Ser | Gly | Ile | Glu | Gly | Ile | Glu | Lys | Pro | Asp | Pro |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Arg | Ile | Phe | Thr | Leu | Ala | Leu | Glu | Arg | Ala | Gly | Asn | Asn | Ile | Ala | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Glu | Val | Leu | His | Ile | Gly | Asp | Ser | Met | Arg | Lys | Asp | Tyr | Val | Pro |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Lys | Ser | Ile | Gly | Met | His | Ala | Leu | Leu | Val | Asp | Arg | Phe | Lys | Thr |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Ala | Ala | Lys | Asp | Trp | Ile | Glu | Ala | Gly | Ala | Ile | Val | Leu | Pro | Asp |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Leu | Val | Ala | Val | Gln | Gln | Leu | Leu | Glu | Ser | Asp | Lys | Leu | Lys | Cys |     |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |

(2) INFORMATION FOR SEQ ID NO:2050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..223
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2050:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Lys | Ala | Ile | Gly | Leu | Pro | Cys | Pro | Asp | Tyr | Lys | Arg | Val |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| His | Glu | Gly | Phe | Lys | Leu | Ala | Tyr | Thr | Asp | Met | Ala | Gln | Lys | Tyr | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Cys | Phe | Gly | Phe | His | Ala | Lys | Met | Pro | Asn | Ile | Val | Trp | Trp | Lys | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Cys | Val | Arg | Asp | Ser | Phe | Val | Lys | Ala | Gly | Tyr | Glu | Tyr | Asp | Glu | Glu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Phe | Glu | Lys | Ile | Phe | Arg | Arg | Ile | Tyr | Ser | Thr | Phe | Gly | Ser | Ala |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Pro | Tyr | Ser | Xaa | Phe | Gln | Asp | Ser | Gln | Pro | Phe | Leu | Arg | Trp | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Arg | Arg | Lys | Gly | Leu | Ile | Val | Gly | Leu | Val | Ser | Asn | Ala | Glu | Tyr | Arg |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Tyr | Gln | Glu | Val | Ile | Leu | Pro | Ser | Phe | Gly | Leu | Ser | Lys | Ala | Glu | Trp |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     | 125 |     |

Asp Phe Gly Val Phe Ser Gly Ile Glu Gly Ile Glu Lys Pro Asp Pro  
130 135 140  
Arg Ile Phe Thr Leu Ala Leu Glu Arg Ala Gly Asn Asn Ile Ala Pro  
145 150 155 160  
Glu Glu Val Leu His Ile Gly Asp Ser Met Arg Lys Asp Tyr Val Pro  
165 170 175  
Ala Lys Ser Ile Gly Met His Ala Leu Leu Val Asp Arg Phe Lys Thr  
180 185 190  
Glu Ala Ala Lys Asp Trp Ile Glu Ala Gly Ala Ile Val Leu Pro Asp  
195 200 205  
Leu Val Ala Val Gln Gln Leu Glu Ser Asp Lys Leu Lys Cys  
210 215 220

(2) INFORMATION FOR SEQ ID NO:2051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2051:

Met Ala Gln Lys Tyr Pro Cys Phe Gly Phe His Ala Lys Met Pro Asn  
1 5 10 15  
Ile Val Trp Trp Lys Thr Cys Val Arg Asp Ser Phe Val Lys Ala Gly  
20 25 30  
Tyr Glu Tyr Asp Glu Glu Thr Phe Glu Lys Ile Phe Arg Arg Ile Tyr  
35 40 45  
Ser Thr Phe Gly Ser Ala Ala Pro Tyr Ser Xaa Phe Gln Asp Ser Gln  
50 55 60  
Pro Phe Leu Arg Trp Ala Arg Arg Lys Gly Leu Ile Val Gly Leu Val  
65 70 75 80  
Ser Asn Ala Glu Tyr Arg Tyr Gln Glu Val Ile Leu Pro Ser Phe Gly  
85 90 95  
Leu Ser Lys Ala Glu Trp Asp Phe Gly Val Phe Ser Gly Ile Glu Gly  
100 105 110  
Ile Glu Lys Pro Asp Pro Arg Ile Phe Thr Leu Ala Leu Glu Arg Ala  
115 120 125  
Gly Asn Asn Ile Ala Pro Glu Glu Val Leu His Ile Gly Asp Ser Met  
130 135 140  
Arg Lys Asp Tyr Val Pro Ala Lys Ser Ile Gly Met His Ala Leu Leu  
145 150 155 160  
Val Asp Arg Phe Lys Thr Glu Ala Ala Lys Asp Trp Ile Glu Ala Gly  
165 170 175  
Ala Ile Val Leu Pro Asp Leu Val Ala Val Gln Gln Leu Leu Glu Ser  
180 185 190  
Asp Lys Leu Lys Cys  
195

(2) INFORMATION FOR SEQ ID NO:2052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1604
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2052:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| atttttagatc | cgatattatt  | agaaagcaac  | caaaactccgg | ctccggttac  | tcggggagttc | 60   |
| aagtttttggg | ttttgtatggg | tactgtctcga | actcgtaccg  | gtatcatctc  | cgctcgtttt  | 120  |
| aaattcttcca | ggtctctgtt  | ccctcgccat  | caccgtacta  | acagcatgaa  | gataaaaaaca | 180  |
| ggaaacgtttt | tgggggtttt  | gatatcatgt  | attcttataa  | acttagctgc  | gatcatggaa  | 240  |
| cgtgcagacg  | agaatctcatt | gccttcgggt  | tataaagaag  | tgagtgaaag  | attttaaagca | 300  |
| ggaccatcag  | atttaggtcta | cttaacattc  | gttagaaaact | ttgttcaagg  | acttgcacata | 360  |
| ccattagcag  | gagttctctgt | cattacotat  | gatcgtccca  | ttgttcttgc  | aataggtaact | 420  |
| gtctgttggg  | ctttatcaac  | tgctgcagtt  | ggagccagca  | gctacttcac  | tcaggttgct  | 480  |
| ttatggagag  | cagtgaaatgg | ttttggaatt  | gcaattgtta  | taccgcgct   | tcaactcgtt  | 540  |
| attgcagata  | gttataaagga | tggtgcgaga  | ggagctggtt  | tcggaattgt  | gaacctcatt  | 600  |
| ggtaacaatcg | gtgttatagg  | aggaggtgtt  | gtagcaactg  | ttatggctgg  | ttcagagattt | 660  |
| tggggcctac  | cgggatggcg  | ttgtgctttt  | ataatgatgg  | cagcgctcag  | cgcagtgatc  | 720  |
| ggattactgt  | tctttctctt  | cgtgtgtgac  | ccgagaaga   | acattgaacg  | agaggaacta  | 780  |
| ttggctcata  | agatgaattc  | gaactcgggt  | tggaaatgatt | cattagcagc  | tgcaaaatct  | 840  |
| ctgcgtcaaa  | taagtacctt  | tcagataaat  | gtcgcgcaag  | gaatcattgg  | ttcgtttccg  | 900  |
| tggaccgcga  | tggttttctt  | tacaatgtgg  | tttgagctta  | ttggcttcga  | tcataaccag  | 960  |
| actgcagctt  | tgcttggggt  | atttgtaca   | ggaggagcga  | taggaacatt  | aatgggaggg  | 1020 |
| ataatagcgg  | ataaaatgtc  | gcggatatat  | ccgaattcgg  | gtagagtgat  | gtgtgcgcag  | 1080 |
| ttcagtgcat  | tcattgggaat | cccattctct  | attattcttc  | tgaagatgat  | cccaacaaag  | 1140 |
| acaacagcgt  | actcaatctt  | ctcgataaact | ctcttctctga | tgggtctttac | cataactttg  | 1200 |
| tcgggatcag  | cggtttaatgc | accgatgttt  | gcagaagtgg  | ttcctccaa   | gcacgcgtata | 1260 |
| atgatctacg  | cgtttgacgc  | tgcttttcgaa | gggtcattct  | catctttttg  | tgccgctttt  | 1320 |
| gtgggaattt  | tgtctgagaa  | aattgtttggg | tatgactcaa  | gaggtattga  | tcctttgaaa  | 1380 |
| ggttctctct  | ttcgtgaggg  | tgatgcctct  | tcaaaagggg  | ttctgtcaat  | gatgctgctt  | 1440 |
| ccgttttggc  | ctgtttgtct  | ctgtttacat  | ccgtttgcat  | ttgttttttc  | gaagatcaga  | 1500 |
| gaaaaacgcga | aaatcgcgag  | ctctaaagaa  | actgaaatga  | tcagagagac  | ttgtctcatgt | 1560 |
| agtcacgttt  | tgattctttt  | tataaccaca  | acgattttta  | aacc        |             |      |

(2) INFORMATION FOR SEQ ID NO:2053:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 514 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..514

(D) OTHER INFORMATION: / Ceres Seq. ID 1571688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2053:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Leu | Asp | Pro | Ile | Phe | Ile | Glu | Ser | Asn | Gln | Thr | Pro | Ala | Pro | Val |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Arg | Glu | Phe | Lys | Phe | Trp | Ile | Leu | Met | Gly | His | Ala | Arg | Thr | Arg |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Thr | Gly | Ile | Ile | Ser | Val | Ala | Phe | Lys | Phe | Phe | Arg | Ser | Leu | Phe | Pro |
|     |     |     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |
| Arg | His | His | Arg | Thr | Asn | Ser | Met | Lys | Ile | Lys | Thr | Gly | Thr | Phe | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Gly | Val | Ser | Ile | Ser | Leu | Ile | Leu | Ile | Asn | Leu | Ala | Ala | Ile | Met | Glu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Ala | Asp | Glu | Asn | Leu | Leu | Pro | Ser | Val | Tyr | Lys | Glu | Val | Ser | Glu |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     | 95  |     |     |
| Ala | Phe | Asn | Ala | Gly | Pro | Ser | Asp | Leu | Gly | Tyr | Leu | Thr | Phe | Val | Arg |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |
| Asn | Phe | Val | Gln | Gly | Leu | Ala | Ser | Pro | Leu | Ala | Gly | Val | Leu | Val | Ile |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Tyr | Asp | Arg | Pro | Ile | Val | Leu | Ala | Ile | Gly | Thr | Val | Cys | Trp | Ala |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Leu | Ser | Thr | Ala | Ala | Val | Gly | Ala | Ser | Ser | Tyr | Phe | Ile | Gln | Val | Ala |
|     |     |     | 145 |     |     |     | 150 |     |     | 155 |     |     |     | 160 |     |
| Leu | Trp | Arg | Ala | Val | Asn | Gly | Phe | Gly | Leu | Ala | Ile | Val | Ile | Pro | Ala |

# COLETTI

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
```

(A) NAME/KEY: peptide  
(B) LOCATION: 1..489  
(D) OTHER INFORMATION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2054:

Met Gly His Ala Arg Thr Arg Thr Gly Ile Ile Ser Val Ala Phe Lys  
1 5 10 15  
Phe Phe Arg Ser Leu Phe Pro Arg His His Arg Thr Asn Ser Met Lys  
20 25 30



Ile Lys Thr Gly Thr Phe Leu Gly Val Ser Ile Ser Leu Ile Leu Ile  
35 40 45  
Asn Leu Ala Ala Ile Met Glu Arg Ala Asp Glu Asn Leu Leu Pro Ser  
50 55 60  
Val Tyr Lys Glu Val Ser Glu Ala Phe Asn Ala Gly Pro Ser Asp Leu  
65 70 75 80  
Gly Tyr Leu Thr Phe Val Arg Asn Phe Val Gln Gly Leu Ala Ser Pro  
85 90 95  
Leu Ala Gly Val Leu Val Ile Thr Tyr Asp Arg Pro Ile Val Leu Ala  
100 105 110  
Ile Gly Thr Val Cys Trp Ala Leu Ser Thr Ala Ala Val Gly Ala Ser  
115 120 125  
Ser Tyr Phe Ile Gln Val Ala Leu Trp Arg Ala Val Asn Gly Phe Gly  
130 135 140  
Leu Ala Ile Val Ile Pro Ala Leu Gln Ser Phe Ile Ala Asp Ser Tyr  
145 150 155 160  
Lys Asp Gly Ala Arg Gly Ala Gly Phe Gly Met Leu Asn Leu Ile Gly  
165 170 175  
Thr Ile Gly Gly Ile Gly Gly Gly Val Val Ala Thr Val Met Ala Gly  
180 185 190  
Ser Glu Phe Trp Gly Ile Pro Gly Trp Arg Cys Ala Phe Ile Met Met  
195 200 205  
Ala Ala Leu Ser Ala Val Ile Gly Leu Leu Val Phe Leu Phe Val Val  
210 215 220  
Asp Pro Arg Lys Asn Ile Glu Arg Glu Glu Met Ala His Lys Met  
225 230 235 240  
Asn Ser Asn Ser Val Trp Asn Asp Ser Leu Ala Ala Ala Lys Ser Val  
245 250 255  
Val Lys Val Ser Thr Phe Gln Ile Ile Val Ala Gln Gly Ile Ile Gly  
260 265 270  
Ser Phe Pro Trp Thr Ala Met Val Phe Phe Thr Met Trp Phe Glu Leu  
275 280 285  
Ile Gly Phe Asp His Asn Gln Thr Ala Ala Leu Leu Gly Val Phe Ala  
290 295 300  
Thr Gly Gly Ala Ile Gly Thr Leu Met Gly Gly Ile Ile Ala Asp Lys  
305 310 315 320  
Met Ser Arg Ile Tyr Pro Asn Ser Gly Arg Val Met Cys Ala Gln Phe  
325 330 335  
Ser Ala Phe Met Gly Ile Pro Phe Ser Ile Ile Leu Leu Lys Val Ile  
340 345 350  
Pro Gln Ser Thr Ser Ser Tyr Ser Ile Phe Ser Ile Thr Leu Phe Leu  
355 360 365  
Met Gly Leu Thr Ile Thr Trp Cys Gly Ser Ala Val Asn Ala Pro Met  
370 375 380  
Phe Ala Glu Val Val Pro Pro Arg His Arg Thr Met Ile Tyr Ala Phe  
385 390 395 400  
Asp Arg Ala Phe Glu Gly Ser Phe Ser Ser Phe Ala Ala Pro Leu Val  
405 410 415  
Gly Ile Leu Ser Glu Lys Met Phe Gly Tyr Asp Ser Arg Gly Ile Asp  
420 425 430  
Pro Leu Lys Gly Ser Ser Val Arg Glu Ala Asp Ala Leu Ser Lys Gly  
435 440 445  
Leu Leu Ser Met Met Ala Val Pro Phe Gly Leu Cys Cys Leu Cys Tyr  
450 455 460  
Thr Pro Leu His Phe Val Phe Gln Lys Asp Arg Glu Asn Ala Lys Ile  
465 470 475 480  
Ala Ser Ser Lys Glu Thr Glu Met Ile  
485

(2) INFORMATION FOR SEQ ID NO:2055:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 459 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..459  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571690  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2055:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ile | Lys | Thr | Gly | Thr | Phe | Leu | Gly | Val | Ser | Ile | Ser | Leu | Ile |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ile | Asn | Leu | Ala | Ala | Ile | Met | Glu | Arg | Ala | Asp | Glu | Asn | Leu | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Pro | Ser | Val | Tyr | Lys | Glu | Val | Ser | Glu | Ala | Phe | Asn | Ala | Gly | Pro | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Leu | Gly | Tyr | Leu | Thr | Phe | Val | Arg | Asn | Phe | Val | Gln | Gly | Leu | Ala |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ser | Pro | Leu | Ala | Gly | Val | Leu | Val | Ile | Thr | Tyr | Asp | Arg | Pro | Ile | Val |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Ala | Ile | Gly | Thr | Val | Cys | Trp | Ala | Leu | Ser | Thr | Ala | Ala | Val | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Ser | Ser | Tyr | Phe | Ile | Gln | Val | Ala | Leu | Trp | Arg | Ala | Val | Asn | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Gly | Leu | Ala | Ile | Val | Ile | Pro | Ala | Leu | Gln | Ser | Phe | Ile | Ala | Asp |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Tyr | Lys | Asp | Gly | Ala | Arg | Gly | Ala | Gly | Phe | Gly | Met | Leu | Asn | Leu |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Ile | Gly | Thr | Ile | Gly | Gly | Ile | Gly | Gly | Gly | Val | Val | Ala | Thr | Val | Met |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Ala | Gly | Ser | Glu | Phe | Trp | Gly | Ile | Pro | Gly | Trp | Arg | Cys | Ala | Phe | Ile |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Met | Met | Ala | Ala | Leu | Ser | Ala | Val | Ile | Gly | Leu | Leu | Val | Phe | Leu | Phe |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Val | Val | Asp | Pro | Arg | Lys | Asn | Ile | Glu | Arg | Glu | Glu | Leu | Met | Ala | His |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Met | Asn | Ser | Asn | Ser | Val | Trp | Asn | Asp | Ser | Leu | Ala | Ala | Ala | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Val | Val | Lys | Val | Ser | Thr | Phe | Gln | Ile | Ile | Val | Ala | Gln | Gly | Ile |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ile | Gly | Ser | Phe | Pro | Trp | Thr | Ala | Met | Val | Phe | Phe | Thr | Met | Trp | Phe |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Leu | Ile | Gly | Phe | Asp | His | Asn | Gln | Thr | Ala | Ala | Leu | Leu | Gly | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Phe | Ala | Thr | Gly | Gly | Ala | Ile | Gly | Thr | Leu | Met | Gly | Gly | Ile | Ile | Ala |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asp | Lys | Met | Ser | Arg | Ile | Tyr | Pro | Asn | Ser | Gly | Arg | Val | Met | Cys | Ala |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Gln | Phe | Ser | Ala | Phe | Met | Gly | Ile | Pro | Phe | Ser | Ile | Ile | Leu | Leu | Lys |
|     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |     |
| Val | Ile | Pro | Gln | Ser | Thr | Ser | Ser | Tyr | Ser | Ile | Phe | Ser | Ile | Thr | Leu |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Phe | Leu | Met | Gly | Leu | Thr | Ile | Thr | Trp | Cys | Gly | Ser | Ala | Val | Asn | Ala |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     |     | 350 |     |     |
| Pro | Met | Phe | Ala | Glu | Val | Val | Pro | Pro | Arg | His | Arg | Thr | Met | Ile | Tyr |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ala | Phe | Asp | Arg | Ala | Phe | Glu | Gly | Ser | Phe | Ser | Ser | Phe | Ala | Ala | Pro |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Leu | Val | Gly | Ile | Leu | Ser | Glu | Lys | Met | Phe | Gly | Tyr | Asp | Ser | Arg | Gly |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Ile | Asp | Pro | Leu | Lys | Gly | Ser | Ser | Val | Arg | Glu | Ala | Asp | Ala | Leu | Ser |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |

Lys Gly Leu Leu Ser Met Met Ala Val Pro Phe Gly Leu Cys Cys Leu  
420 425 430  
Cys Tyr Thr Pro Leu His Phe Val Phe Gln Lys Asp Arg Glu Asn Ala  
435 440 445  
Lys Ile Ala Ser Ser Lys Glu Thr Glu Met Ile  
450 455

(2) INFORMATION FOR SEQ ID NO:2056:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1305 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1305

(D) OTHER INFORMATION: / Ceres Seq. ID 1571691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2056:

aatggaatca cactatacaca atcataacca caaaaacaaa cactatggga cacctcaaaa 60  
gtctcttctac tattcttttc ctaatagcta tgtcgtcaac cgttaacatt gccggtaaaa 120  
taccgcgat catcgtgttt gccgactctt ccgttgatgc cgggaacaaa aactatatcc 180  
caactgttgc tagaagaac tttgagccat atggacggga ctttgttgtt ggaagccga 240  
cgggacggtt ttgtaacgga aagattgcga cggattttat gtccgaagcc ttagggtcta 300  
aaccaatcat tccggcatac ttggatcctt cttataacat ttcagacttt gcaacagggt 360  
ttacctttgc ttctgtctgc actggctatg acaacgccac ttctgatgtt ctgtcggcat 420  
tacctctatg gaacacaact gaatactaca aagaatacca acaaaaactt aaagcatacc 480  
aaggaagaag cagacgcaca gagactatag aaagctctct ctacctcata agcataggga 540  
ccaacgattt cctcgagaat tactttgtct ttcggggcgc ttcttcgcaa tattccgtca 600  
gtctttacca agattttcta gccggaatcg cgaaagaatt tgtgaagaag ttgcatggac 660  
ttggtgtcag aaagatctca ctagggtgggt tactccaat gggatgcatt cctttagaga 720  
gagccaccaa caattggcaat ggaggtgagt cgcgtaggac gtacaaagac atagccgttc 780  
agttcaacag caagcttgat aagattggtt agaagctgaa caaagagctt cctgttctca 840  
acctogtttt ctcaaatcca tatgagccat ttatgcggat catcaagaac cctctctctt 900  
ttgggttcga ggtggtggga gccgcatgCt gcgcgacagg gatgtctcag atgggatgatg 960  
gttgtcaaaag gaataaccca ttacatgta caaacgcaga caagtatgtg ttttgggact 1020  
catttcaccc aacacagaag actaatcaca tcatggccaa tgctctcatg aacagcacat 1080  
tcctcactt cctctaaatg atttttatgt ttgtgtgtgg aaactaaata gatataagag 1140  
taatattatt attagggatt gcttttgata tgcactctgt atgtatttat atttaagtag 1200  
attttgctct tgtgttagtt agcgaaacct acgtttcttt tctagattat ggtgtgccta 1260  
tttatgtacg ttattttatc ctctttagtt attctcaata tatcc

(2) INFORMATION FOR SEQ ID NO:2057:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 364 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..364

(D) OTHER INFORMATION: / Ceres Seq. ID 1571692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2057:

Trp Asn His Thr Ile Thr Ile Ile Thr Thr Lys Thr Asn Thr Met Gly  
1 5 10  
His Leu Lys Ser Leu Phe Thr Ile Leu Phe Leu Ile Ala Met Ser Ser  
20 25 30  
Thr Val Thr Phe Ala Gly Lys Ile Pro Ala Ile Ile Val Phe Gly Asp  
35 40 45  
Ser Ser Val Asp Ala Gly Asn Asn Asn Tyr Ile Pro Thr Val Ala Arg  
50 55 60  
Ser Asn Phe Glu Pro Tyr Gly Arg Asp Phe Val Gly Gly Lys Pro Thr

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Arg | Phe | Cys | Asn | Gly | Lys | Ile | Ala | Thr | Asp | Phe | Met | Ser | Glu | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Gly | Leu | Lys | Pro | Ile | Ile | Pro | Ala | Tyr | Leu | Asp | Pro | Ser | Tyr | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Ser | Asp | Phe | Ala | Thr | Gly | Val | Thr | Phe | Ala | Ser | Ala | Ala | Thr | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Tyr | Asp | Asn | Ala | Thr | Ser | Asp | Val | Leu | Ser | Val | Leu | Pro | Leu | Trp | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Leu | Glu | Tyr | Tyr | Lys | Glu | Tyr | Gln | Thr | Lys | Leu | Lys | Ala | Tyr | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Lys | Asp | Arg | Ala | Thr | Glu | Thr | Ile | Glu | Ser | Ser | Leu | Tyr | Leu | Ile |
|     |     | 165 |     |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Ile | Gly | Thr | Asn | Asp | Phe | Leu | Glu | Asn | Tyr | Phe | Val | Phe | Pro | Gly |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Ser | Ser | Gln | Tyr | Ser | Val | Ser | Leu | Tyr | Gln | Asp | Phe | Leu | Ala | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Ala | Lys | Glu | Phe | Val | Lys | Lys | Leu | His | Gly | Leu | Gly | Ala | Arg | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Ser | Leu | Gly | Gly | Leu | Pro | Pro | Met | Gly | Cys | Met | Pro | Leu | Glu | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ala | Thr | Asn | Ile | Gly | Thr | Gly | Gly | Glu | Cys | Val | Gly | Arg | Tyr | Asn | Asp |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ile | Ala | Val | Gln | Phe | Asn | Ser | Lys | Leu | Asp | Lys | Met | Val | Glu | Lys | Leu |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asn | Lys | Glu | Leu | Pro | Gly | Ser | Asn | Leu | Val | Phe | Ser | Asn | Pro | Tyr | Glu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Pro | Phe | Met | Arg | Ile | Ile | Lys | Asn | Pro | Ser | Ser | Phe | Gly | Phe | Glu | Val |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Val | Gly | Ala | Ala | Cys | Cys | Ala | Thr | Gly | Met | Phe | Glu | Met | Gly | Tyr | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Cys | Gln | Arg | Asn | Asn | Pro | Phe | Thr | Cys | Thr | Asn | Ala | Asp | Lys | Tyr | Val |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Phe | Trp | Asp | Ser | Phe | His | Pro | Thr | Gln | Lys | Thr | Asn | His | Ile | Met | Ala |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Asn | Ala | Leu | Met | Asn | Ser | Thr | Phe | Pro | His | Phe | Leu |     |     |     |     |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2058:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..350

(D) OTHER INFORMATION: / Ceres Seq. ID 1571693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2058:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | His | Leu | Lys | Ser | Leu | Phe | Thr | Ile | Leu | Phe | Leu | Ile | Ala | Met |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Ser | Thr | Val | Thr | Phe | Ala | Gly | Lys | Ile | Pro | Ala | Ile | Ile | Val | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Asp | Ser | Ser | Val | Asp | Ala | Gly | Asn | Asn | Asn | Tyr | Ile | Pro | Thr | Val |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Arg | Ser | Asn | Phe | Glu | Pro | Tyr | Gly | Arg | Asp | Phe | Val | Gly | Gly | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Thr | Gly | Arg | Phe | Cys | Asn | Gly | Lys | Ile | Ala | Thr | Asp | Phe | Met | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Ala | Leu | Gly | Leu | Lys | Pro | Ile | Ile | Pro | Ala | Tyr | Leu | Asp | Pro | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |

Tyr Asn Ile Ser Asp Phe Ala Thr Gly Val Thr Phe Ala Ser Ala Ala  
100 105 110  
Thr Gly Tyr Asp Asn Ala Thr Ser Asp Val Leu Ser Val Leu Pro Leu  
115 120 125  
Trp Lys Gln Leu Glu Tyr Tyr Lys Glu Tyr Gln Thr Lys Leu Lys Ala  
130 135 140  
Tyr Gln Gly Lys Asp Arg Ala Thr Glu Thr Ile Glu Ser Ser Leu Tyr  
145 150 155 160  
Leu Ile Ser Ile Gly Thr Asn Asp Phe Leu Glu Asn Tyr Phe Val Phe  
165 170 175  
Pro Gly Arg Ser Ser Gln Tyr Ser Val Ser Leu Tyr Gln Asp Phe Leu  
180 185 190  
Ala Gly Ile Ala Lys Glu Phe Val Lys Lys Leu His Gly Leu Gly Ala  
195 200 205  
Arg Lys Ile Ser Leu Gly Gly Leu Pro Pro Met Gly Cys Met Pro Leu  
210 215 220  
Glu Arg Ala Thr Asn Ile Gly Thr Gly Gly Glu Cys Val Gly Arg Tyr  
225 230 235 240  
Asn Asp Ile Ala Val Gln Phe Asn Ser Lys Leu Asp Lys Met Val Glu  
245 250 255  
Lys Leu Asn Lys Glu Leu Pro Gly Ser Asn Leu Val Phe Ser Asn Pro  
260 265 270  
Tyr Glu Pro Phe Met Arg Ile Ile Lys Asn Pro Ser Ser Phe Gly Phe  
275 280 285  
Glu Val Val Gly Ala Ala Cys Cys Ala Thr Gly Met Phe Glu Met Gly  
290 295 300  
Tyr Gly Cys Gln Arg Asn Asn Pro Phe Thr Cys Thr Asn Ala Asp Lys  
305 310 315 320  
Tyr Val Phe Trp Asp Ser Phe His Pro Thr Gln Lys Thr Asn His Ile  
325 330 335  
Met Ala Asn Ala Leu Met Asn Ser Thr Phe Pro His Phe Leu  
340 345 350

(2) INFORMATION FOR SEQ ID NO:2059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..335

(D) OTHER INFORMATION: / Ceres Seq. ID 1571694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2059:

Met Ser Ser Thr Val Thr Phe Ala Gly Lys Ile Pro Ala Ile Val  
1 5 10 15  
Phe Gly Asp Ser Ser Val Asp Ala Gly Asn Asn Asn Tyr Ile Pro Thr  
20 25 30  
Val Ala Arg Ser Asn Phe Glu Pro Tyr Gly Arg Asp Phe Val Gly Gly  
35 40 45  
Lys Pro Thr Gly Arg Phe Cys Asn Gly Lys Ile Ala Thr Asp Phe Met  
50 55 60  
Ser Glu Ala Leu Gly Leu Lys Pro Ile Ile Pro Ala Tyr Leu Asp Pro  
65 70 75 80  
Ser Tyr Asn Ile Ser Asp Phe Ala Thr Gly Val Thr Phe Ala Ser Ala  
85 90 95  
Ala Thr Gly Tyr Asp Asn Ala Thr Ser Asp Val Leu Ser Val Leu Pro  
100 105 110  
Leu Trp Lys Gln Leu Glu Tyr Tyr Lys Glu Tyr Gln Thr Lys Leu Lys  
115 120 125  
Ala Tyr Gln Gly Lys Asp Arg Ala Thr Glu Thr Ile Glu Ser Ser Leu

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 130                                                             | 135 | 140 |
| Tyr Leu Ile Ser Ile Gly Thr Asn Asp Phe Leu Glu Asn Tyr Phe Val |     |     |
| 145                                                             | 150 | 155 |
| Phe Pro Gly Arg Ser Ser Gln Tyr Ser Val Ser Leu Tyr Gln Asp Phe |     |     |
|                                                                 | 165 | 170 |
| Leu Ala Gly Ile Ala Lys Glu Phe Val Lys Lys Leu His Gly Leu Gly |     |     |
|                                                                 | 180 | 185 |
| Ala Arg Lys Ile Ser Leu Gly Gly Leu Pro Pro Met Gly Cys Met Pro |     |     |
|                                                                 | 195 | 200 |
| Leu Glu Arg Ala Thr Asn Ile Gly Thr Gly Gly Glu Cys Val Gly Arg |     |     |
|                                                                 | 210 | 215 |
| Tyr Asn Asp Ile Ala Val Gln Phe Asn Ser Lys Leu Asp Lys Met Val |     |     |
|                                                                 | 225 | 230 |
| Glu Lys Leu Asn Lys Glu Leu Pro Gly Ser Asn Leu Val Phe Ser Asn |     |     |
|                                                                 | 245 | 250 |
| Pro Tyr Glu Pro Phe Met Arg Ile Ile Lys Asn Pro Ser Ser Phe Gly |     |     |
|                                                                 | 260 | 265 |
| Phe Glu Val Val Gly Ala Ala Cys Cys Ala Thr Gly Met Phe Glu Met |     |     |
|                                                                 | 275 | 280 |
| Gly Tyr Gly Cys Gln Arg Asn Asn Pro Phe Thr Cys Thr Asn Ala Asp |     |     |
|                                                                 | 290 | 295 |
| Lys Tyr Val Phe Trp Asp Ser Phe His Pro Thr Gln Lys Thr Asn His |     |     |
|                                                                 | 305 | 310 |
| Ile Met Ala Asn Ala Leu Met Asn Ser Thr Phe Pro His Phe Leu     |     |     |
|                                                                 | 325 | 330 |
|                                                                 |     | 335 |

(2) INFORMATION FOR SEQ ID NO:2060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2060:

|             |            |             |             |            |            |      |
|-------------|------------|-------------|-------------|------------|------------|------|
| atagattacg  | taagagtctc | tctctctctc  | tctctggaag  | agggccttgk | gattgttttc | 60   |
| tctctctctc  | tcagctctct | atcgaaattc  | ttatcgaaat  | gaaagtctcg | acccttcgtc | 120  |
| gttgctccctc | aatacgcctc | attcttttga  | ttagcatccc  | taaaactaaa | atcgacagaa | 180  |
| gaatttctcc  | gtttggaatc | ctaccaaatt  | ggggcgcttt  | tggaataaat | gccaccgttt | 240  |
| atgtccggtc  | tcagagctgt | atcttctcta  | ctttcatgtc  | gaaacgcgat | tagcaggaaa | 300  |
| ctcgttagtc  | gttctgggag | ctctcgaggg  | agttttgtat  | cagatcaaat | taggagattt | 360  |
| ggttctcttt  | coggcgctga | gagatgttct  | tctaatttgt  | tgatgtccaa | tgatgacgct | 420  |
| agagctctct  | tcgggagatt | gcctggctct  | gtgagcctac  | ttcagagacg | gcattttctg | 480  |
| gggtgcggag  | atggggaaga | aggtggttgt  | gagttatcaa  | agatctatga | agagagacgt | 540  |
| gtcttagggt  | atactccgga | gcacaattgt  | aacgtagtgt  | cagctgtaga | cttgtagcat | 600  |
| ggatttgttc  | cttggtgtca | gcgctctgag  | gttcttaaa   | aataccctga | tggttcattt | 660  |
| gatgctgaat  | tggagattgt | tttcaagtgt  | ctcgttgaga  | gttacatttc | ccatgtcgaa | 720  |
| tcggagaggg  | cgaaatggat | taagaactaca | gcgagggaca  | ctggcctgtt | tgaccatttg | 780  |
| ataaacctct  | ggcaatttaa | gccaggggcc  | attcctggaa  | cctgcgacct | tcacttccat | 840  |
| gtagatttca  | aattcaattc | accctctcat  | cgccagggtg  | cgtaattgtt | cttcaaggag | 900  |
| gtagcatcaa  | gacttgtggg | ggcattcagt  | gatcgatgcc  | gactagtgtg | tggtccagaa | 960  |
| gtcccgagtag | atgaaaacgc | atatgagcaa  | agagccttgag | acatatctat | atataatat  | 1020 |
| catggaagta  | acaacacatc | agtttagttt  | tcactctgtt  | ttctagagag | cgattgcgca | 1080 |
| tagcatgttt  | tgttttctta | aatatatagt  | aatgctgttt  | cataagaaga | tgaacacatt | 1140 |
| agatgtttgt  | ttaaatgtta | agcagaaaaa  | ataaacacat  | ccatttctct | gttggaattc | 1200 |
| tttttttcac  | tc         |             |             |            |            |      |

(2) INFORMATION FOR SEQ ID NO:2061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..256  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1571704  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2061:  
Met Pro Pro Phe Met Ser Gly Leu Arg Ala Val Ser Ser Leu Leu Ser  
1                  5                  10                  15  
Cys Arg Asn Ala Ile Ser Arg Lys Leu Val Ser Arg Ser Gly Ile Ser  
                  20                  25                  30  
Arg Gly Ser Phe Val Ser Asp Gln Ile Arg Arg Phe Gly Ser Leu Ser  
                  35                  40                  45  
Gly Val Glu Arg Cys Ser Ser Asn Trp Leu Met Ser Asn Asp Asp Ala  
50                  55                  60  
Arg Val Ser Phe Arg Arg Leu Pro Gly Ser Val Ser Leu Leu Gln Arg  
65                  70                  75                  80  
Arg His Phe Leu Gly Cys Gly Asp Gly Glu Glu Gly Gly Gly Glu Leu  
                  85                  90                  95  
Ser Lys Ile Tyr Glu Glu Arg Arg Val Leu Gly Tyr Thr Pro Glu Gln  
                  100                  105                  110  
Met Phe Asn Val Val Ala Ala Val Asp Leu Tyr His Gly Phe Val Pro  
                  115                  120                  125  
Trp Cys Gln Arg Ser Glu Val Leu Lys Glu Tyr Pro Asp Gly Ser Phe  
130                  135                  140  
Asp Ala Glu Leu Glu Ile Gly Phe Lys Phe Leu Val Glu Ser Tyr Ile  
145                  150                  155                  160  
Ser His Val Glu Ser Glu Arg Pro Lys Trp Ile Lys Thr Thr Ala Arg  
                  165                  170                  175  
Asp Thr Gly Leu Phe Asp His Leu Ile Asn Leu Trp Gln Phe Lys Pro  
                  180                  185                  190  
Gly Pro Ile Pro Gly Thr Cys Asp Leu His Phe His Val Asp Phe Lys  
                  195                  200                  205  
Phe Asn Ser Pro Leu Tyr Arg Gln Val Ala Ser Met Phe Phe Lys Glu  
210                  215                  220  
Val Ala Ser Arg Leu Val Gly Ala Phe Ser Asp Arg Cys Arg Leu Val  
225                  230                  235                  240  
Tyr Gly Pro Gly Val Arg Val Asp Glu Asn Ala Tyr Glu Gln Arg Ala  
                  245                  250                  255

(2) INFORMATION FOR SEQ ID NO:2062:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 252 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..252  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1571705  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2062:  
Met Ser Gly Leu Arg Ala Val Ser Ser Leu Leu Ser Cys Arg Asn Ala  
1                  5                  10                  15  
Ile Ser Arg Lys Leu Val Ser Arg Ser Gly Ile Ser Arg Gly Ser Phe  
                  20                  25                  30  
Val Ser Asp Gln Ile Arg Arg Phe Gly Ser Leu Ser Gly Val Glu Arg  
35                  40                  45

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Cys | Ser | Ser | Asn | Trp | Leu | Met | Ser | Asn | Asp | Asp | Ala | Arg | Val | Ser | Phe |  |  |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Arg | Arg | Leu | Pro | Gly | Ser | Val | Ser | Leu | Leu | Gln | Arg | Arg | His | Phe | Leu |  |  |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |  |  |
| Gly | Cys | Gly | Asp | Gly | Glu | Glu | Gly | Gly | Gly | Glu | Leu | Ser | Lys | Ile | Tyr |  |  |
|     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |  |  |
| Glu | Glu | Arg | Arg | Val | Leu | Gly | Tyr | Thr | Pro | Glu | Gln | Met | Phe | Asn | Val |  |  |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |  |  |
| Val | Ala | Ala | Val | Asp | Leu | Tyr | His | Gly | Phe | Val | Pro | Trp | Cys | Gln | Arg |  |  |
|     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |  |  |
| Ser | Glu | Val | Leu | Lys | Glu | Tyr | Pro | Asp | Gly | Ser | Phe | Asp | Ala | Glu | Leu |  |  |
|     |     |     |     |     |     |     |     | 135 |     |     |     |     |     | 140 |     |  |  |
| Glu | Ile | Gly | Phe | Lys | Phe | Leu | Val | Glu | Ser | Tyr | Ile | Ser | His | Val | Glu |  |  |
|     |     |     |     |     |     |     |     | 150 |     |     |     |     |     | 160 |     |  |  |
| Ser | Glu | Arg | Pro | Lys | Trp | Ile | Lys | Thr | Thr | Ala | Arg | Asp | Thr | Gly | Leu |  |  |
|     |     |     |     |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Phe | Asp | His | Leu | Ile | Asn | Leu | Trp | Gln | Phe | Lys | Pro | Gly | Pro | Ile | Pro |  |  |
|     |     |     |     |     |     |     |     |     | 185 |     |     |     |     | 190 |     |  |  |
| Gly | Thr | Cys | Asp | Leu | His | Phe | His | Val | Asp | Phe | Lys | Phe | Asn | Ser | Pro |  |  |
|     |     |     |     |     |     |     |     | 200 |     |     |     |     |     | 205 |     |  |  |
| Leu | Tyr | Arg | Gln | Val | Ala | Ser | Met | Phe | Phe | Lys | Glu | Val | Ala | Ser | Arg |  |  |
|     |     |     |     |     |     |     |     | 215 |     |     |     |     |     | 220 |     |  |  |
| Leu | Val | Gly | Ala | Phe | Ser | Asp | Arg | Cys | Arg | Leu | Val | Tyr | Gly | Pro | Gly |  |  |
|     |     |     |     |     |     |     |     | 230 |     |     |     |     |     |     | 240 |  |  |
| Val | Arg | Val | Asp | Glu | Asn | Ala | Tyr | Glu | Gln | Arg | Ala |     |     |     |     |  |  |
|     |     |     |     |     |     |     |     | 245 |     |     |     |     |     |     |     |  |  |
|     |     |     |     |     |     |     |     |     | 250 |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:2063:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..198

(D) OTHER INFORMATION: / Ceres Seq. ID 1571706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2063:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Ser | Asn | Asp | Asp | Ala | Arg | Val | Ser | Phe | Arg | Arg | Leu | Pro | Gly | Ser |  |  |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Val | Ser | Leu | Leu | Gln | Arg | Arg | His | Phe | Leu | Gly | Cys | Gly | Asp | Gly | Glu |  |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Glu | Gly | Gly | Gly | Glu | Leu | Ser | Lys | Ile | Tyr | Glu | Glu | Arg | Arg | Val | Leu |  |  |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |  |  |
| Gly | Tyr | Thr | Pro | Glu | Gln | Met | Phe | Asn | Val | Val | Ala | Ala | Val | Asp | Leu |  |  |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |  |  |
| Tyr | His | Gly | Phe | Val | Pro | Trp | Cys | Gln | Arg | Ser | Glu | Val | Leu | Lys | Glu |  |  |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     | 75  |     | 80  |  |  |
| Tyr | Pro | Asp | Gly | Ser | Phe | Asp | Ala | Glu | Leu | Glu | Ile | Gly | Phe | Lys | Phe |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Leu | Val | Glu | Ser | Tyr | Ile | Ser | His | Val | Glu | Ser | Glu | Arg | Pro | Lys | Trp |  |  |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |  |  |
| Ile | Lys | Thr | Thr | Ala | Arg | Asp | Thr | Gly | Leu | Phe | Asp | His | Leu | Ile | Asn |  |  |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |  |  |
| Leu | Trp | Gln | Phe | Lys | Pro | Gly | Pro | Ile | Pro | Gly | Thr | Cys | Asp | Leu | His |  |  |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |  |  |
| Phe | His | Val | Asp | Phe | Lys | Phe | Asn | Ser | Pro | Leu | Tyr | Arg | Gln | Val | Ala |  |  |
|     |     |     |     | 145 |     |     |     |     | 155 |     |     |     |     | 160 |     |  |  |
| Ser | Met | Phe | Phe | Lys | Glu | Val | Ala | Ser | Arg | Leu | Val | Gly | Ala | Phe | Ser |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Asp | Arg | Cys | Arg | Leu | Val | Tyr | Gly | Pro | Gly | Val | Arg | Val | Asp | Glu | Asn |  |  |



180  
Ala Tyr Glu Gln Arg Ala  
195

185

190

(2) INFORMATION FOR SEQ ID NO:2064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1592

(D) OTHER INFORMATION: / Ceres Seq. ID 1571707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2064:

```
gatttcgcat ttaactatcct gggtatgtct caattcttct tcaattctct ccttcagttc
gtgtctctgt tctgattgat tactctcaca aaactcatct ttctaatgtc taaagggtcta
atcttttagt ataactcaaa atctgtttct aagttctgac aagttttctga aacgaaattc
aagttttttt atacatatgt tcaattctca gaacagggtt taattaaaca agagatgtca
attttggcga tggttttcgt aacataaaca tgagatttga ttgttctgtg cagatctcat
agtttaactg gtttgagtct agaaatttgc agtgatgcag ctgcacgcc attgttacc
actgagaaga tagataccat ggctcaagat tcaacctga actcaagaac ttcttcttca
agaaaaagaa gattgcgtcg ctctagaagt gtcctctctg gtgattgtat gtacaatgat
gatgtcaaaa tgcagcaaac acctctcat ccgagtaaaa tcccaatgtt cagtgtcta
aaccgcgaat tcaaggcagat gatcatgttc ttggctttat attcttaccat tggatctctc
tgtttctacc tctgtgagaga ccagatctcc ggctcataaaa ccagtgggtg ggtagatgct
ctctattctt gtatagttaac gatgacaaat gttggatacg gtgaccttgt ccttaagtgt
tcgcctctaa ggctacttgc ttgtgccttc gtcttctcgg gaatggctct cgttggctac
ctcttaagtc gaggcgcgga ttatctagtg gagaacaag aggcctttct cgttggggct
ttcattttgc gtcaaaagctt tgggtccaaca gacattctca aggagttgca tctaacaag
ttgagatata aatgctatgc tacatgcctt gtctctgtat tctcttctat tgttggcagc
taatttcctg taatgggtga gaaaatgcgc gttatctcag ttcttctact gctctgctcc
acgggtacaa cattgggtta tggagataag agttttaact cggaaagccgc acgcctttt
gctgtgtttt ggcatttgac gaggaccata tgtttTggc tcagtttttc ctctatgtaA
gctgagctaa atacagaaaa caaacagagg gcgttgggtg aatgggtttt aacgcgaaga
atcacaacaa atgatctcga agcagctgat ctcatggaag atggmgtgtg tggagctgca
gagttttat tgtataaact gaaagaaatg ggtaagattg atgagaaga taattctggg
ataatggaat agttcgaaga acttgattac gatgaatcag gaactctcac gactctgac
atcgtttttg ctacagaccac gtctcagatt caaaggtaag cctcattatc atcatcatca
tcatcttgcc aagacgaatc agaattcttg tttagttata ccttcacaca acaaaaagcc
aaagagatgt aacagttttt tggaaatttt gtttgtttt cctgtttgtg ttgtgaagt
aatgccacag tctaactctt tgcattgttc t
```

(2) INFORMATION FOR SEQ ID NO:2065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..253

(D) OTHER INFORMATION: / Ceres Seq. ID 1571708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2065:

```
Met Ala Gln Asp Phe Asn Leu Asn Ser Arg Thr Ser Ser Ser Arg Lys
1 5 10 15
Arg Arg Leu Arg Arg Ser Arg Ser Ala Pro Arg Gly Asp Cys Met Tyr
20 25 30
Asn Asp Asp Val Lys Ile Asn Glu Pro Pro Pro His Pro Ser Lys Ile
35 40 45
Pro Met Phe Ser Asp Leu Asn Pro Asn Leu Arg Arg Val Ile Met Phe
```

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 50                                                              | 55  | 60  |
| Leu Ala Leu Tyr Leu Thr Ile Gly Thr Leu Cys Phe Tyr Leu Val Arg |     |     |
| 65                                                              | 70  | 75  |
| Asp Gln Ile Ser Gly His Lys Thr Ser Gly Val Val Asp Ala Leu Tyr |     | 80  |
|                                                                 | 85  | 90  |
| Phe Cys Ile Val Thr Met Thr Thr Val Gly Tyr Gly Asp Leu Val Pro |     | 95  |
|                                                                 | 100 | 105 |
| Asn Ser Ser Ala Ser Arg Leu Leu Ala Cys Ala Phe Val Phe Ser Gly |     | 110 |
|                                                                 | 115 | 120 |
| Met Val Leu Val Gly His Leu Leu Ser Arg Ala Ala Asp Tyr Leu Val |     | 125 |
|                                                                 | 130 | 135 |
| Glu Lys Gln Glu Ala Leu Leu Val Arg Ala Phe His Leu Arg Gln Ser |     | 140 |
|                                                                 | 145 | 150 |
| Phe Gly Pro Thr Asp Ile Leu Lys Glu Leu His Thr Asn Lys Leu Arg |     | 155 |
|                                                                 | 165 | 170 |
| Tyr Lys Cys Tyr Ala Thr Cys Leu Val Leu Val Val Leu Phe Ile Val |     | 175 |
|                                                                 | 180 | 185 |
| Gly Thr Ile Phe Leu Val Met Val Glu Lys Met Pro Val Ile Ser Ala |     | 190 |
|                                                                 | 195 | 200 |
| Phe Tyr Cys Val Cys Ser Thr Val Thr Thr Leu Gly Tyr Gly Asp Lys |     | 205 |
|                                                                 | 210 | 215 |
| Ser Phe Asn Ser Glu Ala Gly Arg Leu Phe Ala Val Phe Trp Ile Leu |     | 220 |
|                                                                 | 225 | 230 |
| Thr Ser Thr Ile Cys Phe Trp Leu Ser Phe Ser Ser Met             |     | 235 |
|                                                                 | 245 | 250 |

(2) INFORMATION FOR SEQ ID NO:2066:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1571709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2066:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Tyr Asn Asp Asp Val Lys Ile Asp Glu Pro Pro Pro His Pro Ser |     |
| 1                                                               | 5   |
| Lys Ile Pro Met Phe Ser Asp Leu Asn Pro Asn Leu Arg Arg Val Ile | 10  |
|                                                                 | 15  |
| Met Phe Leu Ala Leu Tyr Leu Thr Ile Gly Thr Leu Cys Phe Tyr Leu | 20  |
|                                                                 | 25  |
| Val Arg Asp Gln Ile Ser Gly His Lys Thr Ser Gly Val Val Asp Ala | 30  |
|                                                                 | 35  |
| Leu Tyr Phe Cys Ile Val Thr Met Thr Thr Val Gly Tyr Gly Asp Leu | 40  |
|                                                                 | 45  |
| Val Pro Asn Ser Ser Ala Ser Arg Leu Leu Ala Cys Ala Phe Val Phe | 50  |
|                                                                 | 55  |
| Ser Gly Met Val Leu Val Gly His Leu Leu Ser Arg Ala Ala Asp Tyr | 60  |
|                                                                 | 65  |
| Leu Val Glu Lys Gln Glu Ala Leu Leu Val Arg Ala Phe His Leu Arg | 70  |
|                                                                 | 75  |
| Gln Ser Phe Gly Pro Thr Asp Ile Leu Lys Glu Leu His Thr Asn Lys | 80  |
|                                                                 | 85  |
| Leu Arg Tyr Lys Cys Tyr Ala Thr Cys Leu Val Leu Val Val Leu Phe | 90  |
|                                                                 | 95  |
| Ile Val Gly Thr Ile Phe Leu Val Met Val Glu Lys Met Pro Val Ile | 100 |
|                                                                 | 105 |
| Ser Ala Phe Tyr Cys Val Cys Ser Thr Val Thr Thr Leu Gly Tyr Gly | 110 |
|                                                                 | 115 |
|                                                                 | 120 |
|                                                                 | 125 |
|                                                                 | 130 |
|                                                                 | 135 |
|                                                                 | 140 |
|                                                                 | 145 |
|                                                                 | 150 |
|                                                                 | 155 |
|                                                                 | 160 |
|                                                                 | 165 |
|                                                                 | 170 |
|                                                                 | 175 |
|                                                                 | 180 |
|                                                                 | 185 |
|                                                                 | 190 |

2025 RELEASE UNDER E.O. 14176

Asp Lys Ser Phe Asn Ser Glu Ala Gly Arg Leu Phe Ala Val Phe Trp  
195 200 205  
Ile Leu Thr Ser Thr Ile Cys Phe Trp Leu Ser Phe Ser Ser Met  
210 215 220

(2) INFORMATION FOR SEQ ID NO:2067:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..204
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2067:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Ser | Asp | Leu | Asn | Pro | Asn | Leu | Arg | Val | Ile | Met | Phe | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Ala | Leu | Tyr | Leu | Thr | Ile | Gly | Thr | Leu | Cys | Phe | Tyr | Leu | Val | Arg |
|     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Ile | Ser | Gly | His | Lys | Thr | Ser | Gly | Val | Val | Asp | Ala | Leu | Tyr |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Ile | Val | Thr | Met | Thr | Thr | Val | Gly | Tyr | Gly | Asp | Leu | Val | Pro |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |
| Ser | Ser | Ala | Ser | Arg | Leu | Ala | Cys | Ala | Phe | Val | Phe | Ser | Gly | Met |
|     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| Val | Leu | Val | Gly | His | Leu | Leu | Ser | Arg | Ala | Ala | Asp | Tyr | Leu | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Lys | Gln | Glu | Ala | Leu | Leu | Val | Arg | Ala | Phe | His | Leu | Arg | Gln | Ser |
|     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Pro | Thr | Asp | Ile | Leu | Lys | Glu | Leu | His | Thr | Asn | Lys | Leu | Arg |
|     | 115 |     |     |     | 120 |     |     |     |     |     |     | 125 |     |     |
| Lys | Cys | Tyr | Ala | Thr | Cys | Leu | Val | Leu | Val | Val | Leu | Phe | Ile | Val |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Thr | Ile | Phe | Leu | Val | Met | Val | Glu | Lys | Met | Pro | Val | Ile | Ser | Ala |
|     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Tyr | Cys | Val | Cys | Ser | Thr | Val | Thr | Thr | Leu | Gly | Tyr | Gly | Asp | Lys |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Phe | Asn | Ser | Glu | Ala | Gly | Arg | Leu | Phe | Ala | Val | Phe | Trp | Ile | Leu |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Thr | Ile | Cys | Phe | Trp | Leu | Ser | Phe | Ser | Ser | Met |     |     |     |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1324
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2068:

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| ctatcgaaac | tctctctgac  | ttgtttgtgt | tctctcaaat | cctctgataa | gaatcaatgg  | 60  |
| cgaaggaatt | agcagagaaa  | gctaaagaag | ctYttctaga | tgatgacttc | gatgttgctg  | 120 |
| ttgacttata | ctccaaagcc  | attgacttgg | atcccaattg | gcgccctctc | ttcgccgcatc | 180 |
| gtgctcaggc | caacatcaaa  | atcgataact | tcactgaagc | tgttgtagat | gcgaacaaag  | 240 |
| ccattgagtt | ggagccaaag  | ggtgcaaaag | cctatctcag | aaagggcact | gcttgtagta  | 300 |
| agctagaaga | atatagtact  | gctaaagcag | cctcgaaaaa | gggagctctc | gttgcaaccga | 360 |
| atgaacccaa | gttttaagaag | atgatagatg | aatgcgatct | tcgtattgca | gaagaagaga  | 420 |

|             |            |            |             |            |            |      |
|-------------|------------|------------|-------------|------------|------------|------|
| aagatttgggt | tcagccgatg | ccaccgagtt | tgccttcaag  | ctctacaaca | ccactagcaa | 480  |
| cggaagctga  | tgctctcctt | gttccaatto | ctgcagcacc  | tgccaaaccg | atgttcaggc | 540  |
| acgagttcta  | ccagaaacca | gaagaagcgg | tggtgacaat  | tttcgccaaa | aaagtaccta | 600  |
| agggaacgt   | aactgtcgag | tttggtgagc | agattctgag  | tggtgtcatt | gatgttgctg | 660  |
| gagaggaagc  | ttatcatctc | cagccgagat | tggtcgggaa  | gataatacca | gagaagtgcg | 720  |
| gatttgaagt  | attgtcgacc | aaagttgaga | tccgtcttgc  | gaaagcagag | ataatcacct | 780  |
| gggcctccct  | tgaatatggt | aaagggcaca | gtgttttgcc  | caaaccacca | gtctcatcag | 840  |
| cgctgtcgca  | gagaccagtg | taccatcttt | ctaagccagc  | aaaagactgg | gacaagttgg | 900  |
| aagctggaat  | gaagaacacg | gagaagggat | agaagcttga  | tgagagtgca | gctatgaaca | 960  |
| aatttttcag  | cgacatatac | tcgagtgca  | atgaagacat  | gagcggggca | atgaacaaat | 1020 |
| catttgcaga  | gtcgaatggg | acggtaactg | cgacaaactg  | gaaagaagtt | gggactaaga | 1080 |
| aagtggagag  | cactccacca | gatggcatgg | agctcaagaa  | gtgggagtat | tgatctcttt | 1140 |
| aaaaatccct  | tttctgggtt | ttgttataaa | aaagtctgac  | aaatcttttg | aacttttaag | 1200 |
| gtgttttttt  | ttttggtttc | tgctcgaaat | tgctctcttc  | cattcttgcg | ttgtgtgtct | 1260 |
| aaagaaacgt  | ctgatacttt | gatttggat  | tagaaaaacta | aaactcgcaa | gtctgttgg  | 1320 |

(2) INFORMATION FOR SEQ ID NO:2069:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 358 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..358

(D) OTHER INFORMATION: / Ceres Seq. ID 1571735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2069:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Glu | Leu | Ala | Glu | Lys | Ala | Lys | Glu | Ala | Xaa | Leu | Asp | Asp |
| 1   |     |     | 5   |     |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Asp | Phe | Asp | Val | Ala | Val | Asp | Leu | Tyr | Ser | Lys | Ala | Ile | Asp | Leu | Asp |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Pro | Asn | Cys | Ala | Ala | Phe | Phe | Ala | Asp | Arg | Ala | Gln | Ala | Asn | Ile | Lys |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Ile | Asp | Asn | Phe | Thr | Glu | Ala | Val | Val | Asp | Ala | Asn | Lys | Ala | Ile | Glu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Glu | Pro | Thr | Leu | Ala | Lys | Ala | Tyr | Leu | Arg | Lys | Gly | Thr | Ala | Cys |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Met | Lys | Leu | Glu | Glu | Tyr | Ser | Thr | Ala | Lys | Ala | Ala | Leu | Glu | Lys | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Ser | Val | Ala | Pro | Asn | Glu | Pro | Lys | Phe | Lys | Lys | Met | Ile | Asp | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Asp | Leu | Arg | Ile | Ala | Glu | Glu | Lys | Asp | Leu | Val | Gln | Pro | Met |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Pro | Pro | Ser | Leu | Pro | Ser | Ser | Ser | Thr | Thr | Pro | Leu | Ala | Thr | Glu | Ala |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Asp | Ala | Pro | Pro | Val | Pro | Ile | Pro | Ala | Ala | Pro | Ala | Lys | Pro | Met | Phe |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Arg | His | Glu | Phe | Tyr | Gln | Lys | Pro | Glu | Glu | Ala | Val | Val | Thr | Ile | Phe |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Lys | Lys | Val | Pro | Lys | Glu | Asn | Val | Thr | Val | Glu | Phe | Gly | Glu | Gln |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Leu | Ser | Val | Val | Ile | Asp | Val | Ala | Gly | Glu | Glu | Ala | Tyr | His | Leu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gln | Pro | Arg | Leu | Phe | Gly | Lys | Ile | Ile | Pro | Glu | Lys | Cys | Arg | Phe | Glu |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Leu | Ser | Thr | Lys | Val | Glu | Ile | Arg | Leu | Ala | Lys | Ala | Glu | Ile | Ile |
|     |     |     | 225 |     |     | 230 |     |     |     | 235 |     |     |     | 240 |     |
| Thr | Trp | Ala | Ser | Leu | Glu | Tyr | Gly | Lys | Gly | Gln | Ser | Val | Leu | Pro | Lys |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Pro | Asn | Val | Ser | Ser | Ala | Leu | Ser | Gln | Arg | Pro | Val | Tyr | Pro | Ser | Ser |

[illegible]

(2) INFORMATION FOR SEQ ID NO:2071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..250
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2071:

Met Ile Asp Glu Cys Asp Leu Arg Ile Ala Glu Glu Glu Lys Asp Leu  
1 5 10 15  
Val Gln Pro Met Pro Pro Ser Leu Pro Ser Ser Ser Thr Thr Pro Leu  
20 25 30  
Ala Thr Glu Ala Asp Ala Pro Pro Val Pro Ile Pro Ala Ala Pro Ala  
35 40 45  
Lys Pro Met Phe Arg His Glu Phe Tyr Gln Lys Pro Glu Glu Ala Val  
50 55 60  
Val Thr Ile Phe Ala Lys Lys Val Pro Lys Glu Asn Val Thr Val Glu  
65 70 75 80  
Phe Gly Glu Gln Ile Leu Ser Val Val Ile Asp Val Ala Gly Glu Glu  
85 90 95  
Ala Tyr His Leu Gln Pro Arg Leu Phe Gly Lys Ile Ile Pro Glu Lys  
100 105 110  
Cys Arg Phe Glu Val Leu Ser Thr Lys Val Glu Ile Arg Leu Ala Lys  
115 120 125  
Ala Glu Ile Ile Thr Trp Ala Ser Leu Glu Tyr Gly Lys Gly Gln Ser  
130 135 140  
Val Leu Pro Lys Pro Asn Val Ser Ser Ala Leu Ser Gln Arg Pro Val  
145 150 155 160  
Tyr Pro Ser Ser Lys Pro Ala Lys Asp Trp Asp Lys Leu Glu Ala Glu  
165 170 175  
Val Lys Lys Gln Glu Lys Asp Glu Lys Leu Asp Gly Asp Ala Ala Met  
180 185 190  
Asn Lys Phe Phe Ser Asp Ile Tyr Ser Ser Ala Asp Glu Asp Met Arg  
195 200 205  
Arg Ala Met Asn Lys Ser Phe Ala Glu Ser Asn Gly Thr Val Leu Ser  
210 215 220  
Thr Asn Trp Lys Glu Val Gly Thr Lys Lys Val Glu Ser Thr Pro Pro  
225 230 235 240  
Asp Gly Met Glu Leu Lys Lys Trp Glu Tyr  
245 250

(2) INFORMATION FOR SEQ ID NO:2072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..767
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2072:

atcatcacaa ctactatcac accaaactca aaaaacacaa accacaagag gatcatattca 60  
ttttttattg ttctgtttta atcatcatca tcagaagaaa aatggtttgcg atatcggaga 120  
tcaagtcgac ggtggatgac acggcggcga attgtttgat gcttttatct agagtgggac 180  
aagaaaaacgt tgacgggtggc gatcaaaaaa gcgttttcac atgtaaaacg tgtttgaagc 240  
agtttcattc gttccaagcc ttaggaggtc accgtgcgag tcacaagaag cctaacaacg 300

```

acgcgtttgtc gtctagattg atgaagaagg tgaaaaacgtc gtcgcacatc tgtcccatat 360
gtggagtgga gtttccgatg ggacaagcgt tgggaggaga catgaggaga cacaggaacg 420
agagtggNgg ctgctgggtg cgcgttggtt acacgcgctt tgttgccgga gccacgggtg 480
actacgttga agaaatctav cagtgggaag agagtggctt gtttgatct gagtctaggg 540
atgtgtgaca atttgaatct caagttggag cttggaagaa cagtttattg attttattta 600
ttttccttaa attttcga tttatttggg tctctcattc tttgaatttt tcttaatttt 660
ctagattata catacatccg cagatttagg aaactttcat agagtgtaat cttttctttc 720
tgtaaaaata tattttactt gtacgattgg agatttgta tgagatc

```

(2) INFORMATION FOR SEQ ID NO:2073:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 217 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1571751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2073:

```

His His Asn Tyr Tyr His Thr Lys Leu Lys Lys His Lys Pro Gln Glu
1 5 10 15
Asp His Phe Ile Phe Tyr Cys Phe Val Leu Ile Ile Ile Arg Arg
20 25 30
Lys Met Val Ala Ile Ser Glu Ile Lys Ser Thr Val Asp Val Thr Ala
35 40 45
Ala Asn Cys Leu Met Leu Leu Ser Arg Val Gly Gln Glu Asn Val Asp
50 55 60
Gly Gly Asp Gln Lys Arg Val Phe Thr Cys Lys Thr Cys Leu Lys Gln
65 70 75 80
Phe His Ser Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys
85 90 95
Pro Asn Asn Asp Ala Leu Ser Ser Arg Leu Met Lys Lys Val Lys Thr
100 105 110
Ser Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met Gly Gln
115 120 125
Ala Leu Gly Gly His Met Arg Arg His Arg Asn Glu Ser Xaa Gly Cys
130 135 140
Trp Trp Arg Val Gly Tyr Thr Arg Phe Val Ala Gly Ala His Gly Asp
145 150 155 160
Tyr Val Glu Glu Ile Xaa Gln Trp Glu Glu Ser Gly Leu Phe Gly Ser
165 170 175
Glu Ser Arg Asp Gly Gly Gln Phe Glu Ser Gln Val Gly Ala Trp Lys
180 185 190
Asn Ser Leu Ile Leu Phe Ile Phe Leu Lys Phe Ser Glu Tyr Ile
195 200 205
Cys Phe Ser His Ser Leu Asn Phe Ser
210 215

```

(2) INFORMATION FOR SEQ ID NO:2074:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 184 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..184

(D) OTHER INFORMATION: / Ceres Seq. ID 1571752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2074:

```

Met Val Ala Ile Ser Glu Ile Lys Ser Thr Val Asp Val Thr Ala Ala

```

|                 |                     |                     |                 |
|-----------------|---------------------|---------------------|-----------------|
| 1               | 5                   | 10                  | 15              |
| Asn Cys Leu Met | Leu Leu Ser Arg Val | Gly Gln Glu Asn Val | Asp Gly         |
| 20              | 25                  | 30                  |                 |
| Gly Asp Gln Lys | Arg Val Phe Thr Cys | Lys Thr Cys Leu Lys | Gln Phe         |
| 35              | 40                  | 45                  |                 |
| His Ser Phe Gln | Ala Leu Gly Gly     | His Arg Ala Ser     | His Lys Lys Pro |
| 50              | 55                  | 60                  |                 |
| Asn Asn Asp Ala | Leu Ser Ser Arg     | Leu Met Lys Lys     | Val Lys Thr Ser |
| 65              | 70                  | 75                  | 80              |
| Ser His Pro Cys | Pro Ile Cys Gly     | Val Glu Phe Pro     | Met Gly Gln Ala |
| 85              | 90                  | 95                  |                 |
| Leu Gly Gly His | Met Arg Arg His     | Arg Asn Glu Ser     | Xaa Gly Cys Trp |
| 100             | 105                 | 110                 |                 |
| Trp Arg Val Gly | Tyr Thr Arg Phe     | Val Ala Gly Ala     | His Gly Asp Tyr |
| 115             | 120                 | 125                 |                 |
| Val Glu Glu Ile | Xaa Gln Trp Glu     | Glu Ser Gly Leu     | Phe Gly Ser Glu |
| 130             | 135                 | 140                 |                 |
| Ser Arg Asp Gly | Gly Gln Phe Glu     | Ser Gln Val Gly     | Ala Trp Lys Asn |
| 145             | 150                 | 155                 | 160             |
| Ser Leu Leu Ile | Leu Phe Ile Phe     | Leu Lys Phe Ser     | Glu Tyr Ile Cys |
| 165             | 170                 | 175                 |                 |
| Phe Ser His Ser | Leu Asn Phe Ser     |                     |                 |
| 180             |                     |                     |                 |

(2) INFORMATION FOR SEQ ID NO:2075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1571753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2075:

|                 |                     |                 |             |
|-----------------|---------------------|-----------------|-------------|
| Met Leu Leu Ser | Arg Val Gly Gln Glu | Asn Val Asp Gly | Gly Asp Gln |
| 1               | 5                   | 10              | 15          |
| Lys Arg Val Phe | Thr Cys Lys Thr Cys | Leu Lys Gln Phe | His Ser Phe |
| 20              | 25                  | 30              |             |
| Gln Ala Leu Gly | Gly His Arg Ala Ser | His Lys Lys Pro | Asn Asn Asp |
| 35              | 40                  | 45              |             |
| Ala Leu Ser Ser | Arg Leu Met Lys Lys | Val Lys Thr Ser | Ser His Pro |
| 50              | 55                  | 60              |             |
| Cys Pro Ile Cys | Gly Val Glu Phe Pro | Met Gly Gln Ala | Leu Gly Gly |
| 65              | 70                  | 75              | 80          |
| His Met Arg Arg | His Arg Asn Glu Ser | Xaa Gly Cys Trp | Trp Arg Val |
| 85              | 90                  | 95              |             |
| Gly Tyr Thr Arg | Phe Val Ala Gly Ala | His Gly Asp Tyr | Val Glu Glu |
| 100             | 105                 | 110             |             |
| Ile Xaa Gln Trp | Glu Glu Ser Gly Leu | Phe Gly Ser Glu | Ser Arg Asp |
| 115             | 120                 | 125             |             |
| Gly Gly Gln Phe | Glu Ser Gln Val Gly | Ala Trp Lys Asn | Ser Leu Leu |
| 130             | 135                 | 140             |             |
| Ile Leu Phe Ile | Phe Leu Lys Phe Ser | Glu Tyr Ile Cys | Phe Ser His |
| 145             | 150                 | 155             | 160         |
| Ser Leu Asn Phe | Ser                 |                 |             |
| 165             |                     |                 |             |

(2) INFORMATION FOR SEQ ID NO:2076:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 949 base pairs

(B) TYPE: nucleic acid



(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1.949  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571770  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2076:

|             |            |             |            |             |            |     |
|-------------|------------|-------------|------------|-------------|------------|-----|
| ctccacgatt  | ctgacacaaa | aaaggagaag  | gaataagaga | aaagtgaagt  | tgtgtttgt  | 60  |
| atcgatcaga  | aaatggcgac | gtcgatgata  | cagaggatgt | tcaagcaagg  | gacgaaaatc | 120 |
| gtctgcgtcg  | gcgctaacta | cgccgctcac  | gccaaaaga  | taggcacgcg  | cgtccccaag | 180 |
| gaaccagtta  | tattcttgaa | gccaaacatca | tcatacttag | aaaatggagg  | aacaattgag | 240 |
| atcccacatc  | ctttggattc | acttcaccaa  | gaagtagaac | tcgctttagt  | gattggacag | 300 |
| aaagctagag  | atgtacctga | atcaatagcc  | atggattaca | tggaggagata | tgccggtgtc | 360 |
| cttgatatga  | ctgctaggga | actccaaagt  | tcgtctaagg | catctgggtc  | cccatggacg | 420 |
| gttgcgaaag  | gacaagatgc | cttcactcct  | atcagctctg | ttctgcacaa  | ggcgatgggt | 480 |
| cgtgatcccg  | ataatctaga | actttggctc  | aaggttgatg | gtgaacaacg  | acagaagggt | 540 |
| tggacaaaag  | atatgatatt | caagggtccc  | tacctcatta | gctacataag  | ttctataatg | 600 |
| accctttacg  | aaggagatgt | catcttgaca  | ggcacaccag | aaggtgttgg  | acctgtaaa  | 660 |
| ataggtcaga  | agataacggc | cggaatcacc  | ggtctatctg | aagttcaatt  | cgatgtggag | 720 |
| agggcgtgtaa | agcccttgag | ctaataagtg  | gttttattta | tctttcatac  | aaaaatgtca | 780 |
| attttataaaa | agcatctcta | aaattttcat  | cacttactgt | gtttccctaag | gaaggagaaa | 840 |
| ataaaacctcg | ttactcaatt | tatttgtaat  | ctctataaca | atggctctaa  | gaccggttta | 900 |
| aattgtttat  | atgggagagt | atttgtaaag  | ttgtgatatt | tactgttgc   |            |     |

(2) INFORMATION FOR SEQ ID NO:2077:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 223 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1.223  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571771  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2077:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Thr | Ser | Met | Ile | Gln | Arg | Met | Phe | Lys | Gln | Gly | Thr | Lys | Ile |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Val | Cys | Val | Gly | Arg | Asn | Tyr | Ala | Ala | His | Ala | Lys | Glu | Leu | Gly | Asn |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |  |
| Ala | Val | Pro | Lys | Glu | Pro | Val | Ile | Phe | Leu | Lys | Pro | Thr | Ser | Ser | Tyr |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Leu | Glu | Asn | Gly | Gly | Thr | Ile | Glu | Ile | Pro | His | Pro | Leu | Asp | Ser | Leu |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| His | His | Glu | Val | Glu | Leu | Ala | Leu | Val | Ile | Gly | Gln | Lys | Ala | Arg | Asp |  |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |  |
| Val | Pro | Glu | Ser | Ile | Ala | Met | Asp | Tyr | Ile | Gly | Gly | Tyr | Ala | Val | Ala |  |
|     |     |     | 85  |     |     |     | 90  |     |     |     | 95  |     |     |     |     |  |
| Leu | Asp | Met | Thr | Ala | Arg | Glu | Leu | Gln | Ala | Ser | Ala | Lys | Ala | Ser | Gly |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     | 110 |     |     |     |     |  |
| Leu | Pro | Trp | Thr | Val | Ala | Lys | Gly | Gln | Asp | Thr | Phe | Thr | Pro | Ile | Ser |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |     |  |
| Ser | Val | Leu | Pro | Lys | Ala | Met | Val | Arg | Asp | Pro | Asp | Asn | Leu | Glu | Leu |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |  |
| Trp | Leu | Lys | Val | Asp | Gly | Glu | Thr | Arg | Gln | Lys | Gly | Leu | Thr | Lys | Asp |  |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     | 160 |     |  |
| Met | Ile | Phe | Lys | Val | Pro | Tyr | Leu | Ile | Ser | Tyr | Ile | Ser | Ser | Ile | Met |  |
|     |     |     | 165 |     |     |     | 170 |     |     |     | 175 |     |     |     |     |  |
| Thr | Leu | Tyr | Glu | Gly | Asp | Val | Ile | Leu | Thr | Gly | Thr | Pro | Glu | Gly | Val |  |
|     |     |     | 180 |     |     |     | 185 |     |     |     | 190 |     |     |     |     |  |
| Gly | Pro | Val | Lys | Ile | Gly | Gln | Lys | Ile | Thr | Ala | Gly | Ile | Thr | Gly | Leu |  |

195 200 205  
Ser Glu Val Gln Phe Asp Val Glu Arg Arg Val Lys Pro Leu Ser  
210 215 220

(2) INFORMATION FOR SEQ ID NO:2078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..219
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2078:

Met Ile Gln Arg Met Phe Lys Gln Gly Thr Lys Ile Val Cys Val Gly  
1 5 10 15  
Arg Asn Tyr Ala Ala His Ala Lys Glu Leu Gly Asn Ala Val Pro Lys  
20 25 30  
Glu Pro Val Ile Phe Leu Lys Pro Thr Ser Ser Tyr Leu Glu Asn Gly  
35 40 45  
Gly Thr Ile Glu Ile Pro His Pro Leu Asp Ser Leu His His Glu Val  
50 55 60  
Glu Leu Ala Leu Val Ile Gly Gln Lys Ala Arg Asp Val Pro Glu Ser  
65 70 75 80  
Ile Ala Met Asp Tyr Ile Gly Gly Tyr Ala Val Ala Leu Asp Met Thr  
85 90 95  
Ala Arg Glu Leu Gln Ala Ser Ala Lys Ala Ser Gly Leu Pro Trp Thr  
100 105 110  
Val Ala Lys Gly Gln Asp Thr Phe Thr Pro Ile Ser Ser Val Leu Pro  
115 120 125  
Lys Ala Met Val Arg Asp Pro Asp Asn Leu Glu Leu Trp Leu Lys Val  
130 135 140  
Asp Gly Glu Thr Arg Gln Lys Gly Leu Thr Lys Asp Met Ile Phe Lys  
145 150 155 160  
Val Pro Tyr Leu Ile Ser Tyr Ile Ser Ser Ile Met Thr Leu Tyr Glu  
165 170 175  
Gly Asp Val Ile Leu Thr Gly Thr Pro Glu Gly Val Gly Pro Val Lys  
180 185 190  
Ile Gly Gln Lys Ile Thr Ala Gly Ile Thr Gly Leu Ser Glu Val Gln  
195 200 205  
Phe Asp Val Glu Arg Arg Val Lys Pro Leu Ser  
210 215

(2) INFORMATION FOR SEQ ID NO:2079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..215
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2079:

Met Phe Lys Gln Gly Thr Lys Ile Val Cys Val Gly Arg Asn Tyr Ala  
1 5 10 15  
Ala His Ala Lys Glu Leu Gly Asn Ala Val Pro Lys Glu Pro Val Ile  
20 25 30  
Phe Leu Lys Pro Thr Ser Ser Tyr Leu Glu Asn Gly Gly Thr Ile Glu  
35 40 45

```

Ile Pro His Pro Leu Asp Ser Leu His His Glu Val Glu Leu Ala Leu
 50 55 60
Val Ile Gly Gln Lys Ala Arg Asp Val Pro Glu Ser Ile Ala Met Asp
 65 70 75 80
Tyr Ile Gly Gly Tyr Ala Val Ala Leu Asp Met Thr Ala Arg Glu Leu
 85 90 95
Gln Ala Ser Ala Lys Ala Ser Gly Leu Pro Trp Thr Val Ala Lys Gly
 100 105 110
Gln Asp Thr Phe Thr Pro Ile Ser Ser Val Leu Pro Lys Ala Met Val
 115 120 125
Arg Asp Pro Asp Asn Leu Glu Leu Trp Leu Lys Val Asp Gly Glu Thr
 130 135 140
Arg Gln Lys Gly Leu Thr Lys Asp Met Ile Phe Lys Val Pro Tyr Leu
 145 150 155 160
Ile Ser Tyr Ile Ser Ser Ile Met Thr Leu Tyr Glu Gly Asp Val Ile
 165 170 175
Leu Thr Gly Thr Pro Glu Gly Val Gly Pro Val Lys Ile Gly Gln Lys
 180 185 190
Ile Thr Ala Gly Ile Thr Gly Leu Ser Glu Val Gln Phe Asp Val Glu
 195 200 205
Arg Arg Val Lys Pro Leu Ser
 210 215

```

(2) INFORMATION FOR SEQ ID NO:2080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1323
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2080:

```

gtttctaatt gctttcgacg acaatcgatc gtagagaagt ctacctcgta gacatctctc 60
tcacaaatcc aattcaatta coattgtttg ttattatctg atgtcggaata tgcaattctc 120
tcgtgtgttt aatccctttg ttatcttctt ctgtctcgcc gtggttgac caattatctc 180
ggctgatgtc gctatcttga gaacggacta ttacccaaaa acatgtcctg atttcaccaa 240
aattgtgcgt gaagcgttta caaccaaaaa agtccaaaaa ccaacaactg cggcggggac 300
ctctcgcttc tttttccatg attgtttcct tgaagggttg gatgcatctg tcttgatcgc 360
gaccaaactg ttcaacaaag cggaacgvgA tgatgatctc aatgattccc tcccgggaga 420
tgctttttgc atcgtcaccg gcatcaagac agctctcgag ttgtcttgtc ctggtgtgat 480
atctcgcgcg gatattctag cgcaggctac acgtgacctt gtcaacaatg taggaggacc 540
ttactttgac gtaaagcttg gtcgtaaaag cggattcgaa tccaagctc ataaagtacg 600
aggaatgtc ccaatggcaa accagactgt tcttgacatc cacgggatat tcaagaaaaa 660
cggttttagt ctctcgagag ttgtagcatt aagcggggct cacacacttg gattctctca 720
ctgcaaaagg tttttcgaga ggctctacgg atcccgctgt gataaagaaa tcaaccgcgcg 780
attcgcagcc gctctcaaa gctcttgcaa aaaccacacc gtggatgata caatcgccgc 840
gtttaacgac gtgatgatc caggaaagtt cgacacacat tacttcaaga acctaaagcg 900
aggcgtaggg ctttttagcgt ctgaccacat ccttattaaa gacaacagca ccaagccgtt 960
tgtgtgatca tacgcaacta acgagacgac attctttgag gatitcgctc gtgcgatgga 1020
gaaacttgcc acggtcggcg tcaaggcgca taaagatgga gaagtgaagc taaggtgcga 1080
ccaacttcaa aatctcaacg tttaaagaag aaaagaaaaa acaaaaccat ataaatataa 1140
tattatttct gttttatttg cggaggagtt gaggagaaga aaggttttgt ttgtatatat 1200
gtttaataac tactattat aagcaagatc ttgtaacaac tcaagttggg atgttttaatt 1260
tttccatgaa aattcaaac gttgtattga aagtatatag ataaaaaac atattatata 1320
tcg

```

(2) INFORMATION FOR SEQ ID NO:2081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..334  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571789  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2081:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Asn | Met | Gln | Phe | Ser | Arg | Gly | Phe | Asn | Pro | Phe | Val | Ile | Phe |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Phe | Cys | Leu | Ala | Val | Val | Ala | Pro | Ile | Ile | Ser | Ala | Asp | Val | Ala | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Arg | Thr | Asp | Tyr | Tyr | Gln | Lys | Thr | Cys | Pro | Asp | Phe | His | Lys | Ile |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Val | Arg | Glu | Ala | Val | Thr | Thr | Lys | Gln | Val | Gln | Gln | Pro | Thr | Thr | Ala |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Ala | Gly | Thr | Leu | Arg | Leu | Phe | Phe | His | Asp | Cys | Phe | Leu | Glu | Gly | Cys |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     | 80  |
| Asp | Ala | Ser | Val | Leu | Ile | Ala | Thr | Asn | Ser | Phe | Asn | Lys | Ala | Glu | Xaa |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asp | Asp | Asp | Leu | Asn | Asp | Ser | Leu | Pro | Gly | Asp | Ala | Phe | Asp | Ile | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Arg | Ile | Lys | Thr | Ala | Leu | Glu | Leu | Ser | Cys | Pro | Gly | Val | Val | Ser |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Cys | Ala | Asp | Ile | Leu | Ala | Gln | Ala | Thr | Arg | Asp | Leu | Val | Thr | Met | Val |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |
| Gly | Gly | Pro | Tyr | Phe | Asp | Val | Lys | Leu | Gly | Arg | Lys | Asp | Gly | Phe | Glu |
|     |     |     | 145 |     |     |     |     | 150 |     |     |     | 155 |     |     | 160 |
| Ser | Lys | Ala | His | Lys | Val | Arg | Gly | Asn | Val | Pro | Met | Ala | Asn | Gln | Thr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Val | Pro | Asp | Ile | His | Gly | Ile | Phe | Lys | Lys | Asn | Gly | Phe | Ser | Leu | Arg |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Met | Val | Ala | Leu | Ser | Gly | Ala | His | Thr | Ile | Gly | Phe | Ser | His | Cys |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     | 205 |     |     |     |
| Lys | Glu | Phe | Ser | Asp | Arg | Leu | Tyr | Gly | Ser | Arg | Ala | Asp | Lys | Glu | Ile |
|     |     |     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |
| Asn | Pro | Arg | Phe | Ala | Ala | Ala | Leu | Lys | Asp | Leu | Cys | Lys | Asn | His | Thr |
|     |     |     | 225 |     |     |     |     | 230 |     |     |     | 235 |     |     | 240 |
| Val | Asp | Asp | Thr | Ile | Ala | Ala | Phe | Asn | Asp | Val | Met | Thr | Pro | Gly | Lys |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Phe | Asp | Asn | Met | Tyr | Phe | Lys | Asn | Leu | Lys | Arg | Gly | Leu | Gly | Leu | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     | 270 |     |     |     |
| Ala | Ser | Asp | His | Ile | Leu | Ile | Lys | Asp | Asn | Ser | Thr | Lys | Pro | Phe | Val |
|     |     |     | 275 |     |     |     |     | 280 |     |     |     | 285 |     |     |     |
| Asp | Leu | Tyr | Ala | Thr | Asn | Glu | Thr | Ala | Phe | Phe | Glu | Asp | Phe | Ala | Arg |
|     |     |     | 290 |     |     |     |     | 295 |     |     |     | 300 |     |     |     |
| Ala | Met | Glu | Lys | Leu | Gly | Thr | Val | Gly | Val | Lys | Gly | Asp | Lys | Asp | Gly |
|     |     |     | 305 |     |     |     |     | 310 |     |     |     | 315 |     |     | 320 |
| Glu | Val | Arg | Arg | Arg | Cys | Asp | His | Phe | Asn | Asn | Leu | Asn | Val |     |     |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:2082:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 331 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..331  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2082:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Phe | Ser | Arg | Gly | Phe | Asn | Pro | Phe | Val | Ile | Phe | Phe | Cys | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Val | Val | Ala | Pro | Ile | Ile | Ser | Ala | Asp | Val | Ala | Ile | Leu | Arg | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Tyr | Tyr | Gln | Lys | Thr | Cys | Pro | Asp | Phe | His | Lys | Ile | Val | Arg | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Val | Thr | Thr | Lys | Gln | Val | Gln | Gln | Pro | Thr | Thr | Ala | Ala | Gly | Thr |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Leu | Arg | Leu | Phe | Phe | His | Asp | Cys | Phe | Leu | Glu | Gly | Cys | Asp | Ala | Ser |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Leu | Ile | Ala | Thr | Asn | Ser | Phe | Asn | Lys | Ala | Glu | Xaa | Asp | Asp | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Asn | Asp | Ser | Leu | Pro | Gly | Asp | Ala | Phe | Asp | Ile | Val | Thr | Arg | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Thr | Ala | Leu | Glu | Leu | Ser | Cys | Pro | Gly | Val | Val | Ser | Cys | Ala | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Leu | Ala | Gln | Ala | Thr | Arg | Asp | Leu | Val | Thr | Met | Val | Gly | Gly | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Tyr | Phe | Asp | Val | Lys | Leu | Gly | Arg | Lys | Asp | Gly | Phe | Glu | Ser | Lys | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| His | Lys | Val | Arg | Gly | Asn | Val | Pro | Met | Ala | Asn | Gln | Thr | Val | Pro | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | His | Gly | Ile | Phe | Lys | Lys | Asn | Gly | Phe | Ser | Leu | Arg | Glu | Met | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Leu | Ser | Gly | Ala | His | Thr | Ile | Gly | Phe | Ser | His | Cys | Lys | Glu | Phe |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Asp | Arg | Leu | Tyr | Gly | Ser | Arg | Ala | Asp | Lys | Glu | Ile | Asn | Pro | Arg |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Phe | Ala | Ala | Ala | Leu | Lys | Asp | Leu | Cys | Lys | Asn | His | Thr | Val | Asp | Asp |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Thr | Ile | Ala | Ala | Phe | Asn | Asp | Val | Met | Thr | Pro | Gly | Lys | Phe | Asp | Asn |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Met | Tyr | Phe | Lys | Asn | Leu | Lys | Arg | Gly | Leu | Gly | Leu | Leu | Ala | Ser | Asp |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| His | Ile | Leu | Ile | Lys | Asp | Asn | Ser | Thr | Lys | Pro | Phe | Val | Asp | Leu | Tyr |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ala | Thr | Asn | Glu | Thr | Ala | Phe | Phe | Glu | Asp | Phe | Ala | Arg | Ala | Met | Glu |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Lys | Leu | Gly | Thr | Val | Gly | Val | Lys | Gly | Asp | Lys | Asp | Gly | Glu | Val | Arg |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Arg | Arg | Cys | Asp | His | Phe | Asn | Asn | Leu | Asn | Val |     |     |     |     |     |
|     |     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2083:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1571791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2083:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Gly | Gly | Pro | Tyr | Phe | Asp | Val | Lys | Leu | Gly | Arg | Lys | Asp | Gly |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Phe | Glu | Ser | Lys | Ala | His | Lys | Val | Arg | Gly | Asn | Val | Pro | Met | Ala | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Thr | Val | Pro | Asp | Ile | His | Gly | Ile | Phe | Lys | Lys | Asn | Gly | Phe | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Arg | Glu | Met | Val | Ala | Leu | Ser | Gly | Ala | His | Thr | Ile | Gly | Phe | Ser |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His | Cys | Lys | Glu | Phe | Ser | Asp | Arg | Leu | Tyr | Gly | Ser | Arg | Ala | Asp | Lys |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Ile | Asn | Pro | Arg | Phe | Ala | Ala | Ala | Leu | Lys | Asp | Leu | Cys | Lys | Asn |
|     |     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |
| His | Thr | Val | Asp | Asp | Thr | Ile | Ala | Ala | Phe | Asn | Asp | Val | Met | Thr | Pro |
|     |     |     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |
| Gly | Lys | Phe | Asp | Asn | Met | Tyr | Phe | Lys | Asn | Leu | Lys | Arg | Gly | Leu | Gly |
|     |     |     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |
| Leu | Leu | Ala | Ser | Asp | His | Ile | Leu | Ile | Lys | Asp | Asn | Ser | Thr | Lys | Pro |
|     |     |     |     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |
| Phe | Val | Asp | Leu | Tyr | Ala | Thr | Asn | Glu | Thr | Ala | Phe | Phe | Glu | Asp | Phe |
|     |     |     |     |     |     | 145 |     |     |     | 150 |     |     |     |     | 155 |
| Ala | Arg | Ala | Met | Glu | Lys | Leu | Gly | Thr | Val | Gly | Val | Lys | Gly | Asp | Lys |
|     |     |     |     |     |     | 160 |     |     |     | 165 |     |     |     |     | 170 |
| Asp | Gly | Glu | Val | Arg | Arg | Arg | Cys | Asp | His | Phe | Asn | Asn | Leu | Asn | Val |
|     |     |     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |

(2) INFORMATION FOR SEQ ID NO:2084:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1125 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1125

(D) OTHER INFORMATION: / Ceres Seq. ID 1571792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2084:

|            |            |             |            |            |            |      |
|------------|------------|-------------|------------|------------|------------|------|
| acattgcaac | actttctaca | aaaacaagat  | gaagattgca | aagttttctg | ttctactctt | 60   |
| gcttttattt | attttccccc | tgccattagc  | gcagCtgaaa | tttaagtttt | acagtgaatc | 120  |
| gtgcccta   | gcagagacta | tcgtagaaaa  | cctggttcgc | cagcagtttg | ctcgtgaccc | 180  |
| ttcaatcacg | gcgcctttga | ctcgtatgca  | ttttcacgac | tgttttgctc | agggctgcga | 240  |
| cgcttctctc | ctcatagacc | caacgacgtc  | tcaactatcg | gaaaaaaacg | ccggcccaaa | 300  |
| ctttagcgtg | agaggggttc | agctgatgca  | cgagatcaag | acggcactcg | aagctcaatg | 360  |
| tcctctacg  | gtctcgtgtg | cagatatagt  | cacgctcgcc | acacgtgacg | ccgtgtttct | 420  |
| aggtggagga | ccaagctacg | tggtcccccac | cggaacgtcg | gatggctttg | tgtcgaaatc | 480  |
| tgaagacgcc | aatgagatcc | tcctccacc   | attcatatcc | gtcgaaggca | tgtaagtgt  | 540  |
| tttcggcaac | aaaaggaatg | atgtttttga  | ttcgtatgct | cttttggggg | cgacacacgt | 600  |
| tgggatcgcg | tcttgttgga | attttgtgga  | ccgggtcacg | aactttcaag | gaaccggagt | 660  |
| gcccgaccca | tcctatggac | ccactttggc  | tgccagggtg | aggaacacat | gtgcggttcc | 720  |
| agggcgcttc | gcggcactcg | accagtcgat  | gccagtaaac | ccggtctcat | tcgacaactt | 780  |
| gttcttttgt | cagatcacag | agaggaaaag  | aattttgctt | attgaccaac | tgatcgcaag | 840  |
| cgaccocggc | acttctgggt | ttgtacttca  | gtatgcgtcc | aacaacgaac | tattcaaacg | 900  |
| tcagttcgca | atcgcaatgg | tgaagatggg  | agccgttgac | gtgcttaccg | gttcagctcg | 960  |
| tgagatcagg | acgaattgta | gagcattcaa  | ctaaagcttt | ataacaagtt | tctatatctg | 1020 |
| attattgatt | gtttttccct | taatttccgc  | ttctgatgat | gaattgtgaa | tggtgatgtg | 1080 |
| ttgcctatat | atgtatgtac | gtatatcttt  | aaaataaggt | ttggc      |            |      |

(2) INFORMATION FOR SEQ ID NO:2085:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..330

(D) OTHER INFORMATION: / Ceres Seq. ID 1571793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2085:

His Cys Asn Thr Phe Tyr Lys Asn Lys Met Lys Ile Ala Lys Phe Ser  
1 5 10 15  
Val Leu Leu Leu Leu Phe Ile Phe Pro Val Ala Leu Ala Gln Leu  
20 25 30  
Lys Phe Lys Phe Tyr Ser Glu Ser Cys Pro Asn Ala Glu Thr Ile Val  
35 40 45  
Glu Asn Leu Val Arg Gln Gln Phe Ala Arg Asp Pro Ser Ile Thr Ala  
50 55 60  
Ala Leu Thr Arg Met His Phe His Asp Cys Phe Val Gln Gly Cys Asp  
65 70 75 80  
Ala Ser Leu Leu Ile Asp Pro Thr Thr Ser Gln Leu Ser Glu Lys Asn  
85 90 95  
Ala Gly Pro Asn Phe Ser Val Arg Gly Phe Glu Leu Ile Asp Glu Ile  
100 105 110  
Lys Thr Ala Leu Glu Ala Gln Cys Pro Ser Thr Val Ser Cys Ser Asp  
115 120 125  
Ile Val Thr Leu Ala Thr Arg Asp Ala Val Phe Leu Gly Gly Gly Pro  
130 135 140  
Ser Tyr Val Val Pro Thr Gly Arg Arg Asp Gly Phe Val Ser Asn Pro  
145 150 155 160  
Glu Asp Ala Asn Glu Ile Leu Pro Pro Phe Ile Ser Val Glu Gly  
165 170 175  
Met Leu Ser Phe Phe Gly Asn Lys Gly Met Asn Val Phe Asp Ser Val  
180 185 190  
Ala Leu Leu Gly Ala His Thr Val Gly Ile Ala Ser Cys Gly Asn Phe  
195 200 205  
Val Asp Arg Val Thr Asn Phe Gln Gly Thr Gly Leu Pro Asp Pro Ser  
210 215 220  
Met Asp Pro Thr Leu Ala Gly Arg Leu Arg Asn Thr Cys Ala Val Pro  
225 230 235 240  
Gly Gly Phe Ala Ala Leu Asp Gln Ser Met Pro Val Thr Pro Val Ser  
245 250 255  
Phe Asp Asn Leu Phe Phe Gly Gln Ile Arg Glu Arg Lys Gly Ile Leu  
260 265 270  
Leu Ile Asp Gln Leu Ile Ala Ser Asp Pro Ala Thr Ser Gly Val Val  
275 280 285  
Leu Gln Tyr Ala Ser Asn Asn Glu Leu Phe Lys Arg Gln Phe Ala Ile  
290 295 300  
Ala Met Val Lys Met Gly Ala Val Asp Val Leu Thr Gly Ser Ala Gly  
305 310 315 320  
Glu Ile Arg Thr Asn Cys Arg Ala Phe Asn  
325 330

(2) INFORMATION FOR SEQ ID NO:2086:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..321

(D) OTHER INFORMATION: / Ceres Seq. ID 1571794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2086:

Met Lys Ile Ala Lys Phe Ser Val Leu Leu Leu Leu Phe Ile Phe  
1 5 10 15  
Pro Val Ala Leu Ala Gln Leu Lys Phe Lys Phe Tyr Ser Glu Ser Cys  
20 25 30  
Pro Asn Ala Glu Thr Ile Val Glu Asn Leu Val Arg Gln Gln Phe Ala

|                             |                         |                     |
|-----------------------------|-------------------------|---------------------|
| 35                          | 40                      | 45                  |
| Arg Asp Pro Ser Ile Thr     | Ala Leu Thr Arg         | Met His Phe His Asp |
| 50                          | 55                      | 60                  |
| Cys Phe Val Gln Gly Cys Asp | Ala Ser Leu Leu Ile     | Asp Pro Thr Thr     |
| 65                          | 70                      | 75                  |
| Ser Gln Leu Ser Glu Lys Asn | Ala Gly Pro Asn         | Phe Ser Val Arg Gly |
| 85                          | 90                      | 95                  |
| Phe Glu Leu Ile Asp Glu Ile | Lys Thr Ala Leu Glu     | Ala Gln Cys Pro     |
| 100                         | 105                     | 110                 |
| Ser Thr Val Ser Cys Ser Asp | Ile Val Thr Leu Ala Thr | Arg Asp Ala         |
| 115                         | 120                     | 125                 |
| Val Phe Leu Gly Gly Gly Pro | Ser Tyr Val Val Pro     | Thr Gly Arg Arg     |
| 130                         | 135                     | 140                 |
| Asp Gly Phe Val Ser Asn Pro | Glu Asp Ala Asn Glu     | Ile Leu Pro Pro     |
| 145                         | 150                     | 155                 |
| Pro Phe Ile Ser Val Glu Gly | Met Leu Ser Phe         | Phe Gly Asn Lys Gly |
| 165                         | 170                     | 175                 |
| Met Asn Val Phe Asp Ser Val | Ala Leu Leu Gly         | Ala His Thr Val Gly |
| 180                         | 185                     | 190                 |
| Ile Ala Ser Cys Gly Asn Phe | Val Asp Arg Val Thr     | Asn Phe Gln Gly     |
| 195                         | 200                     | 205                 |
| Thr Gly Leu Pro Asp Pro Ser | Met Asp Pro Thr Leu     | Ala Gly Arg Leu     |
| 210                         | 215                     | 220                 |
| Arg Asn Thr Cys Ala Val Pro | Gly Gly Phe Ala Ala Leu | Asp Gln Ser         |
| 225                         | 230                     | 235                 |
| Met Pro Val Thr Pro Val Ser | Phe Asp Asn Leu Phe     | Phe Gly Gln Ile     |
| 245                         | 250                     | 255                 |
| Arg Glu Arg Lys Gly Ile Leu | Leu Ile Asp Gln Leu     | Ile Ala Ser Asp     |
| 260                         | 265                     | 270                 |
| Pro Ala Thr Ser Gly Val Val | Leu Gln Tyr Ala Ser     | Asn Asn Glu Leu     |
| 275                         | 280                     | 285                 |
| Phe Lys Arg Gln Phe Ala Ile | Ala Met Val Lys Met     | Gly Ala Val Asp     |
| 290                         | 295                     | 300                 |
| Val Leu Thr Gly Ser Ala Gly | Glu Ile Arg Thr Asn     | Cys Arg Ala Phe     |
| 305                         | 310                     | 315                 |
| Asn                         |                         | 320                 |

(2) INFORMATION FOR SEQ ID NO:2087:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..262

(D) OTHER INFORMATION: / Ceres Seq. ID 1571795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2087:

|                                                 |                         |
|-------------------------------------------------|-------------------------|
| Met His Phe His Asp Cys Phe Val Gln Gly Cys Asp | Ala Ser Leu Leu         |
| 1                                               | 15                      |
| Ile Asp Pro Thr Ser Gln Leu Ser Glu Lys Asn     | Ala Gly Pro Asn         |
| 20                                              | 30                      |
| Phe Ser Val Arg Gly Phe Glu Leu Ile Asp Glu Ile | Lys Thr Ala Leu         |
| 35                                              | 45                      |
| Glu Ala Gln Cys Pro Ser Thr Val Ser Cys Ser     | Asp Ile Val Thr Leu     |
| 50                                              | 60                      |
| Ala Thr Arg Asp Ala Val Phe Leu Gly Gly Gly     | Pro Ser Tyr Val Val     |
| 65                                              | 80                      |
| Pro Thr Gly Arg Arg Asp Gly Phe Val Ser         | Asn Pro Glu Asp Ala Asn |
| 85                                              | 95                      |



Glu Ile Leu Pro Pro Pro Phe Ile Ser Val Glu Gly Met Leu Ser Phe  
100 105 110  
Phe Gly Asn Lys Gly Met Asn Val Phe Asp Ser Val Ala Leu Leu Gly  
115 120 125  
Ala His Thr Val Gly Ile Ala Ser Cys Gly Asn Phe Val Asp Arg Val  
130 135 140  
Thr Asn Phe Gln Gly Thr Gly Leu Pro Asp Pro Ser Met Asp Pro Thr  
145 150 155 160  
Leu Ala Gly Arg Leu Arg Asn Thr Cys Ala Val Pro Gly Gly Phe Ala  
165 170 175  
Ala Leu Asp Gln Ser Met Pro Val Thr Pro Val Ser Phe Asp Asn Leu  
180 185 190  
Phe Phe Gly Gln Ile Arg Glu Arg Lys Gly Ile Leu Leu Ile Asp Gln  
195 200 205  
Leu Ile Ala Ser Asp Pro Ala Thr Ser Gly Val Val Leu Gln Tyr Ala  
210 215 220  
Ser Asn Asn Glu Leu Phe Lys Arg Gln Phe Ala Ile Ala Met Val Lys  
225 230 235 240  
Met Gly Ala Val Asp Val Leu Thr Gly Ser Ala Gly Glu Ile Arg Thr  
245 250 255  
Asn Cys Arg Ala Phe Asn  
260

(2) INFORMATION FOR SEQ ID NO:2088:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1173
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2088:

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| gttgctgtat  | tcttctggat  | aagagcttgc  | tgatgggttg | aaacctctga  | gtgaagaaga  | 60   |
| agcgccatgg  | ctggggattac | cagcagcacc  | gttggattca | acgcgcctct  | caccggaata  | 120  |
| acocaaacag  | tatcatcaca  | ttcactcttc  | tctgttgatt | ccaaactctg  | tagtcttcgt  | 180  |
| ctctccaaa   | ccgaactgtc  | tttactaat   | ctcactcctt | ctcctgcctg  | tgctttcgcc  | 240  |
| gtcacttgcc  | gcttcggcgg  | tggtgggtga  | ggttatcgat | tctctggaga  | caatagaaga  | 300  |
| ggtagggcga  | aagaagctga  | aattgatgaa  | gctcttgata | tctcctcaat  | taggtcagct  | 360  |
| actgttaagg  | ttatcgatgg  | gcaacaaaaa  | atgcttggtt | tagtgtctaa  | agacgaagcc  | 420  |
| gttcgaatgg  | ctgatgatgc  | tgaacttgat  | ctggtKatac | tatcgccctga | tgccagatcct | 480  |
| ccggttggtta | aaattgatga  | ctacagataa  | tacagatacg | acacgcacaaa | gaggaacaaa  | 540  |
| gatcagcaaa  | agaaaaaac   | tcgcattggat | ttaaaggagc | ttaaaatggg  | ttataatatt  | 600  |
| gatcagcatg  | attattccgt  | tcgtctaaagg | gctgcacaaa | agttcttgca  | agatgggtgac | 660  |
| aaggttaagg  | tgattgtgag  | catgaagaag  | cgagaaaaag | agttcagaaa  | tatcgctatt  | 720  |
| gaactctctca | gacgtttttc  | aaccgaataa  | ggggagcttg | caactgaaga  | gagcaaaaaac | 780  |
| ttcagggaga  | gaaatatggt  | cattatcttg  | gtcccaaaaa | agaaaatgat  | tcggaacaca  | 840  |
| caagaaccac  | ccacaagaaa  | gaagaaaaaa  | acagcggaaa | acgaagcttc  | agcttcagct  | 900  |
| cgacaaaataa | cagctgagcc  | tgagccctgag | ctggaacctg | agcctgagcc  | tgagcctgag  | 960  |
| cctgagcctg  | agcctgagcc  | agagcctcta  | cagatcgatt | cttgagtgtta | aaatctttgtg | 1020 |
| gtagagtttt  | cagagctaaa  | gtaaaagttt  | gtatatattc | ttttctacca  | tgctcaaga   | 1080 |
| gagccaaagag | ctgtataaca  | aatagagtta  | gtcctatttg | aatgatgttc  | ttcgtttgtga | 1140 |
| gatcttttct  | ctaactctatt | ttttgttta   | act        |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..312

(D) OTHER INFORMATION: / Ceres Seq. ID 1571797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2089:

```
Met Ala Gly Ile Thr Ser Ser Thr Val Gly Phe Asn Ala Val Phe Thr
1 5 10 15
Gly Ile Thr Lys Thr Val Ser Ser His Ser Leu Phe Ser Val Asp Ser
20 25
Lys Leu Cys Ser Leu Arg Leu Ser Lys Thr Glu Leu Ser Phe Thr Asn
35 40 45
Leu Thr Pro Ser Pro Arg Arg Ala Phe Ala Val Thr Cys Arg Phe Gly
50 55 60
Gly Gly Gly Gly Tyr Arg Phe Ser Gly Asp Asn Arg Arg Gly Arg
65 70 75 80
Pro Lys Glu Ala Glu Ile Asp Glu Ala Leu Asp Ile Ser Ser Ile Arg
85 90 95
Ser Ala Thr Val Arg Leu Ile Asp Gly Gln Gln Asn Met Leu Gly Leu
100 105 110
Val Ser Lys Asp Glu Ala Val Arg Met Ala Asp Asp Ala Glu Leu Asp
115 120 125
Leu Xaa Ile Leu Ser Pro Asp Ala Asp Pro Pro Val Val Lys Met Met
130 135 140
Asp Tyr Ser Lys Tyr Arg Tyr Glu Gln Gln Lys Arg Lys Lys Asp Gln
145 150 155 160
Gln Lys Lys Thr Thr Arg Met Asp Leu Lys Glu Leu Lys Met Gly Tyr
165 170 175
Asn Ile Asp Gln His Asp Tyr Ser Val Arg Leu Arg Ala Ala Gln Lys
180 185 190
Phe Leu Gln Asp Gly Asp Lys Val Lys Val Ile Val Ser Met Lys Gly
195 200 205
Arg Glu Asn Glu Phe Arg Asn Ile Ala Ile Glu Leu Leu Arg Arg Phe
210 215 220
Gln Thr Glu Ile Gly Glu Leu Ala Thr Glu Glu Ser Lys Asn Phe Arg
225 230 235 240
Asp Arg Asn Met Phe Ile Ile Leu Val Pro Asn Lys Glu Met Ile Arg
245 250 255
Lys Pro Gln Glu Pro Pro Thr Arg Lys Lys Lys Thr Ala Glu Asn
260 265 270
Glu Ala Ser Ala Ser Ala Ala Glu Ile Thr Ala Glu Pro Glu Pro Glu
275 280 285
Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu
290 295 300
Pro Glu Pro Leu Gln Ile Asp Ser
305 310
```

(2) INFORMATION FOR SEQ ID NO:2090:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1571798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2090:

```
Met Leu Gly Leu Val Ser Lys Asp Glu Ala Val Arg Met Ala Asp Asp
1 5 10 15
Ala Glu Leu Asp Leu Xaa Ile Leu Ser Pro Asp Ala Asp Pro Pro Val
20 25 30
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Lys | Met | Met | Asp | Tyr | Ser | Lys | Tyr | Arg | Tyr | Glu | Gln | Gln | Lys | Arg |  |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Lys | Lys | Asp | Gln | Gln | Lys | Lys | Thr | Thr | Arg | Met | Asp | Leu | Lys | Glu | Leu |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Lys | Met | Gly | Tyr | Asn | Ile | Asp | Gln | His | Asp | Tyr | Ser | Val | Arg | Leu | Arg |  |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Ala | Ala | Gln | Lys | Phe | Leu | Gln | Asp | Gly | Asp | Lys | Val | Lys | Val | Ile | Val |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ser | Met | Lys | Gly | Arg | Glu | Asn | Glu | Phe | Arg | Asn | Ile | Ala | Ile | Glu | Leu |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Leu | Arg | Arg | Phe | Gln | Thr | Glu | Ile | Gly | Glu | Leu | Ala | Thr | Glu | Glu | Ser |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Lys | Asn | Phe | Arg | Asp | Arg | Asn | Met | Phe | Ile | Ile | Leu | Val | Pro | Asn | Lys |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Glu | Met | Ile | Arg | Lys | Pro | Gln | Glu | Pro | Pro | Thr | Arg | Lys | Lys | Lys | Lys |  |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Thr | Ala | Glu | Asn | Glu | Ala | Ser | Ala | Ser | Ala | Ala | Glu | Ile | Thr | Ala | Glu |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Pro | Glu | Pro | Glu | Pro | Glu | Pro | Glu | Pro | Glu | Pro | Glu | Pro | Glu | Pro | Glu |  |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |
| Pro | Glu | Pro | Glu | Pro | Glu | Pro | Leu | Gln | Ile | Asp | Ser |     |     |     |     |  |
|     |     |     | 195 |     |     | 200 |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..192
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2091:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Asp | Asp | Ala | Glu | Leu | Asp | Leu | Xaa | Ile | Leu | Ser | Pro | Asp | Ala |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asp | Pro | Pro | Val | Val | Lys | Met | Met | Asp | Tyr | Ser | Lys | Tyr | Arg | Tyr | Glu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gln | Gln | Lys | Arg | Lys | Lys | Asp | Gln | Gln | Lys | Lys | Thr | Thr | Arg | Met | Asp |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Leu | Lys | Glu | Leu | Lys | Met | Gly | Tyr | Asn | Ile | Asp | Gln | His | Asp | Tyr | Ser |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Val | Arg | Leu | Arg | Ala | Ala | Gln | Lys | Phe | Leu | Gln | Asp | Gly | Asp | Lys | Val |  |
|     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Lys | Val | Ile | Val | Ser | Met | Lys | Gly | Arg | Glu | Asn | Glu | Phe | Arg | Asn | Ile |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Ala | Ile | Glu | Leu | Leu | Arg | Arg | Phe | Gln | Thr | Glu | Ile | Gly | Glu | Leu | Ala |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Thr | Glu | Glu | Ser | Lys | Asn | Phe | Arg | Asp | Arg | Asn | Met | Phe | Ile | Ile | Leu |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Val | Pro | Asn | Lys | Glu | Met | Ile | Arg | Lys | Pro | Gln | Glu | Pro | Pro | Thr | Arg |  |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |  |
| Lys | Lys | Lys | Lys | Thr | Ala | Glu | Asn | Glu | Ala | Ser | Ala | Ser | Ala | Ala | Glu |  |
|     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Ile | Thr | Ala | Glu | Pro | Glu | Pro | Glu | Pro | Glu | Pro | Glu | Pro | Glu | Pro | Glu |  |
|     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |     |  |
| Pro | Glu | Pro | Glu | Pro | Glu | Pro | Glu | Pro | Leu | Gln | Ile | Asp | Ser |     |     |  |
|     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2092:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1185  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571800  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2092:  
gacgatgacg atgatgatga tgatgatgaa gttgatggag atgataatga gaaggagaaa 60  
attgggttat acgagctcaa gaagggaat ctaactgtca aattcacaaa ttgggggtgct 120  
tcaatcatat ctctccattt occagacaaa aatggtaaaa tggacgatat tgttcttgge 180  
tatgatagcg tcaaaaacct caagaccgac aaggtttatt tcggagcaac cgttggccga 240  
gtagcaaatg gaattaggaaa gggcaaatc aagttgaatg gtaaaagata caagacaagt 300  
gtcaacgaNt ggaaaaaaca cactccatgg tggcaagaaa ggggttgggg atgtgtgtgtg 360  
ggcagttgca aaacaccagt acgatggcaa gaaaccacac attgtcttca ctacacacaag 420  
tcctgacggc gatcaagggt ttccgggaga actcaagtgc acggtgacat ataaacttgt 480  
caaagacaat gaattgagtg tgggtgatga ggcaaaagCct aaggataaag caactccggt 540  
gaacttagct catcatagtt attggaatct tgggtggtcat aattccggag atattttgtc 600  
tgaagaaaatt caaatccctcg gctcgggtta taccocccgtc gacggtgagc tcattccacc 660  
cgggaaaacat aatccggtga aaggaacagc atacgatttt ctccaactcc gtccattaa 720  
agataaatat aaggatctta aaacaggata tgatataaat tattgcttag atggtaaggc 780  
aaaaaagatg agaaaaatag ttgaactcgt agataagaaa tcaggggagg aaatggagtt 840  
atcccgaaac caagcgggtt tgcaatttca taccggaggg atgttaaaag atgtcaaaag 900  
gaagaattggg gcagtttacc aagctttcgg gggattatgt ttagaacac aaagttaatc 960  
agacgcatgt aacctccca aatttccttc acagattgtc gagccaggga aaaaatacaa 1020  
cacacattgt ctcttcaagt tttctattgt ttcataagat gttttagatg ttgttaaatg 1080  
aacacccttg gaaccatgtc caatgttcat gaacaagaaa ctaaatacat tgtaatat 1140  
tgtaacaagt cttaaatat caaattatat aaacctaacg tgaac  
(2) INFORMATION FOR CERE Seq ID NO:2093:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 141 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..141  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571801  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2093:  
Asp Asp Asp Asp Asp Asp Asp Asp Asp Glu Val Asp Gly Asp Asp Asn  
1 5 10 15  
Glu Lys Glu Lys Ile Gly Leu Tyr Glu Leu Lys Lys Gly Asn Leu Thr  
20 25 30  
Val Lys Phe Thr Asn Trp Gly Ala Ser Ile Ile Ser Leu His Phe Pro  
35 40 45  
Asp Lys Asn Gly Lys Met Asp Asp Ile Val Leu Gly Tyr Asp Ser Val  
50 55 60  
Lys Thr Tyr Lys Thr Asp Lys Val Tyr Phe Gly Ala Thr Val Gly Arg  
65 70 75 80  
Val Ala Asn Arg Ile Gly Lys Gly Lys Phe Lys Leu Asn Gly Lys Glu  
85 90 95  
Tyr Lys Thr Ser Val Asn Xaa Trp Lys Lys His Thr Pro Trp Trp Gln  
100 105 110  
Glu Arg Val Trp Gly Cys Cys Val Gly Ser Cys Lys Thr Pro Val Arg  
115 120 125  
Trp Gln Glu Thr Thr His Cys Leu His Ser His Lys Ser  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..259
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2094:

Met Val Lys Ser Thr Arg Gln Val Ser Thr Xaa Gly Lys Asn Thr Leu  
1 5 10 15  
His Gly Gly Lys Lys Gly Phe Gly Asp Val Val Trp Ala Val Ala Lys  
20 25 30  
His Gln Tyr Asp Gly Lys Lys Pro His Ile Val Phe Thr His Thr Ser  
35 40 45  
Pro Asp Gly Asp Gln Gly Phe Pro Gly Glu Leu Ser Val Thr Val Thr  
50 55 60  
Tyr Lys Leu Val Lys Asp Asn Glu Leu Ser Val Val Met Glu Ala Lys  
65 70 75 80  
Pro Lys Asp Lys Ala Thr Pro Val Asn Leu Ala His His Ser Tyr Trp  
85 90 95  
Asn Leu Gly Gly His Asn Ser Gly Asp Ile Leu Ser Glu Glu Ile Gln  
100 105 110  
Ile Leu Gly Ser Gly Tyr Thr Pro Val Asp Gly Glu Leu Ile Pro Thr  
115 120 125  
Gly Lys Ile Asn Pro Val Lys Gly Thr Ala Tyr Asp Phe Leu Gln Leu  
130 135 140  
Arg Pro Ile Lys Asp Asn Met Lys Asp Leu Lys Thr Gly Tyr Asp Ile  
145 150 155 160  
Asn Tyr Cys Leu Asp Gly Lys Ala Lys Lys Met Arg Lys Ile Val Glu  
165 170 175  
Leu Val Asp Lys Lys Ser Gly Arg Lys Met Glu Leu Ser Gly Asn Gln  
180 185 190  
Ala Gly Leu Gln Phe Tyr Thr Gly Gly Met Leu Lys Asp Val Lys Gly  
195 200 205  
Lys Asn Gly Ala Val Tyr Gln Ala Phe Gly Gly Leu Cys Leu Glu Thr  
210 215 220  
Gln Ser Tyr Pro Asp Ala Leu Asn His Pro Lys Phe Pro Ser Gln Ile  
225 230 235 240  
Val Glu Pro Gly Lys Lys Tyr Lys His Thr Met Leu Phe Lys Phe Ser  
245 250 255  
Ile Val Ser

(2) INFORMATION FOR SEQ ID NO:2095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2095:

Met Glu Ala Lys Pro Lys Asp Lys Ala Thr Pro Val Asn Leu Ala His  
1 5 10 15  
His Ser Tyr Trp Asn Leu Gly Gly His Asn Ser Gly Asp Ile Leu Ser

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| 20  |     |     |     |     |     |     |     |     |     | 25  |     |     |     |     | 30  |  |  |  |  |
| Glu | Glu | Ile | Gln | Ile | Leu | Gly | Ser | Gly | Tyr | Thr | Pro | Val | Asp | Gly | Glu |  |  |  |  |
| 35  |     |     |     |     |     |     | 40  |     |     | 45  |     |     |     |     |     |  |  |  |  |
| Leu | Ile | Pro | Thr | Gly | Lys | Ile | Asn | Pro | Val | Lys | Gly | Thr | Ala | Tyr | Asp |  |  |  |  |
| 50  |     |     |     |     |     |     | 55  |     |     | 60  |     |     |     |     |     |  |  |  |  |
| Phe | Leu | Gln | Leu | Arg | Pro | Ile | Lys | Asp | Asn | Met | Lys | Asp | Leu | Lys | Thr |  |  |  |  |
| 65  |     |     |     |     |     |     | 70  |     |     | 75  |     |     |     |     |     |  |  |  |  |
| Gly | Tyr | Asp | Ile | Asn | Tyr | Cys | Leu | Asp | Gly | Lys | Ala | Lys | Lys | Met | Arg |  |  |  |  |
| 85  |     |     |     |     |     |     | 90  |     |     | 95  |     |     |     |     |     |  |  |  |  |
| Lys | Ile | Val | Glu | Leu | Val | Asp | Lys | Lys | Ser | Gly | Arg | Lys | Met | Glu | Leu |  |  |  |  |
| 100 |     |     |     |     |     |     | 105 |     |     | 110 |     |     |     |     |     |  |  |  |  |
| Ser | Gly | Asn | Gln | Ala | Gly | Leu | Gln | Phe | Tyr | Thr | Gly | Gly | Met | Leu | Lys |  |  |  |  |
| 115 |     |     |     |     |     |     | 120 |     |     | 125 |     |     |     |     |     |  |  |  |  |
| Asp | Val | Lys | Gly | Lys | Asn | Gly | Ala | Val | Tyr | Gln | Ala | Phe | Gly | Gly | Leu |  |  |  |  |
| 130 |     |     |     |     |     |     | 135 |     |     | 140 |     |     |     |     |     |  |  |  |  |
| Cys | Leu | Glu | Thr | Gln | Ser | Tyr | Pro | Asp | Ala | Leu | Asn | His | Pro | Lys | Phe |  |  |  |  |
| 145 |     |     |     |     |     |     | 150 |     |     | 155 |     |     |     |     |     |  |  |  |  |
| Pro | Ser | Gln | Ile | Val | Glu | Pro | Gly | Lys | Lys | Tyr | Lys | His | Thr | Met | Leu |  |  |  |  |
| 165 |     |     |     |     |     |     | 170 |     |     | 175 |     |     |     |     |     |  |  |  |  |
| Phe | Lys | Phe | Ser | Ile | Val | Ser |     |     |     |     |     |     |     |     |     |  |  |  |  |
| 180 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |

(2) INFORMATION FOR SEO ID NO:2096:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: DNA (genomic)
```

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..554  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2096:

|              |              |             |            |             |             |     |
|--------------|--------------|-------------|------------|-------------|-------------|-----|
| actctatcagat | gaaacctcttgg | aggttatgggt | ctatcaccaa | aagtcctagat | gatacaacagg | 60  |
| aagatgagccaa | atgcagcattc  | tgcgaagaaat | aaataacgat | tggagatgaa  | tgtgggacag  | 120 |
| acacgtctgta  | gcacacatcac  | catgtgaagt  | gttgccaaga | gtggttgcg   | ataaagaagt  | 180 |
| tgtgcccaatg  | ctgcaaaagcc  | acagocggctg | ctcctctcaa | tacaacgtct  | tctctctctt  | 240 |
| cctcgtcttgt  | tgttatagtt   | ctctctatca  | aagcctctga | acaaacaatg  | aacctctcgta | 300 |
| aaaagaagcgt  | caccaatttcc  | tttgtgtaca  | taccaattca | cacccgctgt  | tgtctctctt  | 360 |
| cccttttctc   | taatgacaaa   | gcatactcgt  | gtttctcttg | tcatttcttc  | tcttttaactg | 420 |
| tgtgacttcg   | taatgtaaa    | tgggaagaa   | ggaaacgatt | tctttgtgac  | tttgaagact  | 480 |
| cagtaaacat   | tgactKttta   | attcttaaaa  | tggacaatt  | tgttgaaaag  | caacaaaag   | 540 |
| ctcggtctct   | tgat         |             |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2097:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..73  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2097:

Tyr Gln Met Lys Pro Leu Ser Tyr Gly Ser Ile Thr Lys Ser Pro Ser  
1 5 10 15  
Asp Asn Lys Glu Asp Ala Lys Cys Ser Ile Cys Gln Glu Glu Tyr Thr  
20 25 30  
Ile Gly Asp Glu Val Gly Arg Leu His Cys Glu His Thr Tyr His Val  
35 40 45

Lys Cys Val Gln Glu Trp Leu Arg Met Lys Ser Trp Cys Pro Ile Cys  
50 55 60

Lys Ala Thr Ala Glu Thr Ser Ser Lys  
65 70

(2) INFORMATION FOR SEQ ID NO:2098:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1571814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2098:

Met Lys Pro Leu Ser Tyr Gly Ser Ile Thr Lys Ser Pro Ser Asp Asn  
1 5 10 15

Lys Glu Asp Ala Lys Cys Ser Ile Cys Gln Glu Glu Tyr Thr Ile Gly  
20 25 30

Asp Glu Val Gly Arg Leu His Cys Glu His Thr Tyr His Val Lys Cys  
35 40 45

Val Gln Glu Trp Leu Arg Met Lys Ser Trp Cys Pro Ile Cys Lys Ala  
50 55 60

Thr Ala Glu Thr Ser Ser Lys  
65 70

(2) INFORMATION FOR SEQ ID NO:2099:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..40

(D) OTHER INFORMATION: / Ceres Seq. ID 1571815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2099:

Met Gly Leu Ser Pro Lys Val Leu Val Ile Thr Arg Lys Met Pro Asn  
1 5 10 15

Ala Ala Ser Ala Arg Lys Asn Ile Arg Leu Glu Met Lys Leu Gly Gly  
20 25 30

Tyr Thr Val Ser Thr His Thr Met  
35 40

(2) INFORMATION FOR SEQ ID NO:2100:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1617 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1617

(D) OTHER INFORMATION: / Ceres Seq. ID 1571820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2100:

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| cccgacagta | gaaagcaaaa  | attcttcato | gactcaaatt | caaaaaactca | tctctctcta | 60  |
| tctctatttc | tctgtgtcca  | tagctcaccg | tcgcatcgca | gatctactcc  | ttccgcaata | 120 |
| aattttaccg | gcggagggtat | cagatctcgc | cgatctgttg | tagcagctac  | tgatattttg | 180 |
| gcttctcatt | tgatatgtgg  | gaaacgagga | gtagaggacg | atggaaaatc  | tgatctctct | 240 |
| ggttaacaag | atacacagag  | cttgcaaggc | tttaggagac | catggagact  | ccagcgcttt | 300 |

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| acctactctt  | tgggattcc   | tgccgtcgat  | cgccgtcggt  | ggtggtcaga  | gtcaggagaa  | 360  |
| gtcttcagtc  | ctgggagaga  | tgtgtgggaaa | ggacttttta  | ccccgtggat  | ctggcattgt  | 420  |
| tactcgaag   | ccoccttgtct | tacagttgca  | aaagatcgat  | gatggaaCcc  | gggagtagtc  | 480  |
| agagtttctt  | cacctcccca  | ggaaaaagtt  | tactgatttt  | gctgctgtga  | ggaaggagat  | 540  |
| ctaaagttag  | actgacagag  | agactggagc  | cagcaaggct  | atttctagtgt | ttcccaattca | 600  |
| ccttagcata  | tactctccca  | atgttgtcaa  | cttgacaactg | atagatcttc  | cagggtcttac | 660  |
| aaaaagttgt  | gttgatggac  | aatctgatag  | tatagtgaag  | gacattgaaa  | acatggttgc  | 720  |
| tgcttacaat  | gaaaagoccc  | actgcacatc  | tttggcaatc  | tcacctgcaa  | accaagatct  | 780  |
| tgctacccca  | gatgcaatta  | aaatttcccg  | tgaggttgat  | ccactcgggg  | acagaaactt  | 840  |
| tggtgtcttg  | acaaagattg  | atcttatgga  | caaggggacg  | gatgcagttg  | aaattcttga  | 900  |
| agggagatct  | tttaaaactta | aatatccgtg  | ggttggtgtc  | gtcaaccgtt  | cccaagcaga  | 960  |
| tattaaacaag | aatgtcgaca  | tgattgcgcg  | tcggaaaaga  | gagaggaggt  | acttttccaa  | 1020 |
| tactactgag  | tataggcacc  | ttgctaataa  | aatgggttcc  | gagcattttg  | caaagatgct  | 1080 |
| ctccaaagcat | ctagaacgtg  | tgatcaagtc  | gagaatttcc  | ggcatttcagt | cactttattaa | 1140 |
| caaaaacagta | ttagagctgg  | aaactgaact  | aagtgcgcctt | ggaaaagccta | ttgcagctga  | 1200 |
| tgacgggggg  | aagttgtact  | caataatgga  | gatattgtcg  | ctttttgatc  | aaattattcaa | 1260 |
| agagcatctt  | gatggagtgc  | gtgctgtgtg  | tgaaaagtgc  | tacaacgtgt  | ttgataacca  | 1320 |
| ctctctcgcg  | gctctgaaga  | gactccaaat  | tgacaagcag  | ctagcgtatg  | acaacatccg  | 1380 |
| gaagctgttc  | actgaggtcg  | atggttacc   | gcctcacttg  | attgtctctg  | acgaaggtta  | 1440 |
| cgctgtcttc  | attgagctct  | ctattgtctc  | catcagaggc  | ccctgtgaag  | catctgttga  | 1500 |
| caaccgtatg  | actctttact  | ttcatctcta  | aaaagatgta  | tcaaaaacct  | acataaacct  | 1560 |
| aataagcttc  | tctctcgtt   | ttttttttt   | ttctatggtt  | aaatattagg  | ttcatgc     |      |

(2) INFORMATION FOR SEQ ID NO:2101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..429

(D) OTHER INFORMATION: / Ceres Seq. ID 1571821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2101:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asn | Leu | Ile | Ser | Leu | Val | Asn | Lys | Ile | Gln | Arg | Ala | Cys | Thr |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Ala | Leu | Gly | Asp | His | Gly | Asp | Ser | Ser | Ala | Leu | Pro | Thr | Leu | Trp | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Leu | Pro | Ala | Ile | Ala | Val | Val | Gly | Gln | Ser | Ser | Gly | Lys | Ser |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Val | Leu | Glu | Ser | Ile | Val | Gly | Lys | Asp | Phe | Leu | Pro | Arg | Gly | Ser |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly | Ile | Val | Thr | Arg | Arg | Pro | Leu | Val | Leu | Gln | Lys | Ile | Asp |     |     |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     | 80  |     |     |
| Asp | Gly | Thr | Arg | Glu | Tyr | Ala | Glu | Phe | Leu | His | Leu | Pro | Arg | Lys | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Phe | Thr | Asp | Phe | Ala | Ala | Val | Arg | Lys | Glu | Ile | Gln | Asp | Glu | Thr | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Glu | Thr | Gly | Arg | Ser | Lys | Ala | Ile | Ser | Ser | Val | Pro | Ile | His | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Ile | Tyr | Ser | Pro | Asn | Val | Val | Asn | Leu | Thr | Leu | Ile | Asp | Leu | Pro |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Leu | Thr | Lys | Val | Ala | Val | Asp | Gly | Gln | Ser | Asp | Ser | Ile | Val | Lys |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Asp | Ile | Glu | Asn | Met | Val | Arg | Ser | Tyr | Ile | Glu | Lys | Pro | Asn | Cys | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ile | Leu | Ala | Ile | Ser | Pro | Ala | Asn | Gln | Asp | Leu | Ala | Thr | Ser | Asp | Ala |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Ile | Lys | Ile | Ser | Arg | Glu | Val | Asp | Pro | Ser | Gly | Asp | Arg | Thr | Phe | Gly |
|     |     |     | 195 |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Val | Leu | Thr | Lys | Ile | Asp | Leu | Met | Asp | Lys | Gly | Thr | Asp | Ala | Val | Glu |



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 210                                                             | 215 | 220 |
| Ile Leu Glu Gly Arg Ser Phe Lys Leu Lys Tyr Pro Trp Val Gly Val |     |     |
| 225                                                             | 230 | 235 |
| Val Asn Arg Ser Gln Ala Asp Ile Asn Lys Asn Val Asp Met Ile Ala |     |     |
|                                                                 | 245 | 250 |
| Ala Arg Lys Arg Glu Arg Glu Tyr Phe Ser Asn Thr Thr Glu Tyr Arg |     |     |
|                                                                 | 260 | 265 |
| His Leu Ala Asn Lys Met Gly Ser Glu His Leu Ala Lys Met Leu Ser |     |     |
|                                                                 | 275 | 280 |
| Lys His Leu Glu Arg Val Ile Lys Ser Arg Ile Pro Gly Ile Gln Ser |     |     |
|                                                                 | 290 | 295 |
| Leu Ile Asn Lys Thr Val Leu Glu Leu Glu Thr Glu Leu Ser Arg Leu |     |     |
| 305                                                             | 310 | 315 |
| Gly Lys Pro Ile Ala Ala Asp Ala Gly Gly Lys Leu Tyr Ser Ile Met |     |     |
|                                                                 | 325 | 330 |
| Glu Ile Cys Arg Leu Phe Asp Gln Ile Phe Lys Glu His Leu Asp Gly |     |     |
|                                                                 | 340 | 345 |
| Val Arg Ala Gly Gly Glu Lys Val Tyr Asn Val Phe Asp Asn His Leu |     |     |
|                                                                 | 355 | 360 |
| Pro Ala Ala Leu Lys Arg Leu Gln Phe Asp Lys Gln Leu Ala Met Asp |     |     |
|                                                                 | 370 | 375 |
| Asn Ile Arg Lys Leu Val Thr Glu Ala Asp Gly Tyr Gln Pro His Leu |     |     |
| 385                                                             | 390 | 395 |
| Ile Ala Pro Glu Gln Gly Tyr Arg Arg Leu Ile Glu Ser Ser Ile Val |     |     |
|                                                                 | 405 | 410 |
| Ser Ile Arg Gly Pro Ala Glu Ala Ser Val Asp Thr Val             |     |     |
|                                                                 | 420 | 425 |

(2) INFORMATION FOR SEQ ID NO:2102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..265

(D) OTHER INFORMATION: / Ceres Seq. ID 1571822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2102:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Val Arg Ser Tyr Ile Glu Lys Pro Asn Cys Ile Ile Leu Ala Ile |     |
| 1                                                               | 5   |
| Ser Pro Ala Asn Gln Asp Leu Ala Thr Ser Asp Ala Ile Lys Ile Ser |     |
|                                                                 | 10  |
| Arg Glu Val Asp Pro Ser Gly Asp Arg Thr Phe Gly Val Leu Thr Lys |     |
|                                                                 | 15  |
| Ile Asp Leu Met Asp Lys Gly Thr Asp Ala Val Glu Ile Leu Glu Gly |     |
|                                                                 | 20  |
| Arg Ser Phe Lys Leu Lys Tyr Pro Trp Val Gly Val Val Asn Arg Ser |     |
|                                                                 | 25  |
| Gln Ala Asp Ile Asn Lys Asn Val Asp Met Ile Ala Ala Arg Lys Arg |     |
|                                                                 | 30  |
| Glu Arg Glu Tyr Phe Ser Asn Thr Thr Glu Tyr Arg His Leu Ala Asn |     |
|                                                                 | 35  |
| Lys Met Gly Ser Glu His Leu Ala Lys Met Leu Ser Lys His Leu Glu |     |
|                                                                 | 40  |
| Arg Val Ile Lys Ser Arg Ile Pro Gly Ile Gln Ser Leu Ile Asn Lys |     |
|                                                                 | 45  |
| Thr Val Leu Glu Leu Glu Thr Glu Leu Ser Arg Leu Gly Lys Pro Ile |     |
|                                                                 | 50  |
| Ala Ala Asp Ala Gly Gly Lys Leu Tyr Ser Ile Met Glu Ile Cys Arg |     |
|                                                                 | 55  |
|                                                                 | 60  |
|                                                                 | 65  |
|                                                                 | 70  |
|                                                                 | 75  |
|                                                                 | 80  |
|                                                                 | 85  |
|                                                                 | 90  |
|                                                                 | 95  |
|                                                                 | 100 |
|                                                                 | 105 |
|                                                                 | 110 |
|                                                                 | 115 |
|                                                                 | 120 |
|                                                                 | 125 |
|                                                                 | 130 |
|                                                                 | 135 |
|                                                                 | 140 |
|                                                                 | 145 |
|                                                                 | 150 |
|                                                                 | 155 |
|                                                                 | 160 |
|                                                                 | 165 |
|                                                                 | 170 |
|                                                                 | 175 |

Leu Phe Asp Gln Ile Phe Lys Glu His Leu Asp Gly Val Arg Ala Gly  
180 185 190  
Gly Glu Lys Val Tyr Asn Val Phe Asp Asn His Leu Pro Ala Ala Leu  
195 200 205  
Lys Arg Leu Gln Phe Asp Lys Gln Leu Ala Met Asp Asn Ile Arg Lys  
210 215 220  
Leu Val Thr Glu Ala Asp Gly Tyr Gln Pro His Leu Ile Ala Pro Glu  
225 230 235 240  
Gln Gly Tyr Arg Arg Leu Ile Glu Ser Ser Ile Val Ser Ile Arg Gly  
245 250 255  
Pro Ala Glu Ala Ser Val Asp Thr Val  
260 265

(2) INFORMATION FOR SEQ ID NO:2103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1571823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2103:

Met Asp Lys Gly Thr Asp Ala Val Glu Ile Leu Glu Gly Arg Ser Phe  
1 5 10 15  
Lys Leu Lys Tyr Pro Trp Val Gly Val Val Asn Arg Ser Gln Ala Asp  
20 25 30  
Ile Asn Lys Asn Val Asp Met Ile Ala Ala Arg Lys Arg Glu Arg Glu  
35 40 45  
Tyr Phe Ser Asn Thr Thr Gly Tyr Arg His Leu Ala Asn Lys Met Gly  
50 55 60  
Ser Glu His Leu Ala Lys Met Leu Ser Lys His Leu Glu Arg Val Ile  
65 70 75 80  
Lys Ser Arg Ile Pro Gly Ile Gln Ser Leu Ile Asn Lys Thr Val Leu  
85 90 95  
Glu Leu Glu Thr Glu Leu Ser Arg Leu Gly Lys Pro Ile Ala Ala Asp  
100 105 110  
Ala Gly Gly Lys Leu Tyr Ser Ile Met Glu Ile Cys Arg Leu Phe Asp  
115 120 125  
Gln Ile Phe Lys Glu His Leu Asp Gly Val Arg Ala Gly Gly Glu Lys  
130 135 140  
Val Tyr Asn Val Phe Asp Asn His Leu Pro Ala Ala Leu Lys Arg Leu  
145 150 155 160  
Gln Phe Asp Lys Gln Leu Ala Met Asp Asn Ile Arg Lys Leu Val Thr  
165 170 175  
Glu Ala Asp Gly Tyr Gln Pro His Leu Ile Ala Pro Glu Gln Gly Tyr  
180 185 190  
Arg Arg Leu Ile Glu Ser Ser Ile Val Ser Ile Arg Gly Pro Ala Glu  
195 200 205  
Ala Ser Val Asp Thr Val  
210

(2) INFORMATION FOR SEQ ID NO:2104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..1476

(D) OTHER INFORMATION: / Ceres Seq. ID 1571824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2104:

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| aaaaagtgtgc | gaaGctctct  | cattgagtaa  | actaacggct | atattctctc  | tgatattcaa  | 60   |
| aatttgctcg  | aagaaacgac  | gatggcagcc  | gaaacgaagg | ttcagggtttc | agatccagag  | 120  |
| gcagagtttc  | ttaattcgaa  | gcaggagact  | ggatcacgag | gggagctttt  | caaggagaaac | 180  |
| gtccggccat  | tgaaagagagg | tgcgaatgtt  | ggattctcta | accacgctct  | caaattctcac | 240  |
| tctgaccacc  | aattgagaaa  | gaattctcat  | gagaaaacga | ggaatttgat  | tgaagccatt  | 300  |
| gatgagtagt  | aaggagatga  | ccttttatct  | ccatggatag | agtgtataaa  | atgggtacaa  | 360  |
| gaggcttttc  | caccagaggag | acaagtgtta  | ggactgttag | tgatatatga  | gcaattgtgtt | 420  |
| cgtaaatttt  | ggcactctga  | acgtttacaag | gatgatcttc | gttatcttaa  | agtcctgtgtt | 480  |
| gaatatcggg  | agcattgcgc  | tgtgcggaa   | gtgatttaca | agtttttggg  | ggtcaatgaq  | 540  |
| attggaaga   | cacatgctgt  | ctactatata  | gcttatgctt | tgacacatga  | gtttaagaat  | 600  |
| aaggtaaaaa  | ctgctaata   | gatcttcaat  | cttggaaatc | ctagggatgc  | aaagccagt   | 660  |
| gaaaagtgtg  | atgacgcgta  | caagaagttt  | atggtgagaa | cgatgagaag  | gtccaacaca  | 720  |
| gctgatgaag  | aaccaaaagg  | gaataatgac  | ttaccgtcaa | gaagcttttg  | cactttattg  | 780  |
| tcacggggag  | ataataatgc  | aagaaggcag  | gcgttaggaa | gttctaacc   | acaagccaaa  | 840  |
| aagctaaagc  | caaatcaatc  | atccaagaca  | ccttttgcta | tctacgcaga  | tcagttttca  | 900  |
| gacaccacat  | cagggaatca  | accagagtca  | gacaagtcaa | gaccagagtt  | tggtagttgg  | 960  |
| ctcatgcttg  | gaggcagagc  | agagaggaa   | aaagaaaaca | attctttacc  | tagaaaatgt  | 1020 |
| gcatacttca  | aggttctctc  | gaacccatt   | gtgagaactg | ttgcagcagc  | atctgctttc  | 1080 |
| acccttgagg  | ttttgttcga  | tgaagaagaa  | tgtaacagaa | aggaagaaga  | aaagaagaag  | 1140 |
| aatgatgaaa  | ctatctcatc  | atcatcaaac  | gttctgcccc | ttaatggcgg  | cogtgagata  | 1200 |
| aaaaaagaaa  | cagagctgct  | acgcagaga   | cctttaagac | atttccacc   | caacagcttc  | 1260 |
| ctacgatgat  | gatattggac  | ttctctctc   | acacgatctt | atgggtttgag | atttgagctt  | 1320 |
| ttgtctataa  | agctccttgt  | gtgttttttg  | ctatttggat | ttgtttttgt  | gatgtactgt  | 1380 |
| gatatactat  | cctactatgt  | accatgatgt  | gcctttcatg | ttttgaaatt  | aatgtgactt  | 1440 |

(2) INFORMATION FOR SEQ ID NO:2105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 395 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..395

(D) OTHER INFORMATION: / Ceres Seq. ID 1571825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2105:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Glu | Thr | Lys | Val | Gln | Val | Ser | Asp | Pro | Glu | Ala | Glu | Phe |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Asn | Ser | Lys | Gln | Glu | Thr | Gly | Tyr | Glu | Trp | Glu | Leu | Phe | Lys | Glu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asn | Val | Arg | Pro | Leu | Lys | Arg | Gly | Arg | Asn | Val | Gly | Ile | Leu | Asn | His |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Leu | Lys | Ser | His | Ser | Asp | His | Gln | Leu | Arg | Lys | Asn | Leu | Ile | Glu |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Lys | Arg | Arg | Asn | Leu | Ile | Glu | Ala | Ile | Asp | Gly | Tyr | Glu | Gly | Asp | Asp |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| Pro | Leu | Ser | Pro | Trp | Ile | Glu | Cys | Ile | Lys | Trp | Val | Gln | Glu | Ala | Phe |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Pro | Pro | Gly | Gly | Glu | Cys | Ser | Gly | Leu | Leu | Val | Ile | Tyr | Glu | Gln | Cys |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Val | Arg | Lys | Phe | Trp | His | Ser | Glu | Arg | Tyr | Lys | Asp | Asp | Leu | Arg | Tyr |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Lys | Val | Trp | Leu | Glu | Tyr | Ala | Glu | His | Cys | Ala | Asp | Ala | Glu | Val |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Ile | Tyr | Lys | Phe | Leu | Glu | Val | Asn | Glu | Ile | Gly | Lys | Thr | His | Ala | Val |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |     |
| Tyr | Tyr | Ile | Ala | Tyr | Ala | Leu | His | Ile | Glu | Phe | Lys | Asn | Lys | Val | Lys |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 165 |     | 170 |     | 175 |     |     |     |     |     |     |     |     |     |     |
| Thr | Ala | Asn | Glu | Ile | Phe | Asn | Leu | Gly | Ile | Ser | Arg | Asp | Ala | Lys | Pro |
|     | 180 |     | 185 |     | 190 |     | 195 |     | 200 |     | 205 |     | 210 |     | 215 |
| Val | Glu | Lys | Leu | Asn | Asp | Ala | Tyr | Lys | Lys | Phe | Met | Val | Arg | Thr | Met |
|     | 220 |     | 225 |     | 230 |     | 235 |     | 240 |     | 245 |     | 250 |     | 255 |
| Arg | Arg | Ser | Asn | Thr | Ala | Asp | Glu | Glu | Pro | Lys | Glu | Asn | Asn | Asp | Leu |
|     | 260 |     | 265 |     | 270 |     | 275 |     | 280 |     | 285 |     | 290 |     | 295 |
| Pro | Ser | Arg | Ser | Phe | Gly | Thr | Leu | Leu | Ser | Arg | Gly | Asp | Asn | Asn | Ala |
|     | 300 |     | 305 |     | 310 |     | 315 |     | 320 |     | 325 |     | 330 |     | 335 |
| Arg | Arg | Gln | Ala | Leu | Gly | Ser | Ser | Asn | Pro | Gln | Ala | Lys | Lys | Leu | Lys |
|     | 340 |     | 345 |     | 350 |     | 355 |     | 360 |     | 365 |     | 370 |     | 375 |
| Pro | Asn | Gln | Ser | Ser | Lys | Thr | Pro | Phe | Ala | Ile | Tyr | Ala | Asp | Ala | Val |
|     | 380 |     | 385 |     | 390 |     | 395 |     | 400 |     | 405 |     | 410 |     | 415 |
| Ser | Asp | Thr | Thr | Ser | Gly | Asn | Gln | Pro | Glu | Ser | Asp | Lys | Ser | Arg | Pro |
|     | 420 |     | 425 |     | 430 |     | 435 |     | 440 |     | 445 |     | 450 |     | 455 |
| Glu | Phe | Gly | Ser | Trp | Leu | Met | Leu | Gly | Gly | Arg | Ala | Glu | Arg | Asn | Lys |
|     | 460 |     | 465 |     | 470 |     | 475 |     | 480 |     | 485 |     | 490 |     | 495 |
| Glu | Asn | Asn | Ser | Leu | Pro | Arg | Lys | Trp | Ala | Ser | Phe | Lys | Val | Pro | Gln |
|     | 500 |     | 505 |     | 510 |     | 515 |     | 520 |     | 525 |     | 530 |     | 535 |
| Lys | Pro | Ile | Val | Arg | Thr | Val | Ala | Ala | Ala | Ser | Ala | Phe | Thr | Phe | Glu |
|     | 540 |     | 545 |     | 550 |     | 555 |     | 560 |     | 565 |     | 570 |     | 575 |
| Val | Phe | Val | Asp | Glu | Glu | Glu | Cys | Thr | Glu | Glu | Glu | Glu | Glu | Lys | Lys |
|     | 580 |     | 585 |     | 590 |     | 595 |     | 600 |     | 605 |     | 610 |     | 615 |
| Lys | Asn | Asp | Glu | Thr | Ile | Ser | Ser | Ser | Ser | Asn | Val | Leu | Pro | Leu | Asn |
|     | 620 |     | 625 |     | 630 |     | 635 |     | 640 |     | 645 |     | 650 |     | 655 |
| Gly | Gly | Arg | Glu | Ile | Lys | Lys | Glu | Thr | Glu | Leu | Leu | Arg | Gln | Asn | Pro |
|     | 660 |     | 665 |     | 670 |     | 675 |     | 680 |     | 685 |     | 690 |     | 695 |
| Leu | Arg | His | Phe | Pro | Pro | Asn | Ser | Phe | Leu | Arg |     |     |     |     |     |
|     | 700 |     | 705 |     | 710 |     | 715 |     | 720 |     | 725 |     | 730 |     | 735 |

(2) INFORMATION FOR SEQ ID NO:2106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1641 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1641
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2106:

|             |             |             |             |            |            |      |
|-------------|-------------|-------------|-------------|------------|------------|------|
| ataaagattca | cacatacagct | tactctttt   | gctatttcca  | acccccctta | tgttatttct | 60   |
| ttccttttca  | ggcattttgga | cagccttgga  | actgtttgtg  | gcatacaaac | accaggaggt | 120  |
| taagaaacca  | tataaggata  | ctctgatcaa  | tgtaaagag   | cttgatttct | caaaaccaga | 180  |
| aggtctcttc  | ggatcatctc  | tagatctgg   | tgaaagacca  | cccgtctcca | acgactttgg | 240  |
| aatggttgcc  | tggtgcctag  | atatgtcgac  | cccagagttt  | ccatgggggc | gaaaacttct | 300  |
| ctggtattgc  | aatgatgtca  | ccctcaaaag  | tggttctttt  | ggtcctagag | aggacgcggt | 360  |
| tttctctgtc  | gttactgaac  | tgcgtttgtc  | caagaagctt  | cccttgattt | acttggcagc | 420  |
| aaattctcgt  | gcccgacttg  | gggttgctga  | agaagtcaaa  | gcctgtctca | aatgttgatg | 480  |
| gtcggatgaa  | atttccctcg  | agaatgggtt  | tcagtataata | tacotaaagc | ctgaagacca | 540  |
| cgaagagatt  | ggatcatctg  | tcattgcccc  | tgaagtaaa   | ctccctagat | gggaaactag | 600  |
| gtgggtgatt  | gatacagtcg  | ttggcaaaaga | agatgggtatt | gggtgagaga | acttaacagg | 660  |
| aagtggggcc  | atagcgggtg  | cttactcaaa  | ggcatacaat  | gaaactttta | ctttaacctt | 720  |
| tggtagtggg  | agaacgggtg  | gaattgtgtc  | ttatcttggc  | gcctcaggtg | tgcggtgcat | 780  |
| acagagactt  | gatcagccga  | tcactcttgac | tggtcttctc  | acactcaaca | agttactctg | 840  |
| gcgtgaagtc  | tatatgcttc  | acatgcaact  | gggtggccgc  | aaaatcatgg | gcacaaatgg | 900  |
| tggttttcat  | cttacagctc  | cagatgatct  | tgaaggcgta  | tcagcaattc | tcaactggct | 960  |
| cagctacatt  | ctctgtttaa  | tggttggttc  | tcttctgtgt  | cttgccctct | tagatccacc | 1020 |
| ggagagaatt  | gtggagtatg  | tcccagagaa  | ctcttgcgac  | ccacagcggc | ctgactcgtg | 1080 |
| ggcctaaagac | aataccggta  | aatggcttgg  | aggtatcttt  | gataaaaata | gtttcatatg | 1140 |
| gactcttgaa  | ggctggggca  | ggacggtagt  | gactggtaga  | gccagctcgt | ggggaatacc | 1200 |

|            |            |            |             |             |             |      |
|------------|------------|------------|-------------|-------------|-------------|------|
| cggtggagtt | gttgcagttg | agacacagac | tgatcatgcag | atcatcccgag | cagatcctgg  | 1260 |
| acagottgac | tctcatgaaa | gagtggttcc | gcaagcaggg  | caagtctggt  | ttcctgattc  | 1320 |
| agcggccaag | actgctcaag | cacttatgga | tttcaaccgg  | gaagagcttc  | cattgtttat  | 1380 |
| cctagcgaac | tggaagggtt | tttcaggttg | gcagagagat  | cttttcgaag  | gaatacttca  | 1440 |
| ggcaggttca | actatagtag | aaaatctgag | aacctatcgt  | cagccagtg   | ttgtgtacat  | 1500 |
| cccaatgatg | ggagaGctgc | gcggtggagc | gtgggttgtt  | gttgacagcc  | agataaaattc | 1560 |
| ggattatgtt | gaaatgtatg | ctgatgaaac | agctcgtgga  | aatgtgctcg  | agccagaag   | 1620 |
| gacaatagag | ataaaattta | g          |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..530

(D) OTHER INFORMATION: / Ceres Seq. ID 1571827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2107:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Phe | Leu | Ser | Phe | Ser | Gly | Ile | Trp | Thr | Ala | Leu | Glu | Leu | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Trp | Ala | Ser | Gln | His | Pro | Gly | Val | Lys | Lys | Pro | Tyr | Lys | Asp | Thr | Leu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ile | Asn | Val | Lys | Glu | Leu | Val | Phe | Ser | Lys | Pro | Glu | Gly | Ser | Ser | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Ser | Leu | Asp | Leu | Val | Glu | Arg | Pro | Pro | Gly | Leu | Asn | Asp | Phe | Gly |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Met | Val | Ala | Trp | Cys | Leu | Asp | Met | Ser | Thr | Pro | Glu | Phe | Pro | Met | Gly |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Arg | Lys | Leu | Leu | Val | Ile | Ala | Asn | Asp | Val | Thr | Phe | Lys | Ala | Gly | Ser |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     | 95  |     |
| Phe | Gly | Pro | Arg | Glu | Asp | Ala | Phe | Phe | Leu | Ala | Val | Thr | Glu | Leu | Ala |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Cys | Ala | Lys | Lys | Leu | Pro | Leu | Ile | Tyr | Leu | Ala | Ala | Asn | Ser | Gly | Ala |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Leu | Gly | Val | Ala | Glu | Glu | Val | Lys | Ala | Cys | Phe | Lys | Val | Gly | Trp |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Ser | Asp | Glu | Ile | Ser | Pro | Glu | Asn | Gly | Phe | Gln | Tyr | Ile | Tyr | Leu | Ser |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     | 160 |     |
| Pro | Glu | Asp | His | Glu | Arg | Ile | Gly | Ser | Ser | Val | Ile | Ala | His | Glu | Val |
|     |     |     | 165 |     |     |     | 170 |     |     |     |     |     |     | 175 |     |
| Lys | Leu | Pro | Ser | Gly | Glu | Thr | Arg | Trp | Val | Ile | Asp | Thr | Ile | Val | Gly |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     |     | 190 |     |
| Lys | Glu | Asp | Gly | Ile | Gly | Val | Glu | Asn | Leu | Thr | Gly | Ser | Gly | Ala | Ile |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| Ala | Gly | Ala | Tyr | Ser | Lys | Ala | Tyr | Asn | Glu | Thr | Phe | Thr | Leu | Thr | Phe |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Val | Ser | Gly | Arg | Thr | Val | Gly | Ile | Gly | Ala | Tyr | Leu | Ala | Arg | Leu | Gly |
|     |     |     | 225 |     |     |     | 230 |     |     |     | 235 |     |     | 240 |     |
| Met | Arg | Cys | Ile | Gln | Arg | Leu | Asp | Gln | Pro | Ile | Ile | Leu | Thr | Gly | Phe |
|     |     |     | 245 |     |     |     | 250 |     |     |     |     |     |     | 255 |     |
| Ser | Thr | Leu | Asn | Lys | Leu | Leu | Gly | Arg | Glu | Val | Tyr | Ser | Ser | His | Met |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     |     | 270 |     |
| Gln | Leu | Gly | Gly | Pro | Lys | Ile | Met | Gly | Thr | Asn | Gly | Val | Val | His | Leu |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Thr | Val | Ser | Asp | Asp | Leu | Glu | Gly | Val | Ser | Ala | Ile | Leu | Asn | Trp | Leu |
|     |     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |
| Ser | Tyr | Ile | Pro | Ala | Tyr | Val | Gly | Gly | Pro | Leu | Pro | Val | Leu | Ala | Pro |
|     |     |     | 305 |     |     |     | 310 |     |     |     | 315 |     |     | 320 |     |
| Leu | Asp | Pro | Pro | Glu | Arg | Ile | Val | Glu | Tyr | Val | Pro | Glu | Asn | Ser | Cys |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ala | Trp | Cys | Leu | Asp | Met | Ser | Thr | Pro | Glu | Phe | Pro | Met | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Lys | Leu | Leu | Val | Ile | Ala | Asn | Asp | Val | Thr | Phe | Lys | Ala | Gly | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Gly | Pro | Arg | Glu | Asp | Ala | Phe | Phe | Leu | Ala | Val | Thr | Glu | Leu | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Ala | Lys | Lys | Leu | Pro | Leu | Ile | Tyr | Leu | Ala | Ala | Asn | Ser | Gly | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Leu | Gly | Val | Ala | Glu | Glu | Val | Lys | Ala | Cys | Phe | Lys | Val | Gly | Trp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Asp | Glu | Ile | Ser | Pro | Glu | Asn | Gly | Phe | Gln | Tyr | Ile | Tyr | Leu | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Glu | Asp | His | Glu | Arg | Ile | Gly | Ser | Ser | Val | Ile | Ala | His | Glu | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Leu | Pro | Ser | Gly | Glu | Thr | Arg | Trp | Val | Ile | Asp | Thr | Ile | Val | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Glu | Asp | Gly | Ile | Gly | Val | Glu | Asn | Leu | Thr | Gly | Ser | Gly | Ala | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Gly | Ala | Tyr | Ser | Lys | Ala | Tyr | Asn | Glu | Thr | Phe | Thr | Leu | Thr | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Val | Ser | Gly | Arg | Thr | Val | Gly | Ile | Gly | Ala | Tyr | Leu | Ala | Arg | Leu | Gly |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

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Met Arg Cys Ile Gln Arg Leu Asp Gln Pro Ile Ile Leu Thr Gly Phe
 180 185 190
Ser Thr Leu Asn Lys Leu Leu Gly Arg Glu Val Tyr Ser Ser His Met
 195 200 205
Gln Leu Gly Gly Pro Lys Ile Met Gly Thr Asn Gly Val Val His Leu
 210 215 220
Thr Val Ser Asp Asp Leu Glu Gly Val Ser Ala Ile Leu Asn Trp Leu
 225 230 235 240
Ser Tyr Ile Pro Ala Tyr Val Gly Gly Pro Leu Pro Val Leu Ala Pro
 245 250 255
Leu Asp Pro Pro Glu Arg Ile Val Glu Tyr Val Pro Glu Asn Ser Cys
 260 265 270
Asp Pro Arg Ala Ala Ile Ala Gly Val Lys Asp Asn Thr Gly Lys Trp
 275 280 285
Leu Gly Gly Ile Phe Asp Lys Asn Ser Phe Ile Glu Thr Leu Glu Gly
 290 295 300
Trp Ala Arg Thr Val Val Thr Gly Arg Ala Lys Leu Gly Gly Ile Pro
 305 310 315 320
Val Gly Val Val Ala Val Glu Thr Gln Thr Val Met Gln Ile Ile Pro
 325 330 335
Ala Asp Pro Gly Gln Leu Asp Ser His Glu Arg Val Val Pro Gln Ala
 340 345 350
Gly Gln Val Trp Phe Pro Asp Ser Ala Ala Lys Thr Ala Gln Ala Leu
 355 360 365
Met Asp Phe Asn Arg Glu Glu Leu Pro Leu Phe Ile Leu Ala Asn Trp
 370 375 380
Arg Gly Phe Ser Gly Gly Gln Arg Asp Leu Phe Glu Gly Ile Leu Gln
 385 390 395 400
Ala Gly Ser Thr Ile Val Glu Asn Leu Arg Thr Tyr Arg Gln Pro Val
 405 410 415
Phe Val Tyr Ile Pro Met Met Gly Glu Leu Arg Gly Gly Ala Trp Val
 420 425 430
Val Val Asp Ser Gln Ile Asn Ser Asp Tyr Val Glu Met Tyr Ala Asp
 435 440 445
Glu Thr Ala Arg Gly Asn Val Leu Glu Pro Glu Gly Thr Ile Glu Ile
 450 455 460
Lys Phe
 465

```

(2) INFORMATION FOR SEQ ID NO:2109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 459 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..459

(D) OTHER INFORMATION: / Ceres Seq. ID 1571829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2109:

```

Met Ser Thr Pro Glu Phe Pro Met Gly Arg Lys Leu Leu Val Ile Ala
1 5 10 15
Asn Asp Val Thr Phe Lys Ala Gly Ser Phe Gly Pro Arg Glu Asp Ala
 20 25 30
Phe Phe Leu Ala Val Thr Glu Leu Ala Cys Ala Lys Lys Leu Pro Leu
 35 40 45
Ile Tyr Leu Ala Ala Asn Ser Gly Ala Arg Leu Gly Val Ala Glu Glu
 50 55 60
Val Lys Ala Cys Phe Lys Val Gly Trp Ser Asp Glu Ile Ser Pro Glu
 65 70 75 80
Asn Gly Phe Gln Tyr Ile Tyr Leu Ser Pro Glu Asp His Glu Arg Ile

```

120



tccggccaag actgtaaaaa ctccgggtggt gatggcgggtg gcggttccgt taccocgact 180  
agcattctcc cggaggttcc ttctccttat tctacgtcg agattctcca agcgtttaag 240  
ttgatagaca gagacaacga cggagcgtgtc tctagacacg atcttgagtc gttacttagc 300  
cggttaggtc ctgactcttt gaaggaggag gagatcaacg ttatgcttaa agaggtggac 360  
tgcgacggcg acggtacgat cgtcttgaa gagcttgca gtcgtgtagt ctctttagat 420  
ccggctcgtg actcgactga gctgaaggag actttcgagt tctttgacgc ggatcgtaac 480  
ggtttgatct cggctgatga gcttctacga gttttctcga ccattggaga tgaRcggtgc 540  
acgttagatg attgtaagcg tatgatgca gatgttgatg aggacgggtg t

(2) INFORMATION FOR SEQ ID NO:2111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..197

(D) OTHER INFORMATION: / Ceres Seq. ID 1571831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2111:

Lys Ile His Thr Met Lys Leu Ala Lys Leu Ile Pro Lys Arg Phe Phe  
1 5 10 15  
Ile Arg Ser Lys Asp Arg Ser Thr Val Ser Lys Ser Pro Thr Ala Phe  
20 25 30  
Ser Phe Gly Ser Ala Ser Ser Ser Gly Gln Asp Cys Lys Asn Ser  
35 40 45  
Gly Gly Asp Gly Gly Gly Gly Ser Val Thr Pro Thr Ser Ile Leu Pro  
50 55 60  
Glu Val Pro Ser Pro Tyr Ser Tyr Val Glu Ile Leu Gln Ala Phe Lys  
65 70 75 80  
Leu Ile Asp Arg Asp Asn Asp Gly Ala Val Ser Arg His Asp Leu Glu  
85 90 95  
Ser Leu Leu Ser Arg Leu Gly Pro Asp Pro Leu Thr Glu Glu Glu Ile  
100 105 110  
Asn Val Met Leu Lys Glu Val Asp Cys Asp Gly Asp Gly Thr Ile Arg  
115 120 125  
Leu Glu Glu Leu Ala Ser Arg Val Val Ser Leu Asp Pro Ala Arg Asp  
130 135 140  
Ser Thr Glu Leu Lys Glu Thr Phe Glu Phe Phe Asp Ala Asp Arg Asn  
145 150 155 160  
Gly Leu Ile Ser Ala Asp Glu Leu Leu Arg Val Phe Ser Thr Ile Gly  
165 170 175  
Asp Xaa Arg Cys Thr Leu Asp Asp Cys Lys Arg Met Ile Ala Asp Val  
180 185 190  
Asp Glu Asp Gly Asp  
195

(2) INFORMATION FOR SEQ ID NO:2112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1571832

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2112:

Met Lys Leu Ala Lys Leu Ile Pro Lys Arg Phe Phe Ile Arg Ser Lys  
1 5 10 15  
Asp Arg Ser Thr Val Ser Lys Ser Pro Thr Ala Phe Ser Phe Gly Ser

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| atataaaaa   | taagagattt  | taagggctct  | catattttgc | tttttgctca  | ctcttttttt  | 60   |
| gcctatctgt  | acaaacaccca | aactctctcg  | attcatcagt | tttttgctct  | cttcaagctc  | 120  |
| cagggtacat  | ccatccaatg  | gctcagatct  | tagcacgtct | ttccaacatg  | cagatgagag  | 180  |
| tgcttaaaaa  | ctctcagctc  | attcgatcat  | accaccaagt | atggagctct  | gttgtgttga  | 240  |
| acagacaaga  | gcagagcaac  | acaaaagtca  | gagggtttag | aggtctctgt  | ctccactctg  | 300  |
| ataacagctac | tgtcaataga  | gttgagactc  | tcttcaattt | agacacacaa  | octtactctg  | 360  |
| acaggatgat  | tgtcgaatca  | attttggatc  | gaggatctgg | atttgacctc  | agaagaagaat | 420  |
| cgaggactat  | cgaaaagccg  | gttgaggact  | ctcttgagct | acctaaagtct | aactatgatg  | 480  |
| cttctcagct  | ccgtcaagca  | ctctgtgaag  | atagtgaagt | gtctctatac  | cgcagactga  | 540  |
| tctttcacaga | tccttttcgt  | gaggagcaata | atctcttggt | tatctgtgat  | acttggaacac | 600  |
| cagctcgtgga | gccaatctca  | acaaaacaac  | gcgttaaaag | ctctgagatc  | ttcagtaaca  | 660  |
| agaagtgctc  | tgggcaggtt  | ccaatggctg  | gcgatgaaca | agagatcacct | ttactctcagc | 720  |
| aaaacgtcaa  | attgctctta  | gtgtggctct  | tggaagcgtt | octctgctct  | cagggtctct  | 780  |
| actaotgtgt  | agttggagct  | gacaagaatt  | ggggcgctga | catttcaagt  | gctcatatac  | 840  |
| aagcttgttt  | atactctgga  | attaacatta  | ttgttactaa | tggtgaagtt  | atgcctggac  | 900  |
| agtTggagtt  | ccaagtggc   | accagcgtag  | gaattgatgc | aggttgatct  | gtttgtgttg  | 960  |
| ctagatagat  | tcttgagaga  | ctcacagaca  | aagctgtgtg | gttctcaaca  | cttgatacca  | 1020 |
| aaccgataga  | gggtgactgg  | aacggtgctg  | gttgccacac | caatttaccg  | accaagagca  | 1080 |
| tgagagagga  | agagggattt  | gaagtgatca  | gaagggctat | ctgtgaacct  | tcgctctgct  | 1140 |
| acaaggagca  | catcagtgCc  | tacggttaca  | aaagccgag  | aagtgtagtc  | ggaaagcagc  | 1200 |
| agacagctag  | tattgaccag  | ttctcatagg  | gcgtgcgtaa | acgtggatgc  | ctcatctctg  | 1260 |
| tgggacgtga  | caccagagcg  | aaagaaaggg  | gttacttcta | cagatgcgcg  | tcagatcacta | 1320 |
| acatggagccc | atacatgttg  | acctcacttt  | ttggcagagc | cacactctct  | tgggagccaa  | 1380 |
| ctcttggagc  | tgaagccott  | cgagctcaaa  | ctctcttctt | gaattgttaa  | attatgtgtca | 1440 |
| aactcttcag  | actctgatga  | acacacgtgt  | ctatgtgttc | ttccaagttt  | tttaaacatt  | 1500 |
| cgaattaaaga | caatttttgt  | tctcttttca  | tttcatgttt | taaaaactcag | aatgtatgtg  | 1560 |

acaatgttca tccttttata ttggttcttt tgactgtt

(2) INFORMATION FOR SEQ ID NO:2114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 430 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..430

(D) OTHER INFORMATION: / Ceres Seq. ID 1571838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2114:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gln | Ile | Leu | Ala | Ala | Ser | Pro | Thr | Cys | Gln | Met | Arg | Val | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | His | Ser | Ser | Val | Ile | Ala | Ser | Ser | Ser | Lys | Leu | Trp | Ser | Ser | Val |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Leu | Lys | Gln | Lys | Lys | Gln | Ser | Asn | Asn | Lys | Val | Arg | Gly | Phe | Arg |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Val | Leu | Ala | Leu | Gln | Ser | Asp | Asn | Ser | Thr | Val | Asn | Arg | Val | Glu | Thr |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Leu | Leu | Asn | Leu | Asp | Thr | Lys | Pro | Tyr | Ser | Asp | Arg | Ile | Ile | Ala | Glu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Tyr | Ile | Trp | Ile | Gly | Gly | Ser | Gly | Ile | Asp | Leu | Arg | Ser | Lys | Ser | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Ile | Glu | Lys | Pro | Val | Glu | Asp | Pro | Ser | Glu | Leu | Pro | Lys | Trp | Asn |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Asp | Gly | Ser | Ser | Thr | Gly | Gln | Ala | Pro | Gly | Glu | Asp | Ser | Glu | Val |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Ile | Leu | Tyr | Pro | Gln | Ala | Ile | Phe | Arg | Asp | Pro | Phe | Arg | Gly | Gly | Asn |
|     |     |     |     | 130 |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Asn | Ile | Leu | Val | Ile | Cys | Asp | Thr | Trp | Thr | Pro | Ala | Gly | Glu | Pro | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Thr | Asn | Lys | Arg | Ala | Lys | Ala | Ala | Glu | Ile | Phe | Ser | Asn | Lys | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Ser | Gly | Glu | Val | Pro | Trp | Phe | Gly | Ile | Glu | Gln | Glu | Tyr | Thr | Leu |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Gln | Gln | Asn | Val | Lys | Trp | Pro | Leu | Gly | Trp | Pro | Val | Gly | Ala | Phe |
|     |     |     |     | 195 |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Gly | Pro | Gln | Gly | Pro | Tyr | Tyr | Cys | Gly | Val | Gly | Ala | Asp | Lys | Ile |
|     |     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Trp | Gly | Arg | Asp | Ile | Ser | Asp | Ala | His | Tyr | Lys | Ala | Cys | Leu | Tyr | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Ile | Asn | Ile | Ser | Gly | Thr | Asn | Gly | Glu | Val | Met | Pro | Gly | Gln | Trp |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Phe | Gln | Val | Gly | Pro | Ser | Val | Gly | Ile | Asp | Ala | Gly | Asp | His | Val |
|     |     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Trp | Cys | Ala | Arg | Tyr | Leu | Leu | Glu | Arg | Ile | Thr | Glu | Gln | Ala | Gly | Val |
|     |     |     |     | 275 |     |     |     | 280 |     |     |     | 285 |     |     |     |
| Val | Leu | Thr | Leu | Asp | Pro | Lys | Pro | Ile | Glu | Gly | Asp | Trp | Asn | Gly | Ala |
|     |     |     |     | 290 |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Gly | Cys | His | Thr | Asn | Tyr | Ser | Thr | Lys | Ser | Met | Arg | Glu | Glu | Gly | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Phe | Glu | Val | Ile | Lys | Lys | Ala | Ile | Leu | Asn | Leu | Ser | Leu | Arg | His | Lys |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Glu | His | Ile | Ser | Ala | Tyr | Gly | Glu | Gly | Asn | Glu | Arg | Arg | Leu | Thr | Gly |
|     |     |     |     | 340 |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Lys | His | Glu | Thr | Ala | Ser | Ile | Asp | Gln | Phe | Ser | Trp | Gly | Val | Ala | Asn |
|     |     |     |     | 355 |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Arg | Gly | Cys | Ser | Ile | Arg | Val | Gly | Arg | Asp | Thr | Glu | Ala | Lys | Gly | Lys |
|     |     |     |     | 370 |     |     | 375 |     |     |     |     | 380 |     |     |     |

Gly Tyr Leu Glu Asp Arg Arg Pro Ala Ser Asn Met Asp Pro Tyr Ile  
385 390 395 400  
Val Thr Ser Leu Leu Ala Glu Thr Thr Leu Leu Trp Glu Pro Thr Leu  
405 410 415  
Glu Ala Glu Ala Leu Ala Ala Gln Lys Leu Ser Leu Asn Val  
420 425 430

(2) INFORMATION FOR SEQ ID NO:2115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 418 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..418

(D) OTHER INFORMATION: / Ceres Seq. ID 1571839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2115:

Met Arg Val Pro Lys His Ser Ser Val Ile Ala Ser Ser Ser Lys Leu  
1 5 10 15  
Trp Ser Ser Val Val Leu Lys Gln Lys Lys Gln Ser Asn Asn Lys Val  
20 25 30  
Arg Gly Phe Arg Val Leu Ala Leu Gln Ser Asp Asn Ser Thr Val Asn  
35 40 45  
Arg Val Glu Thr Leu Leu Asn Leu Asp Thr Lys Pro Tyr Ser Asp Arg  
50 55 60  
Ile Ile Ala Glu Tyr Ile Trp Ile Gly Gly Ser Gly Ile Asp Leu Arg  
65 70 75 80  
Ser Lys Ser Arg Thr Ile Glu Lys Pro Val Glu Asp Pro Ser Glu Leu  
85 90 95  
Pro Lys Trp Asn Tyr Asp Gly Ser Ser Thr Gly Gln Ala Pro Gly Glu  
100 105 110  
Asp Ser Glu Val Ile Leu Tyr Pro Gln Ala Ile Phe Arg Asp Pro Phe  
115 120 125  
Arg Gly Gly Asn Asn Ile Leu Val Ile Cys Asp Thr Trp Thr Pro Ala  
130 135 140  
Gly Glu Pro Ile Pro Thr Asn Lys Arg Ala Lys Ala Ala Glu Ile Phe  
145 150 155 160  
Ser Asn Lys Lys Val Ser Gly Glu Val Pro Trp Phe Gly Ile Glu Gln  
165 170 175  
Glu Tyr Thr Leu Leu Gln Gln Asn Val Lys Trp Pro Leu Gly Trp Pro  
180 185 190  
Val Gly Ala Phe Pro Gly Pro Gln Gly Pro Tyr Tyr Cys Gly Val Gly  
195 200 205  
Ala Asp Lys Ile Trp Gly Arg Asp Ile Ser Asp Ala His Tyr Lys Ala  
210 215 220  
Cys Leu Tyr Ala Gly Ile Asn Ile Ser Gly Thr Asn Gly Glu Val Met  
225 230 235 240  
Pro Gly Gln Trp Glu Phe Gln Val Gly Pro Ser Val Gly Ile Asp Ala  
245 250 255  
Gly Asp His Val Trp Cys Ala Arg Tyr Leu Leu Glu Arg Ile Thr Glu  
260 265 270  
Gln Ala Gly Val Val Leu Thr Leu Asp Pro Lys Pro Ile Glu Gly Asp  
275 280 285  
Trp Asn Gly Ala Gly Cys His Thr Asn Tyr Ser Thr Lys Ser Met Arg  
290 295 300  
Glu Glu Gly Gly Phe Glu Val Ile Lys Lys Ala Ile Leu Asn Leu Ser  
305 310 315 320  
Leu Arg His Lys Glu His Ile Ser Ala Tyr Gly Glu Gly Asn Glu Arg  
325 330 335  
Arg Leu Thr Gly Lys His Glu Thr Ala Ser Ile Asp Gln Phe Ser Trp

|         |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 340     |     |     |     | 345 |     |     |     | 350 |     |     |     |     |     |     |     |
| Gly     | Val | Ala | Asn | Arg | Gly | Cys | Ser | Ile | Arg | Val | Gly | Arg | Asp | Thr | Glu |
| 355     |     |     |     | 360 |     |     |     | 365 |     |     |     |     |     |     |     |
| Ala     | Lys | Gly | Lys | Gly | Tyr | Leu | Glu | Asp | Arg | Arg | Pro | Ala | Ser | Asn | Met |
| 370     |     |     |     | 375 |     |     |     | 380 |     |     |     |     |     |     |     |
| Asp     | Pro | Tyr | Ile | Val | Thr | Ser | Leu | Leu | Ala | Glu | Thr | Thr | Leu | Leu | Trp |
| 385     |     |     |     | 390 |     |     |     | 395 |     |     |     | 400 |     |     |     |
| Glu     | Pro | Thr | Leu | Glu | Ala | Glu | Ala | Leu | Ala | Ala | Gln | Lys | Leu | Ser | Leu |
|         |     |     |     | 405 |     |     |     | 410 |     |     |     | 415 |     |     |     |
| Asn Val |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1390
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2116:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| aataataatt  | agactttctg  | actttctcac  | gaacctctct  | gtctcgctcca | ttacttaaaa  | 60   |
| accaaattctt | tcattctctt  | ccttcaccag  | ttgactctct  | ttcaatctat  | ctctgaaatc  | 120  |
| ctcaactctcc | taccgcaaaa  | ccatgaactc  | caacgaccag  | gattccgattc | cggttcagacc | 180  |
| cgaagacaac  | aacttctccg  | gttccaaaaa  | ctacgccatg  | agcgccaaaa  | ctatgctaaag | 240  |
| tgcaatagta  | atctctctct  | tcgtctgcat  | tttaattggtc | ttctctccatc | tttaacgctcg | 300  |
| ttggttatctc | ctccggtgctc | gtagacgtca  | ttctcgtctg  | cgtagccgcta | accgtcgcgcc | 360  |
| tacgattggtt | ttcttcaccg  | ctgatccttc  | caacgccgca  | acttccgtcg  | tcgcttcaag  | 420  |
| tggaacttgat | ccaacagctta | ttaaattctct | ttctgttttc  | actttctccg  | acgagactca  | 480  |
| taaaagatccg | atcgaatgcg  | cggtttggtt  | atcggaattc  | gaagagagcg  | agacgggtcg  | 540  |
| ggttttgcc   | aattgtcaac  | atacttttca  | tgttgattgt  | attgatattg  | ggtttcaatc  | 600  |
| tcattccact  | tgtctctctt  | gtcgatctct  | cgttgagcct  | ctcgccggga  | ttgaatcaac  | 660  |
| ggcgccggcg  | agggagaggg  | aagttgtgat  | tgcggttgat  | tcgtatccgg  | ttttgggtaat | 720  |
| tgaaccgagt  | tctagctctg  | gattgacgga  | tgaaccacat  | ggatctggat  | ctttctcaag  | 780  |
| gctgagggaa  | gattccggga  | gaaaaccggc  | ggcgattgag  | gttccgagga  | ggaacttttag | 840  |
| cgagtttgaa  | gatgagttga  | ctcggagaga  | ctcgccggcg  | agtcagtcgt  | ttaggtctctc | 900  |
| gatgagtcgg  | atgttatctt  | tcactcggat  | gttgagttaga | gatagaagaa  | gcgcttcgctc | 960  |
| tcctatcgcc  | ggaGctccgc  | cgctatcgcc  | gacgttaaagc | tgccggatcac | agatgaccga  | 1020 |
| gtcacatatac | gaacggggag  | gagaaagag   | taggtgactt  | gtcacgtgtt  | gggtctctgat | 1080 |
| tggtttaatg  | ttaacccggg  | gtaaaaaaag  | gaattactac  | aagtcaacag  | gctttttctct | 1140 |
| aggtgttgat  | tctggcgccc  | aaggacacgt  | ggcgtaaac   | gagcttccag  | gaatcaaat   | 1200 |
| tcacggtcta  | ttatgattag  | atagggttaga | tagatttgtg  | taacgatgta  | caaagtcatc  | 1260 |
| tacaatatgt  | aatctgtttc  | catttatttt  | atacatattc  | ttttttttat  | aattttcgaa  | 1320 |
| gttctacaaa  | atcttttatg  | taaaacacaa  | tccaatggtc  | ataattgtga  | taaaagacttt | 1380 |
| gcksawwatt  |             |             |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..304
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2117:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Ser | Asn | Asp | Gln | Asp | Pro | Ile | Pro | Phe | Arg | Pro | Glu | Asp | Asn |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |

```

Asn Phe Ser Gly Ser Lys Thr Tyr Ala Met Ser Gly Lys Ile Met Leu
 20 25 30
Ser Ala Ile Val Ile Leu Phe Phe Val Val Ile Leu Met Val Phe Leu
 35 40 45
His Leu Tyr Ala Arg Trp Tyr Leu Leu Arg Ala Arg Arg His Leu
 50 55 60
Arg Arg Arg Ser Arg Asn Arg Arg Ala Thr Met Val Phe Phe Thr Ala
 65 70 75 80
Asp Pro Ser Thr Ala Ala Thr Ser Val Val Ala Ser Arg Gly Leu Asp
 85 90 95
Pro Asn Val Ile Lys Ser Leu Pro Val Phe Thr Phe Ser Asp Glu Thr
 100 105 110
His Lys Asp Pro Ile Glu Cys Ala Val Cys Leu Ser Glu Phe Glu Glu
 115 120 125
Ser Glu Thr Gly Arg Val Leu Pro Asn Cys Gln His Thr Phe His Val
 130 135 140
Asp Cys Ile Asp Met Trp Phe His Ser His Ser Thr Cys Pro Leu Cys
 145 150 155 160
Arg Ser Leu Val Glu Pro Leu Ala Gly Ile Glu Ser Thr Ala Ala Ala
 165 170 175
Arg Glu Arg Glu Val Val Ile Ala Val Asp Ser Asp Pro Val Leu Val
 180 185 190
Ile Glu Pro Ser Ser Ser Ser Gly Leu Thr Asp Glu Pro His Gly Ser
 195 200 205
Gly Ser Ser Gln Met Leu Arg Glu Asp Ser Gly Arg Lys Pro Ala Ala
 210 215 220
Ile Glu Val Pro Arg Arg Thr Phe Ser Glu Phe Glu Asp Glu Leu Thr
 225 230 235 240
Arg Arg Asp Ser Pro Ala Ser Gln Ser Phe Arg Ser Pro Met Ser Arg
 245 250 255
Met Leu Ser Phe Thr Arg Met Leu Ser Arg Asp Arg Arg Ser Ala Ser
 260 265 270
Ser Pro Ile Ala Gly Ala Pro Pro Leu Ser Pro Thr Leu Ser Cys Arg
 275 280 285
Ile Gln Met Thr Glu Ser Asp Ile Glu Arg Gly Gly Glu Glu Ser Arg
 290 295 300

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(2) INFORMATION FOR SEQ ID NO:2118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..279
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2118:

```

Met Ser Gly Lys Ile Met Leu Ser Ala Ile Val Ile Leu Phe Phe Val
1 5 10 15
Val Ile Leu Met Val Phe Leu His Leu Tyr Ala Arg Trp Tyr Leu Leu
 20 25 30
Arg Ala Arg Arg Arg His Leu Arg Arg Arg Ser Arg Asn Arg Arg Ala
 35 40 45
Thr Met Val Phe Phe Thr Ala Asp Pro Ser Thr Ala Ala Thr Ser Val
 50 55 60
Val Ala Ser Arg Gly Leu Asp Pro Asn Val Ile Lys Ser Leu Pro Val
 65 70 75 80
Phe Thr Phe Ser Asp Glu Thr His Lys Asp Pro Ile Glu Cys Ala Val

```

(2) INFORMATION FOR SEQ ID NO:2119:

(A) LENGTH: 274 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY:  $\lim$

(D) TOPOLOGY: linear  
MOLECULE TYPE: peptide

(B) NAME/KEY: peptide

(A) NAME/KEY: peptide  
(B) LOCATION: 1-234

(B) LOCATION: 1..274

(D) OTHER INFORMATION: 7 Ceres Seq. ID 1371843  
SEQUENCE DESCRIPTION: 370 ID NO: 2110

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ser | Ala | Ile | Val | Ile | Leu | Phe | Phe | Val | Val | Ile | Leu | Met | Val |
|     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Leu | His | Leu | Tyr | Ala | Arg | Trp | Tyr | Leu | Leu | Arg | Ala | Arg | Arg | Arg |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Leu | Arg | Arg | Arg | Ser | Arg | Asn | Arg | Arg | Ala | Thr | Met | Val | Phe | Phe |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Ala | Asp | Pro | Ser | Thr | Ala | Ala | Thr | Ser | Val | Val | Ala | Ser | Arg | Gly |
|     |     |     |     | 50  |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Asp | Pro | Asn | Val | Ile | Lys | Ser | Leu | Pro | Val | Phe | Thr | Phe | Ser | Asp |
|     |     |     |     | 65  |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Thr | His | Lys | Asp | Pro | Ile | Glu | Cys | Ala | Val | Cys | Leu | Ser | Glu | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Glu | Ser | Glu | Thr | Gly | Arg | Val | Leu | Pro | Asn | Cys | Gln | His | Thr | Phe |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Val | Asp | Cys | Ile | Asp | Met | Trp | Phe | His | Ser | His | Ser | Thr | Cys | Pro |
|     |     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Cys | Arg | Ser | Leu | Val | Glu | Pro | Leu | Ala | Gly | Ile | Glu | Ser | Thr | Ala |
|     |     |     |     | 130 |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Ala | Arg | Glu | Arg | Glu | Val | Val | Ile | Ala | Val | Asp | Ser | Asp | Pro | Val |
|     |     |     |     | 145 |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Val | Ile | Glu | Pro | Ser | Ser | Ser | Ser | Gly | Leu | Thr | Asp | Glu | Pro | His |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Ser | Gly | Ser | Ser | Gln | Met | Leu | Arg | Glu | Asp | Ser | Gly | Arg | Lys | Pro |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |

Ala Ala Ile Glu Val Pro Arg Arg Thr Phe Ser Glu Phe Glu Asp Glu  
195 200 205  
Leu Thr Arg Arg Asp Ser Pro Ala Ser Gln Ser Phe Arg Ser Pro Met  
210 215 220  
Ser Arg Met Leu Ser Phe Thr Arg Met Leu Ser Arg Asp Arg Arg Ser  
225 230 235 240  
Ala Ser Ser Pro Ile Ala Gly Ala Pro Pro Leu Ser Pro Thr Leu Ser  
245 250 255  
Cys Arg Ile Gln Met Thr Glu Ser Asp Ile Glu Arg Gly Gly Glu Glu  
260 265 270  
Ser Arg

(2) INFORMATION FOR SEQ ID NO:2120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1405
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2120:

aaaaaatttta tttagccattc gagaaacaag gcatctctat ttttttgctt cttctaataag 60  
actttcttcgt cactgatctc ccacgacgat ctcccaaaact cattttctcta cggttcacga 120  
tctctctcttt tctcgttttgc tctacgaaaa tcagccatgg atgaagagta cgagggtatt 180  
gtttccggcca ccggtctcaa ggagtggtatc ctacgcggtc tcctttccgt cgatgggtgc 240  
aagggtgcttc aatggacacg gaatgactac tatggtggag aatcaacttc tcttaatctc 300  
aatcagctttt ggaagaagtt caggggagaa gagaaggctc ctgagcattt aggtgctagc 360  
cgggattaca atgttgacat gatgcctaag tttatgatgg gaaatggcaa gcttgttcgt 420  
acccttatct atacagatgt tacaagaagt ttgtccttca aagctgttga tggaaagctat 480  
gttttcgtca aaggaaaggt tcaaaagggt ccagctactc ctatggaggc cctgaaactc 540  
tctctcatgg gcatatttga gaaacgtcga gccgcgaagt ttttcagttt tgttcaggaa 600  
tacgatgaga aggacccaaa aacacacgat ggaatggatt tgaccagagt tacaacaag 660  
gaactgattg cgaaatatgg tcttgatggc aacactattg actttattgg tcacgcagtg 720  
gcactTcaca cgaatgacca acatctcgat caaccgcctt ttgatactgt aatgagaatg 780  
aagctctatg cggaatctct tgcacgtttc caaggaaacat ctccatatat ttatcctctc 840  
tatgggttgg gagaactacc ccaggcattt gcacgactta gtgctgtcta tggttggcaca 900  
tatatgttga acaaactcta gtgcaaggta gagtttgacg agggaggtaa gggtattgggt 960  
gtaaacatcg agggagagac tgcataaatgc aaaaagattg tgtgtgacc tcatacactg 1020  
ccgaacaagg ttaggaaagt tggcagggtt gctcgggcca tcgccattat gagccaccgc 1080  
attccaaaac ccaatgatgc tcaactcagt caggctatca taccocgaaa acagtgtggc 1140  
cgcaaatcgg atatgtatgt cttctgttgt tcgtactccc acaacgttgc tcccaaggga 1200  
aaattcattg cattttgtgc tacagatgca gagactgata accctcaaac cgaactaaa 1260  
cctggaactg atcttttggg tctctgttat gagatatct tcgacatgta tgatagatgc 1320  
gagcctgtca acgagccaga gttggacaac tgctttatat caacgagcta tgatgctaca 1380  
acacactttg agacaactgt tgcgg

(2) INFORMATION FOR SEQ ID NO:2121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..416
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2121:

Met Asp Glu Glu Tyr Glu Val Ile Val Leu Gly Thr Gly Leu Lys Glu



|     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   |     |     | 5   |     |     |     | 10  |     |     |     | 15  |
| Cys | Ile | Leu | Ser | Gly | Leu | Leu | Ser | Val | Asp | Gly | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     | 30  |
| Met | Asp | Arg | Asn | Asp | Tyr | Tyr | Gly | Gly | Glu | Ser | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |
| Asn | Gln | Leu | Trp | Lys | Lys | Phe | Arg | Gly | Glu | Glu | Lys |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |
| Leu | Gly | Ala | Ser | Arg | Asp | Tyr | Asn | Val | Asp | Met | Met |
|     |     |     | 65  |     | 70  |     |     |     | 75  |     | 80  |
| Met | Gly | Asn | Gly | Lys | Leu | Val | Arg | Thr | Leu | Ile | His |
|     |     |     | 85  |     |     |     |     | 90  |     |     | 95  |
| Lys | Tyr | Leu | Ser | Phe | Lys | Ala | Val | Asp | Gly | Ser | Tyr |
|     |     |     | 100 |     |     |     | 105 |     |     |     | 110 |
| Gly | Lys | Val | Gln | Lys | Val | Pro | Ala | Thr | Pro | Met | Glu |
|     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |
| Ser | Leu | Met | Gly | Ile | Phe | Glu | Lys | Arg | Arg | Ala | Gly |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |
| Phe | Val | Gln | Glu | Tyr | Asp | Glu | Lys | Asp | Pro | Lys | Thr |
|     |     |     | 145 |     | 150 |     |     |     | 155 |     | 160 |
| Asp | Leu | Thr | Arg | Val | Thr | Thr | Lys | Glu | Leu | Ile | Ala |
|     |     |     | 165 |     |     |     |     | 170 |     |     | 175 |
| Asp | Gly | Asn | Thr | Ile | Asp | Phe | Ile | Gly | His | Ala | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     | 190 |
| Asn | Asp | Gln | His | Leu | Asp | Gln | Pro | Ala | Phe | Asp | Thr |
|     |     |     | 195 |     |     |     | 200 |     |     |     | 205 |
| Lys | Leu | Tyr | Ala | Glu | Ser | Leu | Ala | Arg | Phe | Gln | Gly |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |
| Ile | Tyr | Pro | Leu | Tyr | Gly | Leu | Gly | Glu | Leu | Pro | Gln |
|     |     |     | 225 |     | 230 |     |     |     | 235 |     | 240 |
| Leu | Ser | Ala | Val | Tyr | Gly | Gly | Thr | Tyr | Met | Leu | Asn |
|     |     |     | 245 |     |     |     |     | 250 |     |     | 255 |
| Lys | Val | Glu | Phe | Asp | Glu | Gly | Gly | Lys | Val | Ile | Gly |
|     |     |     | 260 |     |     |     | 265 |     |     |     | 270 |
| Gly | Glu | Thr | Ala | Lys | Cys | Lys | Lys | Ile | Val | Cys | Asp |
|     |     |     | 275 |     |     |     | 280 |     |     |     | 285 |
| Pro | Asn | Lys | Val | Arg | Lys | Ile | Gly | Arg | Val | Ala | Arg |
|     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |
| Met | Ser | His | Pro | Ile | Pro | Asn | Thr | Asn | Asp | Ser | His |
|     |     |     | 305 |     | 310 |     |     |     | 315 |     | 320 |
| Ile | Ile | Pro | Gln | Lys | Gln | Leu | Ala | Arg | Lys | Ser | Asp |
|     |     |     | 325 |     |     |     |     |     | 330 |     | 335 |
| Cys | Cys | Ser | Tyr | Ser | His | Asn | Val | Ala | Pro | Lys | Gly |
|     |     |     | 340 |     |     |     | 345 |     |     |     | 350 |
| Phe | Val | Ser | Thr | Asp | Ala | Glu | Thr | Asp | Asn | Pro | Gln |
|     |     |     | 355 |     |     |     | 360 |     |     |     | 365 |
| Pro | Gly | Thr | Asp | Leu | Leu | Gly | Pro | Val | Asp | Glu | Ile |
|     |     |     | 370 |     | 375 |     |     |     |     |     | 380 |
| Tyr | Asp | Arg | Tyr | Glu | Pro | Val | Asn | Glu | Pro | Glu | Leu |
|     |     |     | 385 |     | 390 |     |     |     | 395 |     | 400 |
| Ile | Ser | Thr | Ser | Tyr | Asp | Ala | Thr | Thr | His | Phe | Glu |
|     |     |     | 405 |     |     |     |     | 410 |     |     | 415 |

(2) INFORMATION FOR SEQ ID NO:2122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1.384

(D) OTHER INFORMATION: / Ceres Seq. ID 1571846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2122:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Arg | Asn | Asp | Tyr | Tyr | Gly | Gly | Glu | Ser | Thr | Ser | Leu | Asn | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Asn | Gln | Leu | Trp | Lys | Lys | Phe | Arg | Gly | Glu | Glu | Lys | Ala | Pro | Glu | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Gly | Ala | Ser | Arg | Asp | Tyr | Asn | Val | Asp | Met | Met | Pro | Lys | Phe | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Met | Gly | Asn | Gly | Lys | Leu | Val | Arg | Thr | Leu | Ile | His | Thr | Asp | Val | Thr |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Lys | Tyr | Leu | Ser | Phe | Lys | Ala | Val | Asp | Gly | Ser | Tyr | Val | Phe | Val | Lys |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Gly | Lys | Val | Gln | Lys | Val | Pro | Ala | Thr | Pro | Met | Glu | Ala | Leu | Lys | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Leu | Met | Gly | Ile | Phe | Glu | Lys | Arg | Arg | Ala | Gly | Lys | Phe | Phe | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Val | Gln | Glu | Tyr | Asp | Glu | Lys | Asp | Pro | Lys | Thr | His | Asp | Gly | Met |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Leu | Thr | Arg | Val | Thr | Thr | Lys | Glu | Leu | Ile | Ala | Lys | Tyr | Gly | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Gly | Asn | Thr | Ile | Asp | Phe | Ile | Gly | His | Ala | Val | Ala | Leu | His | Thr |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Asn | Asp | Gln | His | Leu | Asp | Gln | Pro | Ala | Phe | Asp | Thr | Val | Met | Arg | Met |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Leu | Tyr | Ala | Glu | Ser | Leu | Ala | Arg | Phe | Gln | Gly | Thr | Ser | Pro | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Tyr | Pro | Leu | Tyr | Gly | Leu | Gly | Glu | Leu | Pro | Gln | Ala | Phe | Ala | Arg |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Leu | Ser | Ala | Val | Tyr | Gly | Gly | Thr | Tyr | Met | Leu | Asn | Lys | Pro | Glu | Cys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Val | Glu | Phe | Asp | Glu | Gly | Gly | Lys | Val | Ile | Gly | Val | Thr | Ser | Glu |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |
| Gly | Glu | Thr | Ala | Lys | Cys | Lys | Lys | Ile | Val | Cys | Asp | Pro | Ser | Tyr | Leu |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Asn | Lys | Val | Arg | Lys | Ile | Gly | Arg | Val | Ala | Arg | Ala | Ile | Ala | Ile |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Met | Ser | His | Pro | Ile | Pro | Asn | Thr | Asn | Asp | Ser | His | Ser | Val | Gln | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Ile | Pro | Gln | Lys | Gln | Leu | Ala | Arg | Lys | Ser | Asp | Met | Tyr | Val | Phe |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Cys | Cys | Ser | Tyr | Ser | His | Asn | Val | Ala | Pro | Lys | Gly | Lys | Phe | Ile | Ala |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Phe | Val | Ser | Thr | Asp | Ala | Glu | Thr | Asp | Asn | Pro | Gln | Thr | Glu | Leu | Lys |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Pro | Gly | Thr | Asp | Leu | Leu | Gly | Pro | Val | Asp | Glu | Ile | Phe | Phe | Asp | Met |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Tyr | Asp | Arg | Tyr | Glu | Pro | Val | Asn | Glu | Pro | Glu | Leu | Asp | Asn | Cys | Phe |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ile | Ser | Thr | Ser | Tyr | Asp | Ala | Thr | Thr | His | Phe | Glu | Thr | Thr | Val | Ala |
| 370 |     |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..342

(D) OTHER INFORMATION: / Ceres Seq. ID 1571847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2123:

Met Met Pro Lys Phe Met Met Gly Asn Gly Lys Leu Val Arg Thr Leu  
1 5 10 15  
Ile His Thr Asp Val Thr Lys Tyr Leu Ser Phe Lys Ala Val Asp Gly  
20 25 30  
Ser Tyr Val Phe Val Lys Gly Lys Val Gln Lys Val Pro Ala Thr Pro  
35 40 45  
Met Glu Ala Leu Lys Ser Ser Leu Met Gly Ile Phe Glu Lys Arg Arg  
50 55 60  
Ala Gly Lys Phe Phe Ser Phe Val Gln Glu Tyr Asp Glu Lys Asp Pro  
65 70 75 80  
Lys Thr His Asp Gly Met Asp Leu Thr Arg Val Thr Thr Lys Glu Leu  
85 90 95  
Ile Ala Lys Tyr Gly Leu Asp Gly Asn Thr Ile Asp Phe Ile Gly His  
100 105 110  
Ala Val Ala Leu His Thr Asn Asp Gln His Leu Asp Gln Pro Ala Phe  
115 120 125  
Asp Thr Val Met Arg Met Lys Leu Tyr Ala Glu Ser Leu Ala Arg Phe  
130 135 140  
Gln Gly Thr Ser Pro Tyr Ile Tyr Pro Leu Tyr Gly Leu Gly Glu Leu  
145 150 155 160  
Pro Gln Ala Phe Ala Arg Leu Ser Ala Val Tyr Gly Gly Thr Tyr Met  
165 170 175  
Leu Asn Lys Pro Glu Cys Lys Val Glu Phe Asp Glu Gly Gly Lys Val  
180 185 190  
Ile Gly Val Thr Ser Glu Gly Glu Thr Ala Lys Cys Lys Lys Ile Val  
195 200 205  
Cys Asp Pro Ser Tyr Leu Pro Asn Lys Val Arg Lys Ile Gly Arg Val  
210 215 220  
Ala Arg Ala Ile Ala Ile Met Ser His Pro Ile Pro Asn Thr Asn Asp  
225 230 235 240  
Ser His Ser Val Gln Val Ile Ile Pro Gln Lys Gln Leu Ala Arg Lys  
245 250 255  
Ser Asp Met Tyr Val Phe Cys Cys Ser Tyr Ser His Asn Val Ala Pro  
260 265 270  
Lys Gly Lys Phe Ile Ala Phe Val Ser Thr Asp Ala Glu Thr Asp Asn  
275 280 285  
Pro Gln Thr Glu Leu Lys Pro Gly Thr Asp Leu Leu Gly Pro Val Asp  
290 295 300  
Glu Ile Phe Phe Asp Met Tyr Asp Arg Tyr Glu Pro Val Asn Glu Pro  
305 310 315 320  
Glu Leu Asp Asn Cys Phe Ile Ser Thr Ser Tyr Asp Ala Thr Thr His  
325 330 335  
Phe Glu Thr Thr Val Ala  
340

(2) INFORMATION FOR SEQ ID NO:2124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 884 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..884

(D) OTHER INFORMATION: / Ceres Seq. ID 1571867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2124:

```

acacaattca gattccaatt ttctcaaaat ctaaaatcaa tctctcaaat ctctcaaccg 60
tgatcaagat gcagatcttc gtttaagactc tcaccggaaa gactatcacc ctgcgaggtgg 120
aaagctctcg caccatcgac aacgttaagg ccaagatcca ggataaggaa ggtattctctc 180
cggatcagca gaggcttatt ttccgccgga agcagttgga ggatggccgc acgtttggcgc 240
attacaatat ccagaaggaa tccaccctcc acttggttct caggctccgt ggtgggtatgc 300
agattttcgt taaaaaccCta acgggaaga cgaattactct tgaggtggag agctctgaca 360
ccattgacaa cgctcaaggcc aagatccaag ataaggagggg tattctctcg gaccagcaga 420
ggttgatctt cgccggaaa gcaacttgagg acggcagaaac ttggcgggat tacaacatcc 480
agaaggagtc tacgctttat ttggtcttgc gtctgcgtgg aggtatgcag atctctcgtaa 540
agacttttgc cggaaagacc atcaactctg aagttgagag ctccgacacc attgataacg 600
tgaaggctaa gatccaggac aaggaaggca ttctctcgga ccagcagcgt ctcatctctg 660
cggaagaaga ccttgaggat ggacgtactt tggccgacta caacatccag aaggagtcta 720
ctcttcactt ggtctccgt ctccgtggtg gtttctaaac cttgtctctc tctcttatgg 780
tactgaacc aagttcatgt atcgtttcat ctagtacttt ggtgggttat gttttggggc 840
catgtacagc ctctgataaa taattgatcg actatgttcc cgctc

```

(2) INFORMATION FOR SEQ ID NO:2125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..251

(D) OTHER INFORMATION: / Ceres Seq. ID 1571868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2125:

```

Thr Ile Gln Ile Pro Ile Phe Ser Asn Ser Lys Ile Asn Leu Ser Asn
1 5 10 15
Leu Ser Thr Val Ile Lys Met Gln Ile Phe Val Lys Thr Leu Thr Gly
20 25 30
Lys Thr Ile Thr Leu Glu Val Glu Ser Ser Asp Thr Ile Asp Asn Val
35 40 45
Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg
50 55 60
Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp
65 70 75 80
Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg
85 90 95
Gly Gly Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr
100 105 110
Leu Glu Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile
115 120 125
Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala
130 135 140
Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln
145 150 155 160
Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln
165 170 175 180
Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu
185 190 195
Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu
200 205 210
Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu
215 220 225
Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr
230 235 240 245
Leu His Leu Val Leu Arg Leu Arg Gly Gly Phe
250

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(2) INFORMATION FOR SEQ ID NO:2126:

(i) SEQUENCE CHARACTERISTICS:

2025 RELEASE UNDER E.O. 14176

- (A) LENGTH: 229 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..229  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2126:

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu  
1 5 10 15  
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp  
20 25 30  
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys  
35 40 45  
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu  
50 55 60  
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe  
65 70 75 80  
Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser  
85 90 95  
Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile  
100 105 110  
Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp  
115 120 125  
Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His  
130 135 140  
Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe Val Lys Thr Leu  
145 150 155 160  
Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser Asp Thr Ile Asp  
165 170 175  
Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln  
180 185 190  
Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu  
195 200 205  
Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg  
210 215 220  
Leu Arg Gly Gly Phe  
225

(2) INFORMATION FOR SEQ ID NO:2127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..153  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2127:

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu  
1 5 10 15  
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp  
20 25 30  
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys  
35 40 45  
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu  
50 55 60  
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Met Gln Ile Phe

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asp | Leu | Arg | Asp | Glu | Lys | Gly | Asn | Pro | Ile | His | Leu | Thr | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Gln | Gly | Asn | Pro | Ile | Val | Asp | Leu | Thr | Asp | Glu | His | Gly | Asn | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Tyr | Leu | Thr | Gly | Val | Val | Ser | Ser | Thr | Pro | Gln | His | Lys | Glu | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Thr | Thr | Ser | Asp | Ile | Ala | Glu | His | Pro | Thr | Ser | Thr | Val | Gly | Glu | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| His | Pro | Ala | Ala | Ala | Pro | Thr | Gly | Ala | Gly | Ala | Ala | Thr | Ala | Ala | Thr |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Thr | Gly | Val | Ser | Ala | Gly | Thr | Gly | Ala | Thr | Thr | Thr | Gly | Gln | Gln |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |

His His Gly Ser Leu Glu Glu His Leu Arg Arg Ser Gly Ser Ser Ser  
100 105 110  
Ser Ser Ser Ser Glu Asp Asp Gly Gln Gly Gly Arg Arg Lys Lys Ser  
115 120 125  
Ile Lys Glu Lys Ile Lys Glu Lys Phe Ser Ser Gly Lys His Lys Asp  
130 135 140  
Glu Gln Thr Pro Thr Thr Ala Thr Thr Thr Gly Pro Ala Thr Thr Asp  
145 150 155 160  
Gln Pro His Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Asp Lys Leu  
165 170 175  
Pro Gly His His Asn His Asn His Pro  
180 185

(2) INFORMATION FOR SEQ ID NO:2130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1571873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2130:

Met Tyr Leu Thr Gly Val Val Ser Ser Thr Pro Gln His Lys Glu Ser  
1 5 10 15  
Thr Thr Ser Asp Ile Ala Glu His Pro Thr Ser Thr Val Gly Glu Thr  
20 25 30  
His Pro Ala Ala Ala Pro Thr Gly Ala Gly Ala Ala Thr Ala Ala Thr  
35 40 45  
Ala Thr Gly Val Ser Ala Gly Thr Gly Ala Thr Thr Thr Gly Gln Gln  
50 55 60  
His His Gly Ser Leu Glu Glu His Leu Arg Arg Ser Gly Ser Ser Ser  
65 70 75 80  
Ser Ser Ser Ser Glu Asp Asp Gly Gln Gly Gly Arg Arg Lys Lys Ser  
85 90 95  
Ile Lys Glu Lys Ile Lys Glu Lys Phe Ser Ser Gly Lys His Lys Asp  
100 105 110  
Glu Gln Thr Pro Thr Thr Ala Thr Thr Thr Gly Pro Ala Thr Thr Asp  
115 120 125  
Gln Pro His Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Asp Lys Leu  
130 135 140  
Pro Gly His His Asn His Asn His Pro  
145 150

(2) INFORMATION FOR SEQ ID NO:2131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1091 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..1091

(D) OTHER INFORMATION: / Ceres Seq. ID 1571874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2131:

atcttatctt gctttaaagc ttttggcgag tttgcttggt tgtgagtgtg tggttatgga 60  
gtctccgttc aaacctgatg tcgtcagagg tcaagtggct ctcataccg gtggtggatc 120  
cggtatcggt tttgagatct cttctcagtt ttgcacaacat ggagctctcta tcgctatcat 180  
gggacgcaga aaacaagtcc tcgatcacgc cgtctctgct cttcgatctc ttggaatcca 240  
ggctattgga ttggaaggtg atgttcgtaa gcaagaagat gcgagaagag ttgtggaagc 300

|            |             |            |             |            |            |      |
|------------|-------------|------------|-------------|------------|------------|------|
| aacttatcag | catttttgga  | aacttgatat | tcttggttaac | gccgctgctg | ggaattttct | 360  |
| ggctgctgct | gaggtatttg  | ctcctaattg | cttcagaaca  | gtcttagaca | ttgatcgctg | 420  |
| aggaacatct | aacatgtgtc  | acgcagctct | caagtatctt  | aagaaaggag | cgctggaag  | 480  |
| agactcatca | agcgggtggag | gttcgattat | taacattagc  | gcgactttgc | actacacgpc | 540  |
| ttcttggtac | caaatatcatg | tctctgCagc | caaggctgca  | gttgatgcta | ccacaagaaa | 600  |
| cttggcattg | gagtggggaa  | ctgactatga | tattagagtg  | aacgggattg | ctccaggtcc | 660  |
| tattggagtg | acacctggaa  | tgagtaaaat | tgtacctgag  | gagattgaaa | acaaaaccag | 720  |
| agagtacatg | cctctttata  | aagttggaga | gaagtgggat  | atcgctatgg | ctgcactcta | 780  |
| cctcagctgt | gattctggga  | aatatgtgag | cggactaaca  | atggtggtag | atggaggact | 840  |
| gtggcttagc | aaacctggcc  | acttgcttaa | agaagcggtg  | aagcaactct | ctcgtgcggt | 900  |
| ggagaagag  | tctaggggcca | agcctgtttg | tctcccaacc  | agcaactgtg | agatcatttg | 960  |
| aatttcagat | atcaataaag  | tgcaacttga | aaaaatgttt  | tggtttattg | aattacattg | 1020 |
| gagactgaga | aaatggtatt  | aagattatgt | agatcaaact  | atcttatgca | caataaagta | 1080 |
| gctttctttg | c           |            |             |            |            |      |

(2) INFORMATION FOR SEQ ID NO:2132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..316
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2132:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Tyr | Phe | Val | Leu | Lys | Leu | Leu | Ala | Ser | Leu | Leu | Val | Cys | Glu | Cys |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Val | Met | Glu | Ser | Pro | Phe | Lys | Pro | Asp | Val | Val | Arg | Gly | Gln | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Ile | Thr | Gly | Gly | Gly | Ser | Gly | Ile | Gly | Phe | Glu | Ile | Ser | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Phe | Gly | Lys | His | Gly | Ala | Ser | Ile | Ala | Ile | Met | Gly | Arg | Arg | Lys |
|     |     | 50  |     |     |     | 55  |     |     |     |     |     |     |     |     |     |
| Gln | Val | Leu | Asp | Asp | Ala | Val | Ser | Ala | Leu | Arg | Ser | Leu | Gly | Ile | Gln |
|     |     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Ile | Gly | Leu | Glu | Gly | Asp | Val | Arg | Lys | Gln | Glu | Asp | Ala | Arg | Arg |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Val | Val | Glu | Ala | Thr | Tyr | Gln | His | Phe | Gly | Lys | Leu | Asp | Ile | Leu | Val |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Ala | Ala | Ala | Gly | Asn | Phe | Leu | Ala | Ala | Glu | Asp | Leu | Ser | Pro |     |
|     |     | 115 |     |     |     |     | 120 |     |     | 125 |     |     |     |     |     |
| Asn | Gly | Phe | Arg | Thr | Val | Leu | Asp | Ile | Asp | Ala | Val | Gly | Thr | Phe | Asn |
|     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Met | Cys | His | Ala | Ala | Leu | Lys | Tyr | Leu | Lys | Lys | Gly | Ala | Pro | Gly | Arg |
|     |     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Asp | Ser | Ser | Ser | Gly | Gly | Gly | Ser | Ile | Ile | Asn | Ile | Ser | Ala | Thr | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Tyr | Thr | Ala | Ser | Trp | Tyr | Gln | Ile | His | Val | Ser | Ala | Ala | Lys | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Ala | Val | Asp | Ala | Thr | Thr | Arg | Asn | Leu | Ala | Leu | Glu | Trp | Gly | Thr | Asp |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Tyr | Asp | Ile | Arg | Val | Asn | Gly | Ile | Ala | Pro | Gly | Pro | Ile | Gly | Gly | Thr |
|     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Pro | Gly | Met | Ser | Lys | Leu | Val | Pro | Glu | Glu | Ile | Glu | Asn | Lys | Thr | Arg |
|     |     | 225 |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Glu | Tyr | Met | Pro | Leu | Tyr | Lys | Val | Gly | Glu | Lys | Trp | Asp | Ile | Ala | Met |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Ala | Leu | Tyr | Leu | Ser | Cys | Asp | Ser | Gly | Lys | Tyr | Val | Ser | Gly | Leu |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Met | Val | Val | Asp | Gly | Gly | Leu | Trp | Leu | Ser | Lys | Pro | Arg | His | Leu |



275 280 285  
Pro Lys Glu Ala Val Lys Gln Leu Ser Arg Ala Val Glu Lys Arg Ser  
290 295 300  
Arg Ala Lys Pro Val Gly Leu Pro Thr Ser Lys Leu  
305 310 315

(2) INFORMATION FOR SEQ ID NO:2133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..298
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2133:

Met Glu Ser Pro Phe Lys Pro Asp Val Val Arg Gly Gln Val Ala Leu  
1 5 10 15  
Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Glu Ile Ser Ser Gln Phe  
20 25 30  
Gly Lys His Gly Ala Ser Ile Ala Ile Met Gly Arg Arg Lys Gln Val  
35 40 45  
Leu Asp Asp Ala Val Ser Ala Leu Arg Ser Leu Gly Ile Gln Ala Ile  
50 55 60  
Gly Leu Glu Gly Asp Val Arg Lys Gln Glu Asp Ala Arg Arg Val Val  
65 70 75 80  
Glu Ala Thr Tyr Gln His Phe Gly Lys Leu Asp Ile Leu Val Asn Ala  
85 90 95  
Ala Ala Gly Asn Phe Leu Ala Ala Ala Glu Asp Leu Ser Pro Asn Gly  
100 105 110  
Phe Arg Thr Val Leu Asp Ile Asp Ala Val Gly Thr Phe Asn Met Cys  
115 120 125  
His Ala Ala Leu Lys Tyr Leu Lys Lys Gly Ala Pro Gly Arg Asp Ser  
130 135 140  
Ser Ser Gly Gly Gly Ser Ile Ile Asn Ile Ser Ala Thr Leu His Tyr  
145 150 155 160  
Thr Ala Ser Trp Tyr Gln Ile His Val Ser Ala Ala Lys Ala Ala Val  
165 170 175  
Asp Ala Thr Thr Arg Asn Leu Ala Leu Glu Trp Gly Thr Asp Tyr Asp  
180 185 190  
Ile Arg Val Asn Gly Ile Ala Pro Gly Pro Ile Gly Gly Thr Pro Gly  
195 200 205  
Met Ser Lys Leu Val Pro Glu Glu Ile Glu Asn Lys Thr Arg Glu Tyr  
210 215 220  
Met Pro Leu Tyr Lys Val Gly Glu Lys Trp Asp Ile Ala Met Ala Ala  
225 230 235 240  
Leu Tyr Leu Ser Cys Asp Ser Gly Lys Tyr Val Ser Gly Leu Thr Met  
245 250 255  
Val Val Asp Gly Gly Leu Trp Leu Ser Lys Pro Arg His Leu Pro Lys  
260 265 270  
Glu Ala Val Lys Gln Leu Ser Arg Ala Val Glu Lys Arg Ser Arg Ala  
275 280 285  
Lys Pro Val Gly Leu Pro Thr Ser Lys Leu  
290 295

(2) INFORMATION FOR SEQ ID NO:2134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..257  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571877  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2134:

```
Met Gly Arg Arg Lys Gln Val Leu Asp Asp Ala Val Ser Ala Leu Arg
1 5 10 15
Ser Leu Gly Ile Gln Ala Ile Gly Leu Glu Gly Asp Val Arg Lys Gln
20 25 30
Glu Asp Ala Arg Arg Val Val Glu Ala Thr Tyr Gln His Phe Gly Lys
35 40 45
Leu Asp Ile Leu Val Asn Ala Ala Ala Gly Asn Phe Leu Ala Ala Ala
50 55 60
Glu Asp Leu Ser Pro Asn Gly Phe Arg Thr Val Leu Asp Ile Asp Ala
65 70 75
Val Gly Thr Phe Asn Met Cys His Ala Ala Leu Lys Tyr Leu Lys Lys
85 90 95
Gly Ala Pro Gly Arg Asp Ser Ser Ser Gly Gly Ser Ile Ile Asn
100 105 110
Ile Ser Ala Thr Leu His Tyr Thr Ala Ser Trp Tyr Gln Ile His Val
115 120 125
Ser Ala Ala Lys Ala Ala Val Asp Ala Thr Thr Arg Asn Leu Ala Leu
130 135 140
Glu Trp Gly Thr Asp Tyr Asp Ile Arg Val Asn Gly Ile Ala Pro Gly
145 150 155
Pro Ile Gly Gly Thr Pro Gly Met Ser Lys Leu Val Pro Glu Glu Ile
165 170 175
Glu Asn Lys Thr Arg Glu Tyr Met Pro Leu Tyr Lys Val Gly Glu Lys
180 185 190
Trp Asp Ile Ala Met Ala Ala Leu Tyr Leu Ser Cys Asp Ser Gly Lys
195 200 205
Tyr Val Ser Gly Leu Thr Met Val Val Asp Gly Gly Leu Trp Leu Ser
210 215 220
Lys Pro Arg His Leu Pro Lys Glu Ala Val Lys Gln Leu Ser Arg Ala
225 230 235
Val Glu Lys Arg Ser Arg Ala Lys Pro Val Gly Leu Pro Thr Ser Lys
245 250 255
Leu
```

(2) INFORMATION FOR SEQ ID NO:2135:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1253 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1253  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2135:

```
gaaacataat ttctaagtgc tcaattttct tttggtctct ccaaaactctc tccccggaac 60
gatgtgctta tacagaagag cattcgtttg ttttcaacca gcccttattt gacacttggc 120
actaggggta agaaaaattt gccggccggc tgcaaaattg gagatgttct tttgtttgac 180
ccgaccaagg aagagatagt cacggccccg gacaaaacaa ttcccgaaga gctcatggat 240
gaagaaatga tgggagcttc coattggatg ggatttttct gtgaccggag tgatcgttcc 300
gtacgtatca gcgacatttt caatcctttg gcatccaaaa caaacctgtc catgatcttc 360
ctgcctaggc ttacgggtct gcccaactggc caaacccgaaa aagtttttaa cgtagaccatg 420
tccttctctt ctctctctgg tgagggaagac tgtgtagtgg ctatcaagtt ttccggatgc 480
cagctgagtc tgtgcagacc cggttgtgac cttagtgga ctaacattgt aaccctttc 540
```

|             |             |            |            |             |             |      |
|-------------|-------------|------------|------------|-------------|-------------|------|
| aactgttttg  | acaactcaag  | tctcatgtat | tccaaaagag | acccaaaaatt | ttacttacct  | 600  |
| gccccctggag | gcaactactat | gttctctact | gacctccact | tcaaatcaga  | tgactccccct | 660  |
| gggctccatg  | agttgttcta  | tcgagaccat | ccagtggtgg | atcagtcaga  | gtggagctt   | 720  |
| ttgagttcat  | gttcaggagc  | ggaataccct | gtggagtcac | cttcgtgtgg  | tgaccgtttT  | 780  |
| cctagtcaaa  | tggtatgcgc  | ttggtctttt | tttcgtTcaa | attttaaaagg | aactctacc   | 840  |
| aaaacaaaga  | ggttgatgg   | ttttagagaa | gaggagacga | cggagagaaa  | aattatgtgt  | 900  |
| tacaccgagg  | acattggaga  | catgtgcatt | ttccttgcaa | gcaacgaggc  | ttctgtatc   | 960  |
| ccgcttagct  | cctgcctcgg  | cctcaagcct | aactgcgtct | attatatggg  | acgtgggttt  | 1020 |
| gggttttacc  | atctcactac  | cggagaggca | catcattata | aagctcccaa  | aggtgcacca  | 1080 |
| agcgctctga  | ccgccccotta | ctggcttctc | ccatttgcta | tctagtata   | ctatttctgt  | 1140 |
| ctttgtgtac  | acttgaagtt  | tctctctacc | ggtttaaatt | ggtaacacct  | aaagattggt  | 1200 |
| aatgttctaa  | gttcaatttt  | aagttaaaac | atccagacc  | agaatcccg   | ctt         |      |

(2) INFORMATION FOR SEQ ID NO:2136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..369

(D) OTHER INFORMATION: / Ceres Seq. ID 1571885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2136:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gln | Phe | Leu | Phe | Gly | Leu | Ser | Lys | Leu | Ser | Pro | Arg | Asn | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Leu | Ile | Gln | Lys | Ser | Ile | Arg | Leu | Phe | Ser | Thr | Ser | Pro | Tyr | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Leu | Gly | Thr | Arg | Val | Lys | Lys | Ile | Leu | Pro | Ala | Gly | Cys | Lys | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Asp | Val | Leu | Leu | Phe | Asp | Pro | Thr | Lys | Glu | Glu | Ile | Val | Thr | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Asp | Lys | Thr | Ile | Pro | Glu | Glu | Leu | Met | Asp | Glu | Glu | Met | Met | Gly |
|     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Ser | His | Gly | Trp | Gly | Phe | Phe | Cys | Asp | Arg | Thr | Asp | Arg | Ser | Val |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Ile | Ser | Asp | Ile | Phe | Asn | Pro | Leu | Ala | Ser | Lys | Thr | Asn | Pro | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Met | Ile | Pro | Leu | Pro | Arg | Leu | Thr | Ala | Leu | Pro | Thr | Gly | Gln | Thr | Glu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Val | Phe | Asn | Val | Ala | Met | Ser | Phe | Ser | Ser | Pro | Leu | Gly | Glu | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Cys | Val | Val | Ala | Ile | Lys | Phe | Ser | Gly | Ile | Gln | Leu | Ser | Leu | Cys |
|     | 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |
| Arg | Pro | Gly | Cys | Asp | Leu | Glu | Trp | Thr | Asn | Ile | Val | Thr | Pro | Phe | Asn |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Cys | Leu | Asp | Asn | Ser | Ser | Leu | Met | Tyr | Ser | Lys | Arg | Asp | Gln | Lys | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Tyr | Leu | Pro | Ala | Pro | Gly | Gly | Asn | Tyr | Leu | Phe | Ser | Tyr | Asp | Leu | His |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Phe | Lys | Ser | Asp | Asp | Ser | Pro | Gly | Leu | His | Glu | Leu | Phe | Tyr | Arg | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| His | Pro | Val | Leu | Asp | Gln | Ser | Glu | Trp | Glu | Leu | Leu | Ser | Ser | Cys | Ser |
|     | 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |
| Arg | Thr | Glu | Tyr | Leu | Val | Glu | Ser | Pro | Ser | Gly | Gly | Asp | Arg | Phe | Pro |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ser | Gln | Met | Val | Cys | Ala | Trp | Leu | Leu | Phe | Arg | Ser | Asn | Leu | Lys | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ile | Tyr | His | Lys | Thr | Lys | Arg | Leu | Met | Val | Phe | Arg | Glu | Glu | Glu | Thr |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Thr | Glu | Gly | Lys | Ile | Met | Cys | Tyr | Thr | Glu | Asp | Ile | Gly | Asp | Met | Cys |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 290                                                             | 295 | 300 |
| Ile Phe Leu Ala Ser Asn Glu Ala Phe Cys Ile Pro Ala Ser Ser Cys |     |     |
| 305                                                             | 310 | 315 |
| Leu Gly Leu Lys Pro Asn Cys Val Tyr Tyr Met Gly Arg Gly Phe Gly |     |     |
|                                                                 | 325 | 330 |
| Phe Tyr Asp Leu Thr Thr Gly Glu Ala His His Tyr Lys Ala Pro Lys |     |     |
|                                                                 | 340 | 345 |
| Gly Ala Pro Ser Ala Leu Thr Ala Pro Tyr Trp Leu Pro Pro Phe Ala |     |     |
|                                                                 | 355 | 360 |
|                                                                 |     | 365 |
| Ile                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:2137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..296

- (D) OTHER INFORMATION: / Ceres Seq. ID 1571886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2137:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Asp Glu Glu Met Met Gly Ala Ser His Gly Trp Gly Phe Phe Cys |     |
| 1                                                               | 5   |
| Asp Arg Thr Asp Arg Ser Val Arg Ile Ser Asp Ile Phe Asn Pro Leu | 15  |
|                                                                 | 20  |
| Ala Ser Lys Thr Asn Pro Val Met Ile Pro Leu Pro Arg Leu Thr Ala | 30  |
|                                                                 | 35  |
| Leu Pro Thr Gly Gln Thr Glu Lys Val Phe Asn Val Ala Met Ser Phe | 45  |
|                                                                 | 50  |
| Ser Ser Pro Leu Gly Glu Asp Cys Val Val Ala Ile Lys Phe Ser     | 60  |
|                                                                 | 65  |
| Gly Ile Gln Leu Ser Leu Cys Arg Pro Gly Cys Asp Leu Glu Trp Thr | 75  |
|                                                                 | 80  |
| Asn Ile Val Thr Pro Phe Asn Cys Leu Asp Asn Ser Ser Leu Met Tyr | 85  |
|                                                                 | 90  |
| Ser Lys Arg Asp Gln Lys Phe Tyr Leu Pro Ala Pro Gly Gly Asn Tyr | 95  |
|                                                                 | 100 |
| Leu Phe Ser Tyr Asp Leu His Phe Lys Ser Asp Asp Ser Pro Gly Leu | 105 |
|                                                                 | 110 |
| His Glu Leu Phe Tyr Arg Asp His Pro Val Leu Asp Gln Ser Glu Trp | 115 |
|                                                                 | 120 |
| Glu Leu Leu Ser Ser Cys Ser Arg Thr Glu Tyr Leu Val Glu Ser Pro | 125 |
|                                                                 | 130 |
| Ser Gly Gly Asp Arg Phe Pro Ser Gln Met Val Cys Ala Trp Leu Leu | 135 |
|                                                                 | 140 |
| Phe Arg Ser Asn Leu Lys Gly Ile Tyr His Lys Thr Lys Arg Leu Met | 145 |
|                                                                 | 150 |
| Val Phe Arg Glu Glu Glu Thr Thr Glu Gly Lys Ile Met Cys Tyr Thr | 155 |
|                                                                 | 160 |
| Glu Asp Ile Gly Asp Met Cys Ile Phe Leu Ala Ser Asn Glu Ala Phe | 165 |
|                                                                 | 170 |
| Cys Ile Pro Ala Ser Ser Cys Leu Gly Leu Lys Pro Asn Cys Val Tyr | 175 |
|                                                                 | 180 |
| Tyr Met Gly Arg Gly Phe Gly Phe Tyr Asp Leu Thr Thr Gly Glu Ala | 185 |
|                                                                 | 190 |
| His His Tyr Lys Ala Pro Lys Gly Ala Pro Ser Ala Leu Thr Ala Pro | 195 |
|                                                                 | 200 |
| Tyr Trp Leu Pro Pro Phe Ala Ile                                 | 205 |
|                                                                 | 210 |
|                                                                 | 215 |
|                                                                 | 220 |
|                                                                 | 225 |
|                                                                 | 230 |
|                                                                 | 235 |
|                                                                 | 240 |
|                                                                 | 245 |
|                                                                 | 250 |
|                                                                 | 255 |
|                                                                 | 260 |
|                                                                 | 265 |
|                                                                 | 270 |
|                                                                 | 275 |
|                                                                 | 280 |
|                                                                 | 285 |
|                                                                 | 290 |
|                                                                 | 295 |

(2) INFORMATION FOR SEQ ID NO:2138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..292

(D) OTHER INFORMATION: / Ceres Seq. ID 1571887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2138:

Met Met Gly Ala Ser His Gly Trp Gly Phe Phe Cys Asp Arg Thr Asp  
1 5 10 15  
Arg Ser Val Arg Ile Ser Asp Ile Phe Asn Pro Leu Ala Ser Lys Thr  
20 25 30  
Asn Pro Val Met Ile Pro Leu Pro Arg Leu Thr Ala Leu Pro Thr Gly  
35 40 45  
Gln Thr Gly Lys Val Phe Asn Val Ala Met Ser Phe Ser Ser Pro Leu  
50 55 60  
Gly Glu Glu Asp Cys Val Val Ala Ile Lys Phe Ser Gly Ile Gln Leu  
65 70 75 80  
Ser Leu Cys Arg Pro Gly Cys Asp Leu Glu Trp Thr Asn Ile Val Thr  
85 90 95  
Pro Phe Asn Cys Leu Asp Asn Ser Ser Leu Met Tyr Ser Lys Arg Asp  
100 105 110  
Gln Lys Phe Tyr Leu Pro Ala Pro Gly Gly Asn Tyr Leu Phe Ser Tyr  
115 120 125  
Asp Leu His Phe Lys Ser Asp Asp Ser Pro Gly Leu His Glu Leu Phe  
130 135 140  
Tyr Arg Asp His Pro Val Leu Asp Gln Ser Glu Trp Glu Leu Leu Ser  
145 150 155 160  
Ser Cys Ser Arg Thr Glu Tyr Leu Val Glu Ser Pro Ser Gly Gly Asp  
165 170 175  
Arg Phe Pro Ser Gln Met Val Cys Ala Trp Leu Leu Phe Arg Ser Asn  
180 185 190  
Leu Lys Gly Ile Tyr His Lys Thr Lys Arg Leu Met Val Phe Arg Glu  
195 200 205  
Glu Glu Thr Thr Glu Gly Lys Ile Met Cys Tyr Thr Glu Asp Ile Gly  
210 215 220  
Asp Met Cys Ile Phe Leu Ala Ser Asn Glu Ala Phe Cys Ile Pro Ala  
225 230 235 240  
Ser Ser Cys Leu Gly Leu Lys Pro Asn Cys Val Tyr Tyr Met Gly Arg  
245 250 255  
Gly Phe Gly Phe Tyr Asp Leu Thr Thr Gly Glu Ala His His Tyr Lys  
260 265 270  
Ala Pro Lys Gly Ala Pro Ser Ala Leu Thr Ala Pro Tyr Trp Leu Pro  
275 280 285  
Pro Phe Ala Ile  
290

(2) INFORMATION FOR SEQ ID NO:2139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1312

(D) OTHER INFORMATION: / Ceres Seq. ID 1571888

| (X1)        | SEQUENCE    | DESCRIPTION | SEQ         |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| actctataaca | cacacactct  | caggagagaa  | gtgtatttga  | tgtctctctc  | tttccataaa  | 60   |
| caacactgatt | attttctctc  | cgacgcgcgc  | atgtctctgc  | tctcagatct  | tttcaactcc  | 120  |
| aacctccacog | atgccaccgg  | gaaatcatc   | ccggaataca  | taaggctcgg  | tggatctgga  | 180  |
| atggtatata  | gaagcaaacg  | caggacacta  | ccaggaccag  | tgaactgacc  | atcaagaatt  | 240  |
| cccaagtatca | actacgacgg  | atccagacc   | ggtagcctgt  | ctggagaaga  | caaggaagtc  | 300  |
| attctatacc  | ctcaggcaat  | attcaaggat  | cccttcagga  | aaggccaacaa | catctctTggt | 360  |
| gagtgtgtg   | gottcaacac  | cagctgtgtg  | ctctattcca  | acccaacaaa  | gcgcacaacgc | 420  |
| tgttaagatc  | ttcagccacc  | ccgacgttgc  | caaggaggag  | ctcttggtat  | ggatttgagca | 480  |
| agcaataact  | ttgatcaaa   | aggatgtgaa  | ctgcgaattc  | gggtggccctg | tgtgggtgcta | 540  |
| ccctgcgccct | cagggaacatt | actactgtgt  | tgtggcaggt  | gacaaagcca  | ttggtctgta  | 600  |
| cattgtggat  | gtcactaact  | aggcctctgt  | ttaacgcgcct | attgttgatt  | cttggtataca | 660  |
| tggagaagtc  | atgcaccggc  | agtgggagtt  | ccaagtctgc  | ctctgttgaag | tttattgctc  | 720  |
| tgggtatcaa  | ctctgggttg  | ctcgataact  | ctctcgagag  | atactagaat  | tctctgtgtg  | 780  |
| aattgtctagc | ttcgaccgca  | aaccagtcct  | gggtgactgg  | aatggagctg  | gagctcagct  | 840  |
| caactacacg  | ataagacaaa  | tgagaaacga  | tgaggagata  | gaagtgatca  | agaaacagac  | 900  |
| agggaagctt  | Tcagctgaaa  | caacaaagac  | acattctctc  | tacoggtgaa  | ggaacacgac  | 960  |
| ctgctctcac  | tggaaagcac  | gaaacccagc  | acaatcacac  | attctctgtg  | ggagctcgga  | 1020 |
| acogtctgagc | ctcagtgtag  | ctgggacgtg  | acacagagaa  | ggaaggtgaa  | ggagtaactg  | 1080 |
| aagacagaga  | gccagctctc  | aacatcgatc  | cttactgtgt  | caacctcaat  | atcgctgagta | 1140 |
| gcaccatact  | cggttgatga  | acacatttct  | cttgattatt  | ctctccaatt  | tgtgtttgtt  | 1200 |
| tttttccctt  | gtgattgcac  | ttttcgaata  | taaaaaataa  | attcttataa  | tgcggtattgt | 1260 |
| tttgtacatt  | ttgtttattg  | tttcgaataa  | taaaataagc  | ctctcttaag  | gt          |      |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
MOLECULE TYPE: peptide

MOLECULE TYPE: peptid  
FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..195

(D) OTHER INFORMATION: / Ceres Seq. ID 1571889

[illegible]

(2) INFORMATION FOR SEQ ID NO:2141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2141:

```
Met Gln Lys Asp Val Asn Trp Pro Ile Gly Trp Pro Val Gly Gly Tyr
1 5 10 15
Pro Gly Pro Gln Gly Pro Tyr Tyr Cys Gly Val Gly Ala Asp Lys Ala
20 25 30
Ile Gly Arg Asp Ile Val Asp Ala His Tyr Lys Ala Cys Leu Tyr Ala
35 40 45
Gly Ile Gly Ile Ser Gly Ile Asn Gly Glu Val Met Pro Gly Gln Trp
50 55 60
Glu Phe Gln Val Gly Pro Val Glu Gly Ile Ser Ser Gly Asp Gln Val
65 70 75 80
Trp Val Ala Arg Tyr Leu Leu Glu Arg Ile Thr Glu Ile Ser Gly Val
85 90 95
Ile Val Ser Phe Asp Pro Lys Pro Val Pro Gly Asp Trp Asn Gly Ala
100 105 110
Gly Ala His Cys Asn Tyr Ser Thr Lys Thr Met Arg Asn Asp Gly Gly
115 120 125
Leu Glu Val Ile Lys Lys Ala Ile Gly Lys Leu Ser Ala Glu Thr Gln
130 135 140
Arg Thr His Cys Cys Leu Arg
145 150
```

(2) INFORMATION FOR SEQ ID NO:2142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..657
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2142:

```
ggtggggacca aaggaggagg ccatggggggc cttgacattg atgagctcat gaaacacagg 60
aaaggaggag gagggaggtaa caaggGcaat cataatcata gcgcctaaagg gattgtgggt 120
ggcccaatgg gtccaggcggg tccgatgggt ccaggcggctc cgatgggtca agtggtgccg 180
atgggtatga tgggtccagg tggtcgatg agtatgatgg gtccaggcgg tccatgggt 240
ccaatgggtg gccaaaggcgg ctcttaccoca gcggttcaag gcttgccaat gagtgagggt 300
ggaggatatt atccaggggc gcctcaggca agtcagcaaa tgaaccaaca acaatatatg 360
caaatgatga tgaaccaaca gcagcaacaa caacaacaac aacaagctgc agctcatggt 420
ggctatggcg gtggtcaagg tggcgacatg taccatcoga tgatgtacgc tcggccttat 480
cctgcagtta attatgtcca cctccacca atgcgcgctc ctoactcgga ttcttatact 540
catatgttca gcgatgagaa tccaggtagt tgtagtatta tgtgatcctc ttttgtaatg 600
ttatttagaa tatggacatg tatgcttgct ttagtcttat gttttttttt tttgggg
```

(2) INFORMATION FOR SEQ ID NO:2143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..194

(D) OTHER INFORMATION: / Ceres Seq. ID 1571892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2143:

Gly Gly Thr Lys Gly Gly Gly His Gly Gly Leu Asp Ile Asp Glu Leu  
1 5 10 15  
Met Lys His Ser Lys Gly Gly Gly Gly Asn Lys Gly Asn His Asn  
20 25 30  
His Ser Ala Lys Gly Ile Gly Gly Gly Pro Met Gly Pro Gly Gly Pro  
35 40 45  
Met Gly Pro Gly Gly Pro Met Gly Gln Gly Gly Pro Met Gly Met Met  
50 55 60  
Gly Pro Gly Gly Pro Met Ser Met Met Gly Pro Gly Gly Pro Met Gly  
65 70 75 80  
Pro Met Gly Gly Gln Gly Gly Ser Tyr Pro Ala Val Gln Gly Leu Pro  
85 90 95  
Met Ser Gly Gly Gly Gly Tyr Tyr Pro Gly Pro Pro Gln Ala Ser Gln  
100 105 110  
Gln Met Asn Gln Gln Gln Tyr Met Gln Met Met Met Asn Gln Gln Gln  
115 120 125  
Gln Gln Gln Gln Gln Gln Ala Ala Ala His Gly Gly Tyr Gly Gly  
130 135 140  
Gly His Gly Gly Asp Met Tyr His Pro Met Met Tyr Ala Arg Pro Tyr  
145 150 155 160  
Pro Ala Val Asn Tyr Ala His Pro Pro Pro Met Pro Pro Pro His Ser  
165 170 175  
Asp Ser Tyr Thr His Met Phe Ser Asp Glu Asn Pro Gly Ser Cys Ser  
180 185 190  
Ile Met

(2) INFORMATION FOR SEQ ID NO:2144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1571893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2144:

Met Lys His Ser Lys Gly Gly Gly Gly Gly Asn Lys Gly Asn His Asn  
1 5 10 15  
His Ser Ala Lys Gly Ile Gly Gly Gly Pro Met Gly Pro Gly Gly Pro  
20 25 30  
Met Gly Pro Gly Gly Pro Met Gly Gln Gly Gly Pro Met Gly Met Met  
35 40 45  
Gly Pro Gly Gly Pro Met Ser Met Met Gly Pro Gly Gly Pro Met Gly  
50 55 60  
Pro Met Gly Gly Gln Gly Gly Ser Tyr Pro Ala Val Gln Gly Leu Pro  
65 70 75 80  
Met Ser Gly Gly Gly Gly Tyr Tyr Pro Gly Pro Pro Gln Ala Ser Gln  
85 90 95  
Gln Met Asn Gln Gln Gln Tyr Met Gln Met Met Met Asn Gln Gln Gln  
100 105 110  
Gln Gln Gln Gln Gln Gln Ala Ala Ala His Gly Gly Tyr Gly Gly  
115 120 125  
Gly His Gly Gly Asp Met Tyr His Pro Met Met Tyr Ala Arg Pro Tyr



130 135 140  
Pro Ala Val Asn Tyr Ala His Pro Pro Pro Met Pro Pro Pro His Ser  
145 150 155 160  
Asp Ser Tyr Thr His Met Phe Ser Asp Glu Asn Pro Gly Ser Cys Ser  
165 170 175  
Ile Met

(2) INFORMATION FOR SEQ ID NO:2145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..152  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2145:

Met Gly Pro Gly Gly Pro Met Gly Pro Gly Gly Pro Met Gly Gln Gly  
1 5 10 15  
Gly Pro Met Gly Met Met Gly Pro Gly Gly Pro Met Ser Met Met Gly  
20 25 30  
Pro Gly Gly Pro Met Gly Pro Met Gly Gly Gln Gly Gly Ser Tyr Pro  
35 40 45  
Ala Val Gln Gly Leu Pro Met Ser Gly Gly Gly Gly Tyr Tyr Pro Gly  
50 55 60  
Pro Pro Gln Ala Ser Gln Gln Met Asn Gln Gln Gln Tyr Met Gln Met  
65 70 75 80  
Met Met Asn Gln Gln Gln Gln Gln Gln Gln Gln Ala Ala Ala  
85 90 95  
His Gly Gly Tyr Gly Gly Gly His Gly Gly Asp Met Tyr His Pro Met  
100 105 110  
Met Tyr Ala Arg Pro Tyr Pro Ala Val Asn Tyr Ala His Pro Pro Pro  
115 120 125  
Met Pro Pro Pro His Ser Asp Ser Tyr Thr His Met Phe Ser Asp Glu  
130 135 140  
Asn Pro Gly Ser Cys Ser Ile Met  
145 150

(2) INFORMATION FOR SEQ ID NO:2146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 982 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..982  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2146:

aaagcccaaa tgttgcctcaa ggcctctccc gctctctctc tcttgagctc cggctccacc 60  
ggcggtgGaa atctgtttcc tccgtcgaga aattcgtcga atcgtctggt ttctccgagt 120  
ggatctaagt ttctgtttca ggcggcgaaa ggaacgaaca cgaagtctgt aaccggagt 180  
gtattcgaac cttttgagga agtgaagaaa gaactggacc tcgttcccac tacccctttt 240  
gtttctctcg ctgcgccaca gtctctccgac gatgctgaat ctgcacatcaa cgatcagatc 300  
aacgtggagt acaacgtctc gtatgtctac catgccctgt atgcctactt tgacagagac 360  
aatgtcggtc tgaagggttt cgcgaagttt tttaacgatt cgagtcttga agaacgaggt 420  
atctcgaga tgtttatgga gtatcagaac aagcgtgggt ggagagtga gctcgaagtc 480  
attttgatgc ccgtctctga gtttgatcac gaggagaagg gagatgcatt gcatgcgatg 540  
gagcttgcac tgtcttttga gaaacttaca aatgaaaagc tcttgaagtt acaaaagtgt 600

(2) INFORMATION FOR SEQ ID NO:2147:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1571899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2147:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ala | Gln | Met | Leu | Leu | Lys | Ala | Ser | Pro | Ala | Leu | Ser | Leu | Leu | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Gly | Ser | Thr | Gly | Gly | Gly | Asn | Leu | Phe | Pro | Pro | Ser | Arg | Asn | Ser |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ser | Asn | Arg | Leu | Phe | Ser | Pro | Ser | Gly | Ser | Lys | Phe | Ser | Val | Gln | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Lys | Gly | Thr | Asn | Thr | Lys | Ser | Leu | Thr | Gly | Val | Val | Phe | Glu | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Glu | Glu | Val | Lys | Lys | Glu | Leu | Asp | Leu | Val | Pro | Thr | Thr | Pro | Phe |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Val | Ser | Leu | Ala | Arg | His | Lys | Phe | Ser | Asp | Asp | Ala | Glu | Ser | Ala | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Asp | Gln | Ile | Asn | Val | Glu | Tyr | Asn | Val | Ser | Tyr | Val | Tyr | His | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Tyr | Ala | Tyr | Phe | Asp | Arg | Asp | Asn | Val | Gly | Leu | Lys | Gly | Phe | Ala |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Phe | Phe | Asn | Asp | Ser | Ser | Leu | Glu | Glu | Arg | Gly | His | Ala | Glu | Met |
|     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Phe | Met | Glu | Tyr | Gln | Asn | Lys | Arg | Gly | Gly | Arg | Val | Lys | Leu | Gln | Ser |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Ile | Leu | Met | Pro | Val | Ser | Glu | Phe | Asp | His | Glu | Glu | Lys | Gly | Asp | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | His | Ala | Met | Glu | Leu | Ala | Leu | Ser | Leu | Glu | Lys | Leu | Thr | Asn | Glu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Leu | Leu | Lys | Leu | Gln | Ser | Val | Gly | Val | Lys | Asn | Asn | Asp | Val | Gln |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Val | Asp | Phe | Val | Glu | Ser | Glu | Phe | Leu | Gly | Glu | Gln | Val | Glu | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Lys | Lys | Ile | Ser | Glu | Tyr | Val | Ala | Gln | Leu | Arg | Arg | Ile | Gly | Lys |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Gly | His | Gly | Val | Trp | His | Phe | Asp | Gln | Met | Leu | Leu | Asn | Asp | Glu | Val |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |

(2) INFORMATION FOR SEQ ID NO:2148:

(i) SEQUENCE CHARACTERISTICS:

{A} LENGTH: 253 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..253  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2148:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Leu | Lys | Ala | Ser | Pro | Ala | Leu | Ser | Leu | Leu | Ser | Ser | Gly | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Thr | Gly | Gly | Gly | Asn | Leu | Phe | Pro | Pro | Ser | Arg | Asn | Ser | Ser | Asn | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Leu | Phe | Ser | Pro | Ser | Gly | Ser | Lys | Phe | Ser | Val | Gln | Ala | Ala | Lys | Gly |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Thr | Asn | Thr | Lys | Ser | Leu | Thr | Gly | Val | Val | Phe | Glu | Pro | Phe | Glu | Glu |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Val | Lys | Lys | Glu | Leu | Asp | Leu | Val | Pro | Thr | Thr | Pro | Phe | Val | Ser | Leu |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     |     | 80  |     |
| Ala | Arg | His | Lys | Phe | Ser | Asp | Asp | Ala | Glu | Ser | Ala | Ile | Asn | Asp | Gln |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ile | Asn | Val | Glu | Tyr | Asn | Val | Ser | Tyr | Val | Tyr | His | Ala | Leu | Tyr | Ala |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Tyr | Phe | Asp | Arg | Asp | Asn | Val | Gly | Leu | Lys | Gly | Phe | Ala | Lys | Phe | Phe |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Asn | Asp | Ser | Ser | Leu | Glu | Glu | Arg | Gly | His | Ala | Glu | Met | Phe | Met | Glu |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Tyr | Gln | Asn | Lys | Arg | Gly | Gly | Arg | Val | Lys | Leu | Gln | Ser | Ile | Leu | Met |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Pro | Val | Ser | Glu | Phe | Asp | His | Glu | Glu | Lys | Gly | Asp | Ala | Leu | His | Ala |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Met | Glu | Leu | Ala | Leu | Ser | Leu | Glu | Lys | Leu | Thr | Asn | Glu | Lys | Leu | Leu |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Lys | Leu | Gln | Ser | Val | Gly | Val | Lys | Asn | Asn | Asp | Val | Gln | Leu | Val | Asp |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Phe | Val | Glu | Ser | Glu | Phe | Leu | Gly | Glu | Gln | Val | Glu | Ala | Ile | Lys | Lys |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ile | Ser | Glu | Tyr | Val | Ala | Gln | Leu | Arg | Arg | Ile | Gly | Lys | Gly | His | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Val | Trp | His | Phe | Asp | Gln | Met | Leu | Leu | Asn | Asp | Glu | Val |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1275 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..1275  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2149:

|             |             |             |             |            |            |     |
|-------------|-------------|-------------|-------------|------------|------------|-----|
| aaacaagata  | caacacaatt  | ggaatctttc  | ttctttgaca  | aaaaaaaaag | gaatctctct | 60  |
| ctttctctga  | ttctctcatg  | ttcatgcaac  | aagaaacgtc  | tcacatgacg | gcggctccac | 120 |
| agaccaacgg  | ccatcaaatc  | ttccctgaga  | ttgacatgtc  | cgccggcgat | ttctctctca | 180 |
| tcgtacgagc  | tacagtgcgc  | caagcctcta  | cagtcttcta  | cgatactccc | gccacgtcga | 240 |
| ataaggcaga  | gagactgctt  | tctgaggcag  | cggagaatgg  | atctcagcta | gtgggtgtcc | 300 |
| cggaggcttt  | catcgggtga  | tatccacgtg  | gctctacctt  | tgaattggct | attggtttct | 360 |
| gtaccgcgtaa | agggacgagat | gactttcgca  | agtaccatgc  | ttctgcacct | gatgttctgc | 420 |
| gccctgaagt  | ggaacgaNtt  | agcgtaaatg  | gccaaagaagt | acaaagtata | cttggttatg | 480 |
| ggtgtgatag  | agaggggaag  | ctacacgccta | tactgcacgc  | ttctttttct | cgattcacaa | 540 |
| ggtctgttct  | taggtaagca  | ccgcaaaactc | atgcctacag  | ctcttgaacg | ttgcatttgg | 600 |
| ggatttggag  | atggatacaac | catccctgtg  | ttcgatactc  | ctattgggaa | aatcggtgct | 660 |
| gctattttgt  | gggaaaaatag | gatgccttct  | ttgagaacgc  | caatgtatgc | caaaaggcat | 720 |
| gagatttatt  | gtgcacctac  | tgctgattca  | agagaaactt  | ggctagcatc | aatgactcat | 780 |

|            |            |            |            |            |             |      |
|------------|------------|------------|------------|------------|-------------|------|
| attgcacttg | agggtggatg | ttttgttttg | tcagctaacc | agttttgtcg | tcggaaagac  | 840  |
| tatcctcttc | cgccggaata | catgttttcc | ggttcagaag | agagcctaac | accggactct  | 900  |
| gttgtctgcg | ctcttggaag | ctctatcatt | tcacctttgg | gaattgtttt | agctggacca  | 960  |
| aactatagag | gagaagctct | tatcacagct | gatctagatc | ttggggacat | agcacgagcc  | 1020 |
| aagtttgatt | ttgatgtggg | cggaatttac | tcgaggcctg | aagtgtttag | cttgaacata  | 1080 |
| agggagcatt | cgagaaaaag | ggtcagcttc | aagacgtcaa | aggtaatgga | agatgaatcc  | 1140 |
| gtctaacaaa | tgatcatttg | ttagacccaa | actttctctg | taatttgatg | aagtttatct  | 1200 |
| gtagttaact | tcaagacttg | tgttgtaatt | gaaatcgata | aaaaatccaa | accggttagat | 1260 |
| tgagtgttgt | cttct      |            |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:2150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..255

(D) OTHER INFORMATION: / Ceres Seq. ID 1571906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2150:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Phe | Ala | Ser | Thr | Met | Leu | Leu | Pro | Leu | Met | Phe | Leu | Ala | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Lys | Trp | Asn | Xaa | Leu | Ala | Leu | Met | Ala | Lys | Lys | Tyr | Lys | Val | Tyr | Leu |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Met | Gly | Val | Ile | Glu | Arg | Glu | Gly | Tyr | Thr | Leu | Tyr | Cys | Thr | Val |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Leu | Phe | Phe | Asp | Ser | Gln | Gly | Leu | Phe | Leu | Gly | Lys | His | Arg | Lys | Leu |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Met | Pro | Thr | Ala | Leu | Glu | Arg | Cys | Ile | Trp | Gly | Phe | Gly | Asp | Gly | Ser |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |
| Thr | Ile | Pro | Val | Phe | Asp | Thr | Pro | Ile | Gly | Lys | Ile | Gly | Ala | Ala | Ile |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Cys | Trp | Glu | Asn | Arg | Met | Pro | Ser | Leu | Arg | Thr | Ala | Met | Tyr | Ala | Lys |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Ile | Glu | Ile | Tyr | Cys | Ala | Pro | Thr | Ala | Asp | Ser | Arg | Glu | Thr | Trp |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Leu | Ala | Ser | Met | Thr | His | Ile | Ala | Leu | Glu | Gly | Gly | Cys | Phe | Val | Leu |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |
| Ser | Ala | Asn | Gln | Phe | Cys | Arg | Arg | Lys | Asp | Trp | Pro | Ser | Pro | Pro | Glu |
|     |     |     |     | 145 |     |     |     | 150 |     |     |     |     | 155 |     | 160 |
| Tyr | Met | Phe | Ser | Gly | Ser | Glu | Glu | Ser | Leu | Thr | Pro | Asp | Ser | Val | Val |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Cys | Ala | Gly | Gly | Ser | Ser | Ile | Ile | Ser | Pro | Leu | Gly | Ile | Val | Leu | Ala |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Pro | Asn | Tyr | Arg | Gly | Glu | Ala | Leu | Ile | Thr | Ala | Asp | Leu | Asp | Leu |
|     |     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Gly | Asp | Ile | Ala | Arg | Ala | Lys | Phe | Asp | Phe | Asp | Val | Val | Gly | His | Tyr |
|     |     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |
| Ser | Arg | Pro | Glu | Val | Phe | Ser | Leu | Asn | Ile | Arg | Glu | His | Pro | Arg | Lys |
|     |     |     |     | 225 |     |     |     | 230 |     |     |     |     | 235 |     | 240 |
| Ala | Val | Ser | Phe | Lys | Thr | Ser | Lys | Val | Met | Glu | Asp | Glu | Ser | Val |     |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     | 255 |     |     |

(2) INFORMATION FOR SEQ ID NO:2151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..249  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2151:

```
Met Leu Leu Pro Leu Met Phe Leu Ala Leu Lys Trp Asn Xaa Leu Ala
1 5 10 15
Leu Met Ala Lys Lys Tyr Lys Val Tyr Leu Val Met Gly Val Ile Glu
20 25 30
Arg Glu Gly Tyr Thr Leu Tyr Cys Thr Val Leu Phe Phe Asp Ser Gln
35 40 45
Gly Leu Phe Leu Gly Lys His Arg Lys Leu Met Pro Thr Ala Leu Glu
50 55 60
Arg Cys Ile Trp Gly Phe Gly Asp Gly Ser Thr Ile Pro Val Phe Asp
65 70 75 80
Thr Pro Ile Gly Lys Ile Gly Ala Ala Ile Cys Trp Glu Asn Arg Met
85 90 95
Pro Ser Leu Arg Thr Ala Met Tyr Ala Lys Gly Ile Glu Ile Tyr Cys
100 105 110
Ala Pro Thr Ala Asp Ser Arg Glu Thr Trp Leu Ala Ser Met Thr His
115 120 125
Ile Ala Leu Glu Gly Gly Cys Phe Val Leu Ser Ala Asn Gln Phe Cys
130 135 140
Arg Arg Lys Asp Tyr Pro Ser Pro Pro Glu Tyr Met Phe Ser Gly Ser
145 150 155 160
Glu Glu Ser Leu Thr Pro Asp Ser Val Val Cys Ala Gly Gly Ser Ser
165 170 175
Ile Ile Ser Pro Leu Gly Ile Val Leu Ala Gly Pro Asn Tyr Arg Gly
180 185 190
Glu Ala Leu Ile Thr Ala Asp Leu Asp Leu Gly Asp Ile Ala Arg Ala
195 200 205
Lys Phe Asp Phe Asp Val Val Gly His Tyr Ser Arg Pro Glu Val Phe
210 215 220
Ser Leu Asn Ile Arg Glu His Pro Arg Lys Ala Val Ser Phe Lys Thr
225 230 235 240
Ser Lys Val Met Glu Asp Glu Ser Val
245
```

(2) INFORMATION FOR SEQ ID NO:2152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..244  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2152:

```
Met Phe Leu Ala Leu Lys Trp Asn Xaa Leu Ala Leu Met Ala Lys Lys
1 5 10 15
Tyr Lys Val Tyr Leu Val Met Gly Val Ile Glu Arg Glu Gly Tyr Thr
20 25 30
Leu Tyr Cys Thr Val Leu Phe Phe Asp Ser Gln Gly Leu Phe Leu Gly
35 40 45
Lys His Arg Lys Leu Met Pro Thr Ala Leu Glu Arg Cys Ile Trp Gly
50 55 60
Phe Gly Asp Gly Ser Thr Ile Pro Val Phe Asp Thr Pro Ile Gly Lys
65 70 75 80
Ile Gly Ala Ala Ile Cys Trp Glu Asn Arg Met Pro Ser Leu Arg Thr
85 90 95
Ala Met Tyr Ala Lys Gly Ile Glu Ile Tyr Cys Ala Pro Thr Ala Asp
```

(2) INFORMATION FOR SEQ ID NO:2153:

(A) LENGTH: 1280 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

{B} LOCATION: 1..1280

(D) OTHER INFORMATION: / Ceres Seq. ID 1571909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2153:

| (A1) - 5000 |              |             |             |             |             |      |
|-------------|--------------|-------------|-------------|-------------|-------------|------|
| tcaaaaagtc  | ctctctcggt   | caactttctt  | cttggctccc  | acattcaaac  | atcacaactc  | 60   |
| tctgttattt  | ccaaagagaca  | aaaactctgag | aacacacggc  | cgactcgaaa  | atpgaaactt  | 120  |
| ctcgtttttac | ctctctctcggt | ctcctctcgt  | ccctctcctt  | cttctcaact  | ctctcgcgcc  | 180  |
| aaatgacggc  | aaacttcaac   | tgcagtttgg  | caaactcgac  | gtgtcaatct  | ctcgttgattc | 240  |
| actcaagaaa  | gaacgcaaca   | ctgcttgcca  | atattcaaac  | ctcttttgcc  | gtcaagaacc  | 300  |
| tccgctcgat  | ctctcgagctg  | aacaaattcc  | caactcaaac  | ctcacagtga  | caacgctgta  | 360  |
| accgaatca   | agtgctacgt   | gtcccaactc  | attgtctctg  | ctccaatgac  | accggtgttc  | 420  |
| cgaaacggga  | catcgaatcat  | accatcaaga  | aagacagcat  | actctctttc  | gtcgcgaactg | 480  |
| agattttcgt  | tgtgtctcgtt  | acgtcagaga  | agatcagtga  | gtgttaaacaa | atccctgacc  | 540  |
| cgacacaaat  | cgaaatcogtt  | caaaagtctt  | ggatcccttt  | gcctgttagc  | tgtgtataaat | 600  |
| tgaacgggtg  | ggatgttgtt   | caactgcgac  | attgtagtca  | actcragraag | tctctcgtgct | 660  |
| agatcgtctgc | tgtttttgga   | actgacaaac  | cgacgttggc  | tcagctcaat  | ggaattcattg | 720  |
| gtgactctca  | ctgtttctgt   | gataaaacct  | tcagctctcc  | tctcaaaaga  | tgtagctctt  | 780  |
| ctgtgaggaa  | cgactcgttg   | gatgcacctc  | tgccttctgc  | taaacactca  | taactgtctca | 840  |
| ctgcacaaac  | tgtccgtcga   | tgtacttggt  | agcgtttgaa  | gaattggaat  | taagtgtgtc  | 900  |
| aatcatcatc  | ttagatttaag  | cccttgtaac  | ggcaaaacctg | cccaccattt  | tcacaattgtg | 960  |
| atcagagcttt | gottaaacgcg  | tcttgcagac  | gaacctctgca | tgtcgtctat  | gctgggttat  | 1020 |
| ccaaacaaac  | catcttcaac   | acaagcttcc  | caagtgtgtc  | agattctcgt  | gctctgtgta  | 1080 |
| actatgcatt  | aacgctcagc   | taagacttca  | gttctcgtgat | tgtgttgatt  | cagttgtcgt  | 1140 |
| tctgtgtctg  | ctgcctcttc   | tctaagtgtt  | tgtgtgtgtg  | ttagtagtg   | tattcaagta  | 1200 |
| ctgtctcgat  | taaaataaag   | acattgttct  | acatgaagca  | tcaggtcctt  | gtaccattat  | 1260 |
| tatactggaa  | acattttcagc  |             |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

{ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..350  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2154:

Met Glu Thr Ser Cys Phe Thr Leu Leu Gly Leu Leu Val Ser Leu Ser  
1 5 10 15  
Phe Phe Leu Thr Leu Ser Ala Gln Met Thr Gly Asn Phe Asn Cys Ser  
20 25 30  
Gly Ser Thr Ser Thr Cys Gln Ser Leu Val Gly Tyr Ser Ser Lys Asn  
35 40 45  
Ala Thr Thr Leu Arg Asn Ile Gln Thr Leu Phe Ala Val Lys Asn Leu  
50 55 60  
Arg Ser Ile Leu Gly Ala Asn Asn Leu Pro Leu Asn Thr Ser Arg Asp  
65 70 75 80  
Gln Arg Val Asn Pro Asn Gln Val Val Arg Val Pro Ile His Cys Ser  
85 90 95  
Cys Ser Asn Gly Thr Gly Val Ser Asn Arg Asp Ile Glu Tyr Thr Ile  
100 105 110  
Lys Lys Asp Asp Ile Leu Ser Phe Val Ala Thr Glu Ile Phe Gly Gly  
115 120 125  
Leu Val Thr Tyr Glu Lys Ile Ser Glu Val Asn Lys Ile Pro Asp Pro  
130 135 140  
Asn Lys Ile Glu Ile Gly Gln Lys Phe Trp Ile Pro Leu Pro Cys Ser  
145 150 155 160  
Cys Asp Lys Leu Asn Gly Glu Asp Val Val His Tyr Ala His Val Val  
165 170 175  
Lys Leu Xaa Ser Ser Leu Gly Glu Ile Ala Ala Gln Phe Gly Thr Asp  
180 185 190  
Asn Thr Thr Leu Ala Gln Leu Asn Gly Ile Ile Gly Asp Ser Gln Leu  
195 200 205  
Leu Ala Asp Lys Pro Leu Asp Val Pro Leu Lys Ala Cys Ser Ser Ser  
210 215 220  
Val Arg Asn Asp Ser Leu Asp Ala Pro Leu Leu Ser Asn Asn Ser  
225 230 235 240  
Tyr Val Phe Thr Ala Asn Asn Cys Val Lys Cys Thr Cys Asp Ala Leu  
245 250 255  
Lys Asn Trp Thr Leu Ser Cys Gln Ser Ser Ser Glu Ile Lys Pro Ser  
260 265 270  
Asn Trp Gln Thr Cys Pro Pro Phe Ser Gln Cys Asp Arg Ala Leu Leu  
275 280 285  
Asn Ala Ser Cys Arg Arg Pro Arg Asp Cys Val Tyr Ala Gly Tyr Ser  
290 295 300  
Asn Gln Thr Ile Phe Thr Thr Ala Ser Pro Ala Cys Pro Asp Ser Ala  
305 310 315 320  
Gly Pro Gly Asn Tyr Ala Ser Thr Leu Ser Ser Ser Phe Ser Phe Val  
325 330 335  
Ile Val Leu Ile Gln Cys Ala Leu Leu Cys Leu Cys Leu Leu  
340 345 350

(2) INFORMATION FOR SEQ ID NO:2155:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 326 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..326  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2155:

Met Thr Gly Asn Phe Asn Cys Ser Gly Ser Thr Ser Thr Cys Gln Ser

1 5 10 15  
Leu Val Gly Tyr Ser Ser Lys Asn Ala Thr Thr Leu Arg Asn Ile Gln  
20 25 30  
Thr Leu Phe Ala Val Lys Asn Leu Arg Ser Ile Leu Gly Ala Asn Asn  
35 40 45  
Leu Pro Leu Asn Thr Ser Arg Asp Gln Arg Val Asn Pro Asn Gln Val  
50 55 60  
Val Arg Val Pro Ile His Cys Ser Cys Ser Asn Gly Thr Gly Val Ser  
65 70 75 80  
Asn Arg Asp Ile Glu Tyr Thr Ile Lys Lys Asp Asp Ile Leu Ser Phe  
85 90 95  
Val Ala Thr Glu Ile Phe Gly Gly Leu Val Thr Tyr Glu Lys Ile Ser  
100 105 110  
Glu Val Asn Lys Ile Pro Asp Pro Asn Lys Ile Glu Ile Gly Gln Lys  
115 120 125  
Phe Trp Ile Pro Leu Pro Cys Ser Cys Asp Lys Leu Asn Gly Glu Asp  
130 135 140  
Val Val His Tyr Ala His Val Val Lys Leu Xaa Ser Ser Leu Gly Glu  
145 150 155 160  
Ile Ala Ala Gln Phe Gly Thr Asp Asn Thr Thr Leu Ala Gln Leu Asn  
165 170 175  
Gly Ile Ile Gly Asp Ser Gln Leu Leu Ala Asp Lys Pro Leu Asp Val  
180 185 190  
Pro Leu Lys Ala Cys Ser Ser Ser Val Arg Asn Asp Ser Leu Asp Ala  
195 200 205  
Pro Leu Leu Leu Ser Asn Asn Ser Tyr Val Phe Thr Ala Asn Asn Cys  
210 215 220  
Val Lys Cys Thr Cys Asp Ala Leu Lys Asn Trp Thr Leu Ser Cys Gln  
225 230 235 240  
Ser Ser Ser Glu Ile Lys Pro Ser Asn Trp Gln Thr Cys Pro Pro Phe  
245 250 255  
Ser Gln Cys Asp Arg Ala Leu Leu Asn Ala Ser Cys Arg Arg Pro Arg  
260 265 270  
Asp Cys Val Tyr Ala Gly Tyr Ser Asn Gln Thr Ile Phe Thr Thr Ala  
275 280 285  
Ser Pro Ala Cys Pro Asp Ser Ala Gly Pro Gly Asn Tyr Ala Ser Thr  
290 295 300  
Leu Ser Ser Ser Phe Ser Phe Val Ile Val Leu Ile Gln Cys Ala Leu  
305 310 315 320  
Leu Cys Leu Cys Leu Leu  
325

(2) INFORMATION FOR SEQ ID NO:2156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 914 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..914
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2156:

|             |             |             |            |            |             |     |
|-------------|-------------|-------------|------------|------------|-------------|-----|
| acttcattag  | tctccaagaa  | gaaaacatct  | ctcactctct | aaaatacaca | ctctcatcaa  | 60  |
| aaaccttctc  | ttcgggttcag | aagcatttcaa | gaatccatta | tgagctcatt | tgattccggt  | 120 |
| aaataacggcg | ttaactcacg  | gatgtacttc  | cgtaacccga | gtttcagcaa | cgttatcttta | 180 |
| aacgataact  | ggagcgactt  | gcogttaagt  | gtcgacgatt | ctcaagacat | ggctattttac | 240 |
| aacactctcc  | gtgatcgctt  | tagctccgcc  | tggacaccat | cogttctctc | cgttacctct  | 300 |
| ccggcgaggag | aagataagcc  | tcggcgagcg  | aaggcgagtg | gctcacacgc | gccgaggcag  | 360 |
| aagggggatcg | agttacagag  | agtgaggagg  | aggccgtggg | ggaaattcgc | ggcgagagatt | 420 |
| agggatccga  | agaagaacgg  | agctagggtt  | tggtcgggga | cttacgagac | gccggaGgac  | 480 |



gcggcggttg cgtacgaccg agcggcggtt cagctcagag gatcgaaagc taagctgaat 540  
tttccgcat ttagttgggtc ttgtaagtat gagccgggtta ggattaggcc tcgccgtcgc 600  
tcgcccgaac cgtcagtcct cgtcagttta acgtcggagc agaagaggga aagccacgtg 660  
gatgacggca agtcagtttt ggttgtaccg gagttggatt tcacgggtgga tcagttttac 720  
ttcgtatggtta gttttattaat ggaccaatca gaatgttctt attctgataa tcggatataa 780  
ttagttttaa gattaagcaa aatttgtcca acgagttttg ctgtatgaaa tatctatcga 840  
tgactcaaca ggttttgatc atgatcatat gtaatgtgat gaaattataa tattgacggt 900  
tggttttttc ttcc

(2) INFORMATION FOR SEQ ID NO:2157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..226

(D) OTHER INFORMATION: / Ceres Seq. ID 1571913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2157:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ser | Ser | Asp | Ser | Val | Asn | Asn | Gly | Val | Asn | Ser | Arg | Met | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Arg | Asn | Pro | Ser | Phe | Ser | Asn | Val | Ile | Leu | Asn | Asp | Asn | Trp | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Leu | Pro | Leu | Ser | Val | Asp | Asp | Ser | Gln | Asp | Met | Ala | Ile | Tyr | Asn |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Thr | Leu | Arg | Asp | Ala | Val | Ser | Ser | Ala | Trp | Thr | Pro | Ser | Val | Pro | Pro |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Val | Thr | Ser | Pro | Ala | Glu | Glu | Asp | Lys | Pro | Pro | Ala | Thr | Lys | Ala | Ser |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |
| Gly | Ser | His | Ala | Pro | Arg | Gln | Lys | Gly | Met | Gln | Tyr | Arg | Gly | Val | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Arg | Pro | Trp | Gly | Lys | Phe | Ala | Ala | Glu | Ile | Arg | Asp | Pro | Lys | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Asn | Gly | Ala | Arg | Val | Trp | Leu | Gly | Thr | Tyr | Glu | Thr | Pro | Glu | Asp | Ala |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Ala | Val | Ala | Tyr | Asp | Arg | Ala | Ala | Phe | Gln | Leu | Arg | Gly | Ser | Lys | Ala |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |
| Lys | Leu | Asn | Phe | Pro | His | Leu | Ile | Gly | Ser | Cys | Lys | Tyr | Glu | Pro | Val |
|     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Arg | Ile | Arg | Pro | Arg | Arg | Arg | Ser | Pro | Glu | Pro | Ser | Val | Ser | Asp | Gln |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Leu | Thr | Ser | Glu | Gln | Lys | Arg | Glu | Ser | His | Val | Asp | Asp | Gly | Lys | Ser |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Ser | Leu | Val | Val | Pro | Glu | Leu | Asp | Phe | Thr | Val | Asp | Gln | Phe | Tyr | Phe |
|     |     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |
| Asp | Gly | Ser | Leu | Leu | Met | Asp | Gln | Ser | Glu | Cys | Ser | Tyr | Ser | Asp | Asn |
|     |     |     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |
| Arg | Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 225 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1571914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2158:

Met Tyr Phe Arg Asn Pro Ser Phe Ser Asn Val Ile Leu Asn Asp Asn  
1 5 10 15  
Trp Ser Asp Leu Pro Leu Ser Val Asp Asp Ser Gln Asp Met Ala Ile  
20 25 30  
Tyr Asn Thr Leu Arg Asp Ala Val Ser Ser Ala Trp Thr Pro Ser Val  
35 40 45  
Pro Pro Val Thr Ser Pro Ala Glu Glu Asp Lys Pro Pro Ala Thr Lys  
50 55 60  
Ala Ser Gly Ser His Ala Pro Arg Gln Lys Gly Met Gln Tyr Arg Gly  
65 70 75 80  
Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro  
85 90 95  
Lys Lys Asn Gly Ala Arg Val Trp Leu Gly Thr Tyr Glu Thr Pro Glu  
100 105 110  
Asp Ala Ala Val Ala Tyr Asp Arg Ala Ala Phe Gln Leu Arg Gly Ser  
115 120 125  
Lys Ala Lys Leu Asn Phe Pro His Leu Ile Gly Ser Cys Lys Tyr Glu  
130 135 140  
Pro Val Arg Ile Arg Pro Arg Arg Arg Ser Pro Glu Pro Ser Val Ser  
145 150 155 160  
Asp Gln Leu Thr Ser Glu Gln Lys Arg Glu Ser His Val Asp Asp Gly  
165 170 175  
Lys Ser Ser Leu Val Val Pro Glu Leu Asp Phe Thr Val Asp Gln Phe  
180 185 190  
Tyr Phe Asp Gly Ser Leu Leu Met Asp Gln Ser Glu Cys Ser Tyr Ser  
195 200 205  
Asp Asn Arg Ile  
210

(2) INFORMATION FOR SEQ ID NO:2159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2159:

Met Ala Ile Tyr Asn Thr Leu Arg Asp Ala Val Ser Ser Ala Trp Thr  
1 5 10 15  
Pro Ser Val Pro Pro Val Thr Ser Pro Ala Glu Glu Asp Lys Pro Pro  
20 25 30  
Ala Thr Lys Ala Ser Gly Ser His Ala Pro Arg Gln Lys Gly Met Gln  
35 40 45  
Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile  
50 55 60  
Arg Asp Pro Lys Lys Asn Gly Ala Arg Val Trp Leu Gly Thr Tyr Glu  
65 70 75 80  
Thr Pro Glu Asp Ala Ala Val Ala Tyr Asp Arg Ala Ala Phe Gln Leu  
85 90 95  
Arg Gly Ser Lys Ala Lys Leu Asn Phe Pro His Leu Ile Gly Ser Cys  
100 105 110  
Lys Tyr Glu Pro Val Arg Ile Arg Pro Arg Arg Arg Ser Pro Glu Pro  
115 120 125  
Ser Val Ser Asp Gln Leu Thr Ser Glu Gln Lys Arg Glu Ser His Val  
130 135 140  
Asp Asp Gly Lys Ser Ser Leu Val Val Pro Glu Leu Asp Phe Thr Val  
145 150 155 160

Asp Gln Phe Tyr Phe Asp Gly Ser Leu Leu Met Asp Gln Ser Glu Cys  
165 170 175  
Ser Tyr Ser Asp Asn Arg Ile  
180

(2) INFORMATION FOR SEQ ID NO:2160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571920

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2160:

|            |            |             |            |            |             |      |
|------------|------------|-------------|------------|------------|-------------|------|
| atacgtttgc | tgctccacgt | tgatcttgtt  | gtttactctc | tctctctctc | ccatcgccga  | 60   |
| cgaccaccgg | agatcagcgt | caccgtacca  | aaacatcatt | taccttcttt | aagattttgt  | 120  |
| gttttttaac | cagttgaatc | ggaataaaat  | atcgatcag  | agatgagtaa | cgagcttctc  | 180  |
| accatcgatc | ctgtcgacct | tcaattccct  | tttgaaattg | agaagcagat | ctctgtgtct  | 240  |
| ctctatttgg | gtaacaagac | cgataattat  | gtcgcttcca | aggtaagac  | gacgaatcca  | 300  |
| aagaagtact | gcgttaggcc | taatactggt  | gttggtccat | ccagatcctc | ttctgaagtt  | 360  |
| ttagtaccac | tgaacgtctc | aaaggaagct  | cctgctgac  | tgccagttaa | agataagttc  | 420  |
| ttgtctcaat | gtgtagtcgc | tagtcccgga  | gccaccacca | aggatgttac | tcatgagatg  | 480  |
| tttagcaaa  | agggcaggga | tcgagttgaa  | gagactaaat | tgagagttgt | ctatgttgtct | 540  |
| ccaccacgac | caccatcacc | ggttcgagaa  | ggatctgaa  | agggctcttc | accgagggct  | 600  |
| ctctgtctct | ataatgggaa | gtctctctgat | tttactgctg | ctccaagatt | tagcgacagc  | 660  |
| agggttgatg | ctcaggataa | ctcatctgag  | gcaagagctc | ttgtcacaaa | actcacccag  | 720  |
| gaaaagaact | ctfcggttca | actgaacaac  | aggcttcaac | aagaattgga | ccagttgagg  | 780  |
| cgcgaaaaga | agagaagtga | gagtggttga  | atccctttca | tgtaactgtt | tctggtcgcc  | 840  |
| ctaactcggt | taactctggg | atacattatg  | aagaggacat | gatacagatc | cttcaacaaa  | 900  |
| atactccaaa | agttctcaag | tgcttaaaaa  | agcaattgaa | aggaaagaaa | tcaaattgtg  | 960  |
| tgaggaggac | atactctctc | tctgccttat  | cgctgctatg | caccttttgt | taaaatctga  | 1020 |
| acttagtgcg | ttagaggatt | tgtattacgg  | tttcataaag | acttagaatt | gtcacaataa  | 1080 |
| ctcctttttc | ctctctctta | ttacaacttt  | gtgtagttct | aaacactttt | gttc        |      |

(2) INFORMATION FOR SEQ ID NO:2161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..239
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2161:

|                                                                 |                                 |     |
|-----------------------------------------------------------------|---------------------------------|-----|
| Met Ser Asn Glu Leu Leu Thr Ile Asp                             | Pro Val Asp Leu Gln Phe Pro     |     |
| 1                                                               | 5                               | 10  |
| Phe Glu Leu Lys Lys Gln Ile Ser                                 | Cys Ser Leu Tyr Leu Gly Asn Lys |     |
| 15                                                              | 20                              | 25  |
| Thr Asp Asn Tyr Val Ala Phe Lys Val Lys Thr Thr                 | Asn Pro Lys Lys                 |     |
| 30                                                              | 35                              | 40  |
| Tyr Cys Val Arg Pro Asn Thr Gly Val Val His Pro Arg Ser Ser Ser |                                 |     |
| 45                                                              | 50                              | 55  |
| Glu Val Leu Val Thr Met Gln Ala Gln Lys Glu Ala Pro Ala Asp Leu |                                 |     |
| 60                                                              | 65                              | 70  |
| Gln Cys Lys Asp Lys Phe Leu Leu Gln Cys Val Val Ala Ser Pro Gly |                                 |     |
| 75                                                              | 80                              | 85  |
| Ala Thr Pro Lys Asp Val Thr His Glu Met Phe Ser Lys Glu Ala Gly |                                 |     |
| 90                                                              | 95                              | 100 |
|                                                                 |                                 | 105 |
|                                                                 |                                 | 110 |

His Arg Val Glu Glu Thr Lys Leu Arg Val Val Tyr Val Ala Pro Pro  
115 120 125  
Arg Pro Pro Ser Pro Val Arg Glu Gly Ser Glu Glu Gly Ser Ser Pro  
130 135 140  
Arg Ala Ser Val Ser Asp Asn Gly Asn Ala Ser Asp Phe Thr Ala Ala  
145 150 155 160  
Pro Arg Phe Ser Ala Asp Arg Val Asp Ala Gln Asp Asn Ser Ser Glu  
165 170 175  
Ala Arg Ala Leu Val Thr Lys Leu Thr Glu Glu Lys Asn Ser Ala Val  
180 185 190  
Gln Leu Asn Asn Arg Leu Gln Gln Glu Leu Asp Gln Leu Arg Arg Glu  
195 200 205  
Ser Lys Arg Ser Lys Ser Gly Gly Ile Pro Phe Met Tyr Val Leu Leu  
210 215 220  
Val Gly Leu Ile Gly Leu Ile Leu Gly Tyr Ile Met Lys Arg Thr  
225 230 235

(2) INFORMATION FOR SEQ ID NO:2162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2162:

Met Gln Ala Gln Lys Glu Ala Pro Ala Asp Leu Gln Cys Lys Asp Lys  
1 5 10 15  
Phe Leu Leu Gln Cys Val Val Ala Ser Pro Gly Ala Thr Pro Lys Asp  
20 25 30  
Val Thr His Glu Met Phe Ser Lys Glu Ala Gly His Arg Val Glu Glu  
35 40 45  
Thr Lys Leu Arg Val Val Tyr Val Ala Pro Pro Arg Pro Pro Ser Pro  
50 55 60  
Val Arg Glu Gly Ser Glu Glu Gly Ser Ser Pro Arg Ala Ser Val Ser  
65 70 75 80  
Asp Asn Gly Asn Ala Ser Asp Phe Thr Ala Ala Pro Arg Phe Ser Ala  
85 90 95  
Asp Arg Val Asp Ala Gln Asp Asn Ser Ser Glu Ala Arg Ala Leu Val  
100 105 110  
Thr Lys Leu Thr Glu Glu Lys Asn Ser Ala Val Gln Leu Asn Asn Arg  
115 120 125  
Leu Gln Gln Glu Leu Asp Gln Leu Arg Arg Glu Ser Lys Arg Ser Lys  
130 135 140  
Ser Gly Gly Ile Pro Phe Met Tyr Val Leu Leu Val Gly Leu Ile Gly  
145 150 155 160  
Leu Ile Leu Gly Tyr Ile Met Lys Arg Thr  
165 170

(2) INFORMATION FOR SEQ ID NO:2163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2163:

```

Met Phe Ser Lys Glu Ala Gly His Arg Val Glu Glu Thr Lys Leu Arg
1 5 10 15
Val Val Tyr Val Ala Pro Pro Arg Pro Pro Ser Pro Val Arg Glu Gly
20 25 30
Ser Glu Glu Gly Ser Ser Pro Arg Ala Ser Val Ser Asp Asn Gly Asn
35 40 45
Ala Ser Asp Phe Thr Ala Ala Pro Arg Phe Ser Ala Asp Arg Val Asp
50 55 60
Ala Gln Asp Asn Ser Ser Glu Ala Arg Ala Leu Val Thr Lys Leu Thr
65 70 75 80
Glu Glu Lys Asn Ser Ala Val Gln Leu Asn Asn Arg Leu Gln Gln Glu
85 90 95
Leu Asp Gln Leu Arg Arg Glu Ser Lys Arg Ser Lys Gly Ile
100 105 110
Pro Phe Met Tyr Val Leu Leu Val Gly Leu Ile Gly Leu Ile Leu Gly
115 120 125

Tyr Ile Met Lys Arg Thr
130

```

(2) INFORMATION FOR SEQ ID NO:2164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1623 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1623

(D) OTHER INFORMATION: / Ceres Seq. ID 1571927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2164:

```

attttcgggt attcaagcca caaaacccgt agaatggcgg cagctactca atttctctcc 60
caacctctgt ctctcaatcc acaccaactg aagaacccaaa cctcacaaag ctcacgaagc 120
atccctctgt tgtctcttaa atccacattg aagccactta aacgctctct cgtgaaagcc 180
gccgtggttt cccaaaactc gtccaaaacc gtgaacgaag Tcgatcacgt tttcaagaaa 240
tcatcagatg ggtttctcta ttgtgaagga actaaagttg aggatatcat ggagtcagtg 300
gagagaagac ccttttacct atatagcaaa cctcagatca ctgaaaacct cgaggtctat 360
aaagaagcat tggaaaggagt gagctctgtg attggtttac ctatcaaaag taataacaat 420
cttaagattt tggagcattt gagaagttta ggctgtgggt ctgtgctcgt tagtggaaat 480
gagcttagac ttgctctctg tctgtgtttc gatccacaaa agtgcatttt caatggaaat 540
ggcaagctct tggaaagatt agttctagct gctcaagaag gtgttttctg taatgtcgat 600
agtgaagttg acttgaataa catgttgtaa gcttcaagaa tttctgttaa gcaggtcat 660
gtactgctgc gtatcaatgc ttgatgttat cctcaggtgc atccatgatg tgcactagg 720
aacaagaact caaagttttg tatcaggaa cagaagcttc aatggttttc ggaatcaggt 780
aaggcacatc ccaaagagct gaagcttggt ggagctcatt gccatctagg cctcacatt 840
actaagggtg atatatcag agatgcggca gttctcatga tgaatacat tgaagagatc 900
cggtcgtaag gttttgaagt tagttactgt aacattggtg gtggttttag gattgattat 960
taccatgcgc gcgctgtcct tcccacacc atggatctca tcaacactgt aagagagctt 1020
gttctttcac gagacctgaa tctaataatc gagccaggga gatctctgat tgaacaactt 1080
tgctgtttcg tcaacctagt aactggtgtg aagacgaatg gaactagaa ctctcatgct 1140
attgatggaa gtatgggtga gcttatcogt cccagctctt atgatgcta tcagcacatt 1200
gagttggtct cctctccacc ggctgaagca gaggtttacca aattogaagt cagttggtct 1260
gtctgtgaat ctgctgattt cctgggcaaa gacagagagc ttccactccc tcaacaggga 1320
gtcgggtcgg tggttcatca cgctggtgtc tactgtatga gcatggcttc cacttacaat 1380
ctcaagatgc gtctccggga atactgggtt gaagaagatg ggtcgatcac taagataaag 1440
catgtcgaga cattcgatga ccaattgcgt ttctttgaag tctgatgaac tcttagattt 1500
actcatcatt gtgtcttttt tgattgaatt gtatgattat tccgaatcag gaccataatg 1560
atattgctgt tttagatttt cacattatgt gotttgattc aaagtcaatg aagtgatcat 1620

```

(2) INFORMATION FOR SEQ ID NO:2165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 495 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..495  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2165:

Ile Phe Gly Tyr Gln Ser His Lys Thr Leu Arg Met Ala Ala Ala Thr  
1 5 10 15  
Gln Phe Leu Ser Gln Pro Ser Ser Leu Asn Pro His Gln Leu Lys Asn  
20 25 30  
Gln Thr Ser Gln Arg Ser Arg Ser Ile Pro Val Leu Ser Leu Lys Ser  
35 40 45  
Thr Leu Lys Pro Leu Lys Arg Leu Ser Val Lys Ala Ala Val Val Ser  
50 55 60  
Gln Asn Ser Ser Lys Thr Val Thr Lys Phe Asp His Cys Phe Lys Lys  
65 70 75 80  
Ser Ser Asp Gly Phe Leu Tyr Cys Glu Gly Thr Lys Val Glu Asp Ile  
85 90 95  
Met Glu Ser Val Glu Arg Arg Pro Phe Tyr Leu Tyr Ser Lys Pro Gln  
100 105 110  
Ile Thr Arg Asn Leu Glu Ala Tyr Lys Glu Ala Leu Glu Gly Val Ser  
115 120 125  
Ser Val Ile Gly Tyr Ala Ile Lys Ala Asn Asn Asn Leu Lys Ile Leu  
130 135 140  
Glu His Leu Arg Ser Leu Gly Cys Gly Ala Val Leu Val Ser Gly Asn  
145 150 155 160  
Glu Leu Arg Leu Ala Leu Arg Ala Gly Phe Asp Pro Thr Lys Cys Ile  
165 170 175  
Phe Asn Gly Asn Gly Lys Ser Leu Glu Asp Leu Val Leu Ala Ala Gln  
180 185 190  
Glu Gly Val Phe Val Asn Val Asp Ser Glu Phe Asp Leu Asn Asn Ile  
195 200 205  
Val Glu Ala Ser Arg Ile Ser Gly Lys Gln Val Asn Val Leu Leu Arg  
210 215 220  
Ile Asn Pro Asp Val Asp Pro Gln Val His Pro Tyr Val Ala Thr Gly  
225 230 235 240  
Asn Lys Asn Ser Lys Phe Gly Ile Arg Asn Glu Lys Leu Gln Trp Phe  
245 250 255  
Leu Asp Gln Val Lys Ala His Pro Lys Glu Leu Lys Leu Val Gly Ala  
260 265 270  
His Cys His Leu Gly Ser Thr Ile Thr Lys Val Asp Ile Phe Arg Asp  
275 280 285  
Ala Ala Val Leu Met Ile Glu Tyr Ile Asp Glu Ile Arg Arg Gln Gly  
290 295 300  
Phe Glu Val Ser Tyr Leu Asn Ile Gly Gly Gly Leu Gly Ile Asp Tyr  
305 310 315 320  
Tyr His Ala Gly Ala Val Leu Pro Thr Pro Met Asp Leu Ile Asn Thr  
325 330 335  
Val Arg Glu Leu Val Leu Ser Arg Asp Leu Asn Leu Ile Ile Glu Pro  
340 345 350  
Gly Arg Ser Leu Ile Ala Asn Thr Cys Cys Phe Val Asn His Val Thr  
355 360 365  
Gly Val Lys Thr Asn Gly Thr Lys Asn Phe Ile Val Ile Asp Gly Ser  
370 375 380  
Met Ala Glu Leu Ile Arg Pro Ser Leu Tyr Asp Ala Tyr Gln His Ile  
385 390 395 400  
Glu Leu Val Ser Pro Pro Ala Glu Ala Glu Val Thr Lys Phe Asp

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     | 405 |     |     |     | 410 |     |     |     |     |     | 415 |     |     |
| Val | Val | Gly | Pro | Val | Cys | Glu | Ser | Ala | Asp | Phe | Leu | Gly | Lys | Asp | Arg |
|     |     |     | 420 |     |     |     | 425 |     |     |     |     |     | 430 |     |     |
| Glu | Leu | Pro | Thr | Pro | Pro | Gln | Gly | Ala | Gly | Leu | Val | Val | His | Asp | Ala |
|     |     |     | 435 |     |     |     | 440 |     |     |     |     |     | 445 |     |     |
| Gly | Ala | Tyr | Cys | Met | Ser | Met | Ala | Ser | Thr | Tyr | Asn | Leu | Lys | Met | Arg |
|     |     |     | 450 |     |     |     | 455 |     |     |     |     |     | 460 |     |     |
| Pro | Pro | Glu | Tyr | Trp | Val | Glu | Glu | Asp | Gly | Ser | Ile | Thr | Lys | Ile | Arg |
|     |     |     | 465 |     |     |     | 470 |     |     |     |     |     | 475 |     |     |
| His | Ala | Glu | Thr | Phe | Asp | Asp | His | Leu | Arg | Phe | Phe | Glu | Gly | Leu |     |
|     |     |     | 485 |     |     |     | 490 |     |     |     |     |     | 495 |     |     |

(2) INFORMATION FOR SEQ ID NO:2166:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 484 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..484

(D) OTHER INFORMATION: / Ceres Seq. ID 1571929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2166:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ala | Thr | Gln | Phe | Leu | Ser | Gln | Pro | Ser | Ser | Leu | Asn | Pro |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| His | Gln | Leu | Lys | Asn | Gln | Thr | Ser | Gln | Arg | Ser | Arg | Ser | Ile | Pro | Val |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Leu | Ser | Leu | Lys | Ser | Thr | Leu | Lys | Pro | Leu | Lys | Arg | Leu | Ser | Val | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Ala | Ala | Val | Val | Ser | Gln | Asn | Ser | Ser | Lys | Thr | Val | Thr | Lys | Phe | Asp |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| His | Cys | Phe | Lys | Lys | Ser | Ser | Asp | Gly | Phe | Leu | Tyr | Cys | Glu | Gly | Thr |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Lys | Val | Glu | Asp | Ile | Met | Glu | Ser | Val | Glu | Arg | Arg | Pro | Phe | Tyr | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Tyr | Ser | Lys | Pro | Gln | Ile | Thr | Arg | Asn | Leu | Glu | Ala | Tyr | Lys | Glu | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Glu | Gly | Val | Ser | Ser | Val | Ile | Gly | Tyr | Ala | Ile | Lys | Ala | Asn | Asn |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Leu | Lys | Ile | Leu | Glu | His | Leu | Arg | Ser | Leu | Gly | Cys | Gly | Ala | Val |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Leu | Val | Ser | Gly | Asn | Glu | Leu | Arg | Leu | Ala | Leu | Arg | Ala | Gly | Phe | Asp |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     | 160 |     |
| Pro | Thr | Lys | Cys | Ile | Phe | Asn | Gly | Asn | Gly | Lys | Ser | Leu | Glu | Asp | Leu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Val | Leu | Ala | Ala | Gln | Glu | Gly | Val | Phe | Val | Asn | Val | Asp | Ser | Glu | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | Leu | Asn | Asn | Ile | Val | Glu | Ala | Ser | Arg | Ile | Ser | Gly | Lys | Gln | Val |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | Val | Leu | Leu | Arg | Ile | Asn | Pro | Asp | Val | Asp | Pro | Gln | Val | His | Pro |
|     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Tyr | Val | Ala | Thr | Gly | Asn | Lys | Asn | Ser | Lys | Phe | Gly | Ile | Arg | Asn | Glu |
|     |     |     | 225 |     |     |     | 230 |     |     |     | 235 |     |     | 240 |     |
| Lys | Leu | Gln | Trp | Phe | Leu | Asp | Gln | Val | Lys | Ala | His | Pro | Lys | Glu | Leu |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Lys | Leu | Val | Gly | Ala | His | Cys | His | Leu | Gly | Ser | Thr | Ile | Thr | Lys | Val |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Asp | Ile | Phe | Arg | Asp | Ala | Ala | Val | Leu | Met | Ile | Glu | Tyr | Ile | Asp | Glu |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Arg | Arg | Gln | Gly | Phe | Glu | Val | Ser | Tyr | Leu | Asn | Ile | Gly | Gly | Gly |
|     |     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |

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Leu Gly Ile Asp Tyr Tyr His Ala Gly Ala Val Leu Pro Thr Pro Met
305 310 315 320
Asp Leu Ile Asn Thr Val Arg Glu Leu Val Leu Ser Arg Asp Leu Asn
 325 330 335
Leu Ile Ile Glu Pro Gly Arg Ser Leu Ile Ala Asn Thr Cys Phe
 340 345 350
Val Asn His Val Thr Gly Val Lys Thr Asn Gly Thr Lys Asn Phe Ile
 355 360 365
Val Ile Asp Gly Ser Met Ala Glu Leu Ile Arg Pro Ser Leu Tyr Asp
 370 375 380
Ala Tyr Gln His Ile Glu Leu Val Ser Pro Pro Pro Ala Glu Ala Glu
385 390 395 400
Val Thr Lys Phe Asp Val Val Gly Pro Val Cys Glu Ser Ala Asp Phe
 405 410 415
Leu Gly Lys Asp Arg Glu Leu Pro Thr Pro Pro Gln Gly Ala Gly Leu
 420 425 430
Val Val His Asp Ala Gly Ala Tyr Cys Met Ser Met Ala Ser Thr Tyr
 435 440 445
Asn Leu Lys Met Arg Pro Pro Glu Tyr Trp Val Glu Glu Asp Gly Ser
450 455 460
Ile Thr Lys Ile Arg His Ala Glu Thr Phe Asp Asp His Leu Arg Phe
465 470 475 480
Phe Glu Gly Leu

```

(2) INFORMATION FOR SEQ ID NO:2167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..399

(D) OTHER INFORMATION: / Ceres Seq. ID 1571930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2167:

```

Met Glu Ser Val Glu Arg Arg Pro Phe Tyr Leu Tyr Ser Lys Pro Gln
1 5 10 15
Ile Thr Arg Asn Leu Glu Ala Tyr Lys Glu Ala Leu Glu Gly Val Ser
 20 25 30
Ser Val Ile Gly Tyr Ala Ile Lys Ala Asn Asn Asn Leu Lys Ile Leu
35 40 45
Glu His Leu Arg Ser Leu Gly Cys Gly Ala Val Leu Val Ser Gly Asn
50 55 60
Glu Leu Arg Leu Ala Leu Arg Ala Gly Phe Asp Pro Thr Lys Cys Ile
65 70 75 80
Phe Asn Gly Asn Gly Lys Ser Leu Glu Asp Leu Val Leu Ala Ala Gln
 85 90 95
Glu Gly Val Phe Val Asn Val Asp Ser Glu Phe Asp Leu Asn Asn Ile
100 105 110
Val Glu Ala Ser Arg Ile Ser Gly Lys Gln Val Asn Val Leu Leu Arg
115 120 125
Ile Asn Pro Asp Val Asp Pro Gln Val His Pro Tyr Val Ala Thr Gly
130 135 140
Asn Lys Asn Ser Lys Phe Gly Ile Arg Asn Glu Lys Leu Gln Trp Phe
145 150 155 160
Leu Asp Gln Val Lys Ala His Pro Lys Glu Leu Lys Leu Val Gly Ala
 165 170 175
His Cys His Leu Gly Ser Thr Ile Thr Lys Val Asp Ile Phe Arg Asp
180 185 190
Ala Ala Val Leu Met Ile Glu Tyr Ile Asp Glu Ile Arg Arg Gln Gly

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2025 RELEASE UNDER E.O. 14176



(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

- (B) LOCATION: 1..1383  
(D) OTHER INFORMATION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2168:

tec

(2) INFORMATION FOR SEQ ID NO:2169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..301

(D) OTHER INFORMATION: / Ceres Seq. ID 1571932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2169:

Asp Leu Leu Leu Pro Tyr Val Asn Lys Val Arg Glu Leu Asp Asn Thr  
1 5 10 15  
Thr Leu Tyr Ala Ser Arg Thr Leu Phe Phe Leu Ser Asp Asp Ser Thr  
20 25 30  
Leu Arg Pro Val Ala Ile Glu Leu Thr Cys Pro Pro Asn Ile Asn Lys  
35 40 45  
Pro Gln Trp Lys Lys Val Phe Thr Pro Gly Tyr Asp Ala Thr Ser Cys  
50 55 60  
Trp Leu Trp Asn Leu Ala Lys Thr His Ala Ile Ser His Asp Ala Gly  
65 70 75 80  
Tyr His Gln Leu Ile Ser His Trp Leu Arg Thr His Ala Cys Thr Glu  
85 90 95  
Pro Tyr Ile Ile Ala Ala Asn Arg Gln Leu Ser Ala Met His Pro Ile  
100 105 110  
Tyr Arg Leu Leu His Pro His Phe Arg Tyr Thr Met Glu Ile Asn Ala  
115 120 125  
Arg Ala Arg Gln Ser Leu Val Asn Gly Gly Gly Ile Ile Glu Thr Cys  
130 135 140  
Phe Trp Pro Gly Lys Tyr Ala Leu Glu Leu Xaa Ser Ala Val Tyr Gly  
145 150 155 160  
Lys Leu Trp Arg Phe Asp Gln Glu Gly Leu Pro Ala Asp Leu Ile Lys  
165 170 175  
Arg Gly Leu Ala Glu Glu Asp Lys Thr Ala Glu His Gly Val Arg Leu  
180 185 190  
Thr Ile Pro Asp Tyr Pro Phe Ala Asn Asp Gly Leu Ile Leu Trp Asp  
195 200 205  
Ala Ile Lys Glu Trp Val Thr Asp Tyr Val Lys His Tyr Tyr Pro Asp  
210 215 220  
Glu Glu Leu Ile Thr Ser Asp Glu Glu Leu Gln Gly Trp Trp Ser Glu  
225 230 235 240  
Val Arg Asn Ile Gly His Gly Asp Lys Lys Asp Glu Pro Trp Trp Pro  
245 250 255  
Val Leu Lys Thr Gln Asp Asp Leu Ile Gly Val Val Thr Thr Ile Ala  
260 265 270  
Trp Val Thr Ser Gly His His Ala Ala Val Asn Phe Gly Gln Arg Ile  
275 280 285  
Met Glu Asp Thr Phe Pro Thr Asp Gln Arg Gln Gln Gly  
290 295 300

(2) INFORMATION FOR SEQ ID NO:2170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1571933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2170:

Met His Pro Ile Tyr Arg Leu Leu His Pro His Phe Arg Tyr Thr Met  
1 5 10 15  
Glu Ile Asn Ala Arg Ala Arg Gln Ser Leu Val Asn Gly Gly Gly Ile  
20 25 30  
Ile Glu Thr Cys Phe Trp Pro Gly Lys Tyr Ala Leu Glu Leu Xaa Ser  
35 40 45  
Ala Val Tyr Gly Lys Leu Trp Arg Phe Asp Gln Glu Gly Leu Pro Ala  
50 55 60  
Asp Leu Ile Lys Arg Gly Leu Ala Glu Glu Asp Lys Thr Ala Glu His  
65 70 75 80  
Gly Val Arg Leu Thr Ile Pro Asp Tyr Pro Phe Ala Asn Asp Gly Leu  
85 90 95  
Ile Leu Trp Asp Ala Ile Lys Glu Trp Val Thr Asp Tyr Val Lys His  
100 105 110  
Tyr Tyr Pro Asp Glu Glu Leu Ile Thr Ser Asp Glu Glu Leu Gln Gly  
115 120 125  
Trp Trp Ser Glu Val Arg Asn Ile Gly His Gly Asp Lys Lys Asp Glu  
130 135 140  
Pro Trp Trp Pro Val Leu Lys Thr Gln Asp Asp Leu Ile Gly Val Val  
145 150 155 160  
Thr Thr Ile Ala Trp Val Thr Ser Gly His His Ala Ala Val Asn Phe  
165 170 175  
Gly Gln Arg Ile Met Glu Asp Thr Phe Pro Thr Asp Gln Arg Gln Gln  
180 185 190  
Gly

(2) INFORMATION FOR SEQ ID NO:2171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1571934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2171:

Met Glu Ile Asn Ala Arg Ala Arg Gln Ser Leu Val Asn Gly Gly Gly  
1 5 10 15  
Ile Ile Glu Thr Cys Phe Trp Pro Gly Lys Tyr Ala Leu Glu Leu Xaa  
20 25 30  
Ser Ala Val Tyr Gly Lys Leu Trp Arg Phe Asp Gln Glu Gly Leu Pro  
35 40 45  
Ala Asp Leu Ile Lys Arg Gly Leu Ala Glu Glu Asp Lys Thr Ala Glu  
50 55 60  
His Gly Val Arg Leu Thr Ile Pro Asp Tyr Pro Phe Ala Asn Asp Gly  
65 70 75 80  
Leu Ile Leu Trp Asp Ala Ile Lys Glu Trp Val Thr Asp Tyr Val Lys  
85 90 95  
His Tyr Tyr Pro Asp Glu Glu Leu Ile Thr Ser Asp Glu Glu Leu Gln  
100 105 110  
Gly Trp Trp Ser Glu Val Arg Asn Ile Gly His Gly Asp Lys Lys Asp  
115 120 125  
Glu Pro Trp Trp Pro Val Leu Lys Thr Gln Asp Asp Leu Ile Gly Val  
130 135 140  
Val Thr Thr Ile Ala Trp Val Thr Ser Gly His His Ala Ala Val Asn  
145 150 155 160  
Phe Gly Gln Arg Ile Met Glu Asp Thr Phe Pro Thr Asp Gln Arg Gln  
165 170 175

Gln Gly

(2) INFORMATION FOR SEQ ID NO:2172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1229
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2172:

|            |             |             |             |            |            |      |
|------------|-------------|-------------|-------------|------------|------------|------|
| gtgcgttcgt | agagactgta  | ataaagacgg  | agagattctt  | ctagagtcag | ttctttctct | 60   |
| tcctctctct | cttcccccca  | aatcctctct  | cgctagggtt  | tctcattccg | atccataatt | 120  |
| ctagatgtcg | agggttttta  | ctgagacctg  | tcaataaagc  | taaagctctt | tctaaagagt | 180  |
| ctaaagaaag | cattgcattg  | ttgtagtctt  | gtttgtgtcc  | acagaagcaa | agaagagtga | 240  |
| gaagctcagg | atgtcaaaga  | gtcgaaatac  | ccactgggtg  | cacagatgtc | agcgtgtctg | 300  |
| ccgccttcac | ggccaaagag  | ctgtatgtct  | ttattgcgga  | gggtgatttg | ttgaagaact | 360  |
| tgatatggct | caagccagcc  | cccttgatat  | gttttagatc  | cacaggggtg | ttgtagaacg | 420  |
| tgatcagact | tttgatctca  | tggatgcttt  | ctctgtgttt  | atgaggaacc | gcttagctga | 480  |
| aaggagccac | gacagagaaa  | tcagaggaag  | aacctcagt   | tcaggtctcg | aaaactttcc | 540  |
| tggtctggcc | cccttggtag  | tcaagtccct  | tatagactaa  | ctggcgacaa | gtggttaaac | 600  |
| tgcatcgaaa | gccctcttca  | atggcggtcc  | ccctggcatt  | ggcatcacac | gtggttaaac | 660  |
| cggcgactac | ttcttcggtc  | ccggccttga  | agaattgttc  | gagcaGcttt | cagctggcac | 720  |
| tactcgcgca | ggccccacac  | ccgcacogag  | atcagcaata  | ggcgattgac | caactatcaa | 780  |
| gatcgcgcag | agggcatctta | ggctcatcga  | ctcgaattgt  | ccctgtgtga | aagacgaatt | 840  |
| cgaactcggg | tcagaagcga  | aacagatgcc  | gtgtgaaccac | atctatcatt | ctgactgcgt | 900  |
| tgctccgttg | ctggttcagc  | acaactcttg  | cccggtctgt  | cgccaagagc | taccatcagc | 960  |
| tagcggacct | ctcaagctgc  | aaaacagaac  | caccocctacc | agaaactaca | gaagcagtag | 1020 |
| tagtagtagt | agtagtaaca  | gtcgtgagaa  | cgggaaatga  | agaaaggaac | ctttctcttc | 1080 |
| cttctggcca | ttccgttctg  | cagggttcaag | ctcaagctcc  | actcaaaacc | gtggaggcac | 1140 |
| aagaaactcg | gatacagcgg  | atgagaacca  | taactaccat  | caacagcaac | atcaacaatt | 1200 |
| atatatgggt | tacagtggct  | ggccttttg   |             |            |            |      |

(2) INFORMATION FOR SEQ ID NO:2173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2173:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ser | Ser | Arg | Asn | Thr | His | Trp | Cys | His | Arg | Cys | Gln | Arg | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Arg | Leu | His | Gly | Gln | Glu | Pro | Val | Cys | Ser | Tyr | Cys | Gly | Gly | Gly |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Val | Glu | Glu | Val | Leu | Asp | Met | Ala | Gln | Ala | Ser | Pro | Phe | Asp | Phe |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Arg | Ser | His | Arg | Gly | Val | Val | Glu | Arg | Asp | Gln | Thr | Phe | Asp | Leu | Met |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Asp | Ala | Phe | Ser | Val | Phe | Met | Arg | Asn | Arg | Leu | Ala | Glu | Arg | Ser | His |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |
| Asp | Arg | Glu | Ile | Arg | Gly | Arg | Thr | Ile | Ser | Ser | Gly | Pro | Glu | Asn | Phe |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Pro | Gly | Leu | Ala | Pro | Leu | Leu | Ile | Phe | Gly | Gly | Gln | Val | Pro | Tyr | Arg |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |

Leu Thr Gly Asp Asn Ala Val Glu Ala Leu Phe Asn Gly Gly Ser Pro  
115 120 125  
Gly Ile Gly Ile Thr Arg Gly Asn Thr Gly Asp Tyr Phe Gly Pro  
130 135 140  
Gly Leu Glu Glu Leu Phe Glu Gln Leu Ser Ala Gly Thr Thr Arg Arg  
145 150 155 160  
Gly Pro Pro Pro Ala Pro Arg Ser Ala Ile Asp Ala Leu Pro Thr Ile  
165 170 175  
Lys Ile Ala Gln Arg His Leu Arg Ser Ser Asp Ser Asn Cys Pro Val  
180 185 190  
Cys Lys Asp Glu Phe Glu Leu Gly Ser Glu Ala Lys Gln Met Pro Cys  
195 200 205  
Asn His Ile Tyr His Ser Asp Cys Ile Val Pro Trp Leu Val Gln His  
210 215 220  
Asn Ser Cys Pro Val Cys Arg Gln Glu Leu Pro Ser Ala Ser Gly Pro  
225 230 235 240  
Ser Ser Ser Gln Asn Arg Thr Thr Pro Thr Arg Asn Tyr Arg Ser Ser  
245 250 255  
Ser Ser Ser Ser Ser Ser Asn Ser Arg Glu Asn Gly Asn Glu Arg Arg  
260 265 270  
Asn Pro Phe Ser Ser Phe Trp Pro Phe Arg Ser Ser Gly Ser Ser Ser  
275 280 285  
Ser Ser Thr Gln Asn Arg Gly Gly Thr Arg Asn Ser Asp Thr Ser Asp  
290 295 300  
Glu Asn His Asn Tyr His Gln Gln Gln His Gln Gln Ser Tyr Met Gly  
305 310 315 320  
Tyr Ser Gly Trp Pro Phe  
325

(2) INFORMATION FOR SEQ ID NO:2174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..288

(D) OTHER INFORMATION: / Ceres Seq. ID 1571937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2174:

Met Ala Gln Ala Ser Pro Phe Asp Met Phe Arg Ser His Arg Gly Val  
1 5 10 15  
Val Glu Arg Asp Gln Thr Phe Asp Leu Met Asp Ala Phe Ser Val Phe  
20 25 30  
Met Arg Asn Arg Leu Ala Glu Arg Ser His Asp Arg Glu Ile Arg Gly  
35 40 45  
Arg Thr Ile Ser Ser Gly Pro Glu Asn Phe Pro Gly Leu Ala Pro Leu  
50 55 60  
Leu Ile Phe Gly Gly Gln Val Pro Tyr Arg Leu Thr Gly Asp Asn Ala  
65 70 75 80  
Val Glu Ala Leu Phe Asn Gly Gly Ser Pro Gly Ile Gly Ile Thr Arg  
85 90 95  
Gly Asn Thr Gly Asp Tyr Phe Phe Gly Pro Gly Leu Glu Glu Leu Phe  
100 105 110  
Glu Gln Leu Ser Ala Gly Thr Thr Arg Arg Gly Pro Pro Pro Ala Pro  
115 120 125  
Arg Ser Ala Ile Asp Ala Leu Pro Thr Ile Lys Ile Ala Gln Arg His  
130 135 140  
Leu Arg Ser Ser Asp Ser Asn Cys Pro Val Cys Lys Asp Glu Phe Glu  
145 150 155 160  
Leu Gly Ser Glu Ala Lys Gln Met Pro Cys Asn His Ile Tyr His Ser

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Cys | Ile | Val | Pro | Trp | Leu | Val | Gln | His | Asn | Ser | Cys | Pro | Val | Cys | 165 | 170 | 175 |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     | 190 |     |     |     |
| Arg | Gln | Glu | Leu | Pro | Ser | Ala | Ser | Gly | Pro | Ser | Ser | Ser | Gln | Asn | Arg |     |     |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |     |     |
| Thr | Thr | Pro | Thr | Arg | Asn | Tyr | Arg | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ser |     |     |     |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |     |     |
| Asn | Ser | Arg | Glu | Asn | Gly | Asn | Glu | Arg | Arg | Asn | Pro | Phe | Ser | Ser | Phe |     |     |     |
|     |     | 225 |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |     |     |
| Trp | Pro | Phe | Arg | Ser | Ser | Gly | Ser | Ser | Ser | Ser | Ser | Thr | Gln | Asn | Arg |     |     |     |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |     |     |     |
| Gly | Gly | Thr | Arg | Asn | Ser | Asp | Thr | Ser | Asp | Glu | Asn | His | Asn | Tyr | His |     |     |     |
|     |     | 260 |     |     |     | 265 |     |     |     |     |     |     | 270 |     |     |     |     |     |
| Gln | Gln | Gln | His | Gln | Gln | Ser | Tyr | Met | Gly | Tyr | Ser | Gly | Trp | Pro | Phe |     |     |     |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..280

(D) OTHER INFORMATION: / Ceres Seq. ID 1571938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2175:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| Met | Phe | Arg | Ser | His | Arg | Gly | Val | Val | Glu | Arg | Asp | Gln | Thr | Phe | Asp |  |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |  |
| Leu | Met | Asp | Ala | Phe | Ser | Val | Phe | Met | Arg | Asn | Arg | Leu | Ala | Glu | Arg |  |  |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |  |
| Ser | His | Asp | Arg | Glu | Ile | Arg | Gly | Arg | Thr | Ile | Ser | Ser | Gly | Pro | Glu |  |  |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |  |
| Asn | Phe | Pro | Gly | Leu | Ala | Pro | Leu | Leu | Ile | Phe | Gly | Gly | Gln | Val | Pro |  |  |  |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |  |  |
| Tyr | Arg | Leu | Thr | Gly | Asp | Asn | Ala | Val | Glu | Ala | Leu | Phe | Asn | Gly | Gly |  |  |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |  |  |
| Ser | Pro | Gly | Ile | Gly | Ile | Thr | Arg | Gly | Asn | Thr | Gly | Asp | Tyr | Phe | Phe |  |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |  |  |
| Gly | Pro | Gly | Leu | Glu | Glu | Leu | Phe | Glu | Gln | Leu | Ser | Ala | Gly | Thr | Thr |  |  |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |  |
| Arg | Arg | Gly | Pro | Pro | Pro | Ala | Pro | Arg | Ser | Ala | Ile | Asp | Ala | Leu | Pro |  |  |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |  |  |
| Thr | Ile | Lys | Ile | Ala | Gln | Arg | His | Leu | Arg | Ser | Ser | Asp | Ser | Asn | Cys |  |  |  |
|     |     | 130 |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |  |  |  |
| Pro | Val | Cys | Lys | Asp | Glu | Phe | Glu | Leu | Gly | Ser | Glu | Ala | Lys | Gln | Met |  |  |  |
|     |     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |  |
| Pro | Cys | Asn | His | Ile | Tyr | His | Ser | Asp | Cys | Ile | Val | Pro | Trp | Leu | Val |  |  |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |  |  |
| Gln | His | Asn | Ser | Cys | Pro | Val | Cys | Arg | Gln | Glu | Leu | Pro | Ser | Ala | Ser |  |  |  |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |  |  |
| Gly | Pro | Ser | Ser | Ser | Gln | Asn | Arg | Thr | Thr | Pro | Thr | Arg | Asn | Tyr | Arg |  |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |  |
| Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Asn | Ser | Arg | Glu | Asn | Gly | Asn | Glu |  |  |  |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |  |
| Arg | Arg | Asn | Pro | Phe | Ser | Ser | Phe | Trp | Pro | Phe | Arg | Ser | Ser | Gly | Ser |  |  |  |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |  |  |  |
| Ser | Ser | Ser | Ser | Thr | Gln | Asn | Arg | Gly | Gly | Thr | Arg | Asn | Ser | Asp | Thr |  |  |  |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |  |  |  |

Ser Asp Glu Asn His Asn Tyr His Gln Gln Gln His Gln Gln Ser Tyr  
260 265 270  
Met Gly Tyr Ser Gly Trp Pro Phe  
275 280

(2) INFORMATION FOR SEQ ID NO:2176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1430

(D) OTHER INFORMATION: / Ceres Seq. ID 1571945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2176:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| ctaaactaaa  | atctaaatct  | tgcccttcctg | actttctctc  | tacgacagaa  | tttttgaagc  | 60   |
| ttctctctgc  | ttatcgacac  | tatgggttctc | gaggcgacta  | tgatatgat   | cgacaactcc  | 120  |
| gaagtggatgc | gaaacggaga  | ttactctccg  | tctaggttac  | aggcgcaaac  | ggaagctggt  | 180  |
| aatcttcttt  | gcggagGccaa | aaccacgtcg  | aatccggaga  | atacggtggg  | gattttgaca  | 240  |
| atggtctggca | aaggagttag  | agttattgact | actcctacct  | ctgatcttgg  | caaaattctg  | 300  |
| gcctgtatgc  | acggcctctga | tgtggggagga | gagatcaact  | taaccgcagc  | tatccagatc  | 360  |
| gcccagctag  | ctcttaagca  | tcgccaatac  | aagaatcaac  | gccaaaggat  | tattgttttt  | 420  |
| gctggaaagtc | caatcaaagt  | ogagaagaag  | gccttagaga  | tagttggaaa  | aaggctgaag  | 480  |
| aagaatagtg  | tatctcttga  | tattgtcaat  | ttcggggagg  | atgatgatga  | ggaaaagctc  | 540  |
| cagaaaactcg | agggccctcct | tacagctgtg  | aataacaatg  | acggttagcca | cattgttcat  | 600  |
| gttctctctg  | gagccaatcg  | tctctcagat  | gtgcttctca  | gcacacctgt  | attcaccgggt | 660  |
| gatgagggtg  | caagtggcta  | tgtttctgcg  | gcagctgctg  | cagcgggcgc  | aggtggggag  | 720  |
| ttcgactttg  | gtgtggacc   | aaatatcgat  | ccagaaactg  | ctcttgccct  | tcgggtctcc  | 780  |
| atggaggagg  | agagagcaag  | acaagaagct  | gctgccaaaga | agcgggccga  | tgaggcatgt  | 840  |
| cagaaagaca  | aagatgggga  | cacagcttcc  | gcttcacagg  | agacagtgtc  | taggacaact  | 900  |
| gacaaagaag  | ctgaaccaat  | ggatgaggac  | agtgcgttgc  | tagatcagcg  | aattgctatg  | 960  |
| tctgtgtgtg  | atgtgaatat  | gtcagaagcg  | gctgatgagg  | accagagtct  | ggctttaagt  | 1020 |
| ctgcaaatgt  | caatgagttg  | ggaagagtca  | agtgaagcta  | ctctcatcgc  | aaacaacctc  | 1080 |
| ttgggaaatc  | aagccttcct  | atcgtctggt  | ctctcatcgc  | ttcctggggg  | ggatccaaat  | 1140 |
| gatccggcag  | ttaaagaact  | actagcgtct  | ctgccagacg  | agtcaaaagc  | tcacgaggag  | 1200 |
| gaagagagta  | gtagcaaaaa  | agggcaggat  | gagaagaagt  | gaasaaggat  | ctgagagctc  | 1260 |
| caataaaaa   | tctctctggt  | tcttttggtt  | gataagagatt | ggaactgaat  | ttactaatc   | 1320 |
| tctctgcctt  | gtgaaatttg  | gttttttctc  | tctctctcgc  | ctttttataa  | tgtgtgtatt  | 1380 |
| gtacgagtca  | aggactagct  | tctttttaa   | tttttatgg   | actttatgcc  |             |      |

(2) INFORMATION FOR SEQ ID NO:2177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..386

(D) OTHER INFORMATION: / Ceres Seq. ID 1571946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2177:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Leu | Glu | Ala | Thr | Met | Ile | Cys | Ile | Asp | Asn | Ser | Glu | Trp | Met |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Arg | Asn | Gly | Asp | Tyr | Ser | Pro | Ser | Arg | Leu | Gln | Ala | Gln | Thr | Glu | Ala |
|     |     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |
| Val | Asn | Leu | Leu | Cys | Gly | Ala | Lys | Thr | Gln | Ser | Asn | Pro | Glu | Asn | Thr |
|     |     |     |     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |
| Val | Gly | Ile | Leu | Thr | Met | Ala | Gly | Lys | Gly | Val | Arg | Val | Leu | Thr | Thr |
|     |     |     |     | 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |
| Pro | Thr | Ser | Asp | Leu | Gly | Lys | Ile | Leu | Ala | Cys | Met | His | Gly | Leu | Asp |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |     |
| Val | Gly | Gly | Glu | Ile | Asn | Leu | Thr | Ala | Ala | Ile | Gln | Ile | Ala | Gln | Leu |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ala | Leu | Lys | His | Arg | Gln | Asn | Lys | Asn | Gln | Arg | Gln | Arg | Ile | Ile | Val |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Phe | Ala | Gly | Ser | Pro | Ile | Lys | Tyr | Glu | Lys | Lys | Ala | Leu | Glu | Ile | Val |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Gly | Lys | Arg | Leu | Lys | Lys | Asn | Ser | Val | Ser | Leu | Asp | Ile | Val | Asn | Phe |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |
| Gly | Glu | Asp | Asp | Asp | Glu | Glu | Lys | Pro | Gln | Lys | Leu | Glu | Ala | Leu | Leu |
|     |     |     |     | 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |
| Thr | Ala | Val | Asn | Asn | Asn | Asp | Gly | Ser | His | Ile | Val | His | Val | Pro | Ser |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Gly | Ala | Asn | Ala | Leu | Ser | Asp | Val | Leu | Ser | Thr | Pro | Val | Phe | Thr |     |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Gly | Asp | Glu | Gly | Ala | Ser | Gly | Tyr | Val | Ser | Ala | Ala | Ala | Ala | Ala | Ala |
|     |     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |
| Ala | Ala | Gly | Gly | Asp | Phe | Asp | Phe | Gly | Val | Asp | Pro | Asn | Ile | Asp | Pro |
|     |     |     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |
| Glu | Leu | Ala | Leu | Ala | Leu | Arg | Val | Ser | Met | Glu | Glu | Glu | Arg | Ala | Arg |
|     |     |     |     | 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |
| Gln | Glu | Ala | Ala | Ala | Lys | Lys | Ala | Ala | Asp | Glu | Ala | Cys | Gln | Lys | Asp |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Lys | Asp | Gly | Asp | Thr | Ala | Ser | Ala | Ser | Gln | Glu | Thr | Val | Ala | Arg | Thr |
|     |     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Thr | Asp | Lys | Asn | Ala | Glu | Pro | Met | Asp | Glu | Asp | Ser | Ala | Leu | Leu | Asp |
|     |     |     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |
| Gln | Ala | Ile | Ala | Met | Ser | Xaa | Gly | Asp | Val | Asn | Met | Ser | Glu | Ala | Ala |
|     |     |     |     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |
| Asp | Glu | Asp | Gln | Asp | Leu | Ala | Leu | Ala | Leu | Gln | Met | Ser | Met | Ser | Gly |
|     |     |     |     | 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |
| Glu | Glu | Ser | Ser | Glu | Ala | Thr | Gly | Ala | Gly | Asn | Asn | Leu | Leu | Gly | Asn |
|     |     |     |     | 325 |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Gln | Ala | Phe | Ile | Ser | Ser | Val | Leu | Ser | Ser | Leu | Pro | Gly | Val | Asp | Pro |
|     |     |     |     | 340 |     |     |     | 345 |     |     |     |     |     | 350 |     |
| Asn | Asp | Pro | Ala | Val | Lys | Glu | Leu | Leu | Ala | Ser | Leu | Pro | Asp | Glu | Ser |
|     |     |     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |
| Lys | Arg | His | Glu | Glu | Glu | Glu | Ser | Ser | Ser | Ser | Lys | Lys | Gly | Glu | Asp |
|     |     |     |     | 370 |     |     |     | 375 |     |     |     |     |     | 380 |     |
| Lys | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..380

(D) OTHER INFORMATION: / Ceres Seq. ID 1571947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2178:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Cys | Ile | Asp | Asn | Ser | Glu | Trp | Met | Arg | Asn | Gly | Asp | Tyr | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Ser | Arg | Leu | Gln | Ala | Gln | Thr | Glu | Ala | Val | Asn | Leu | Leu | Cys | Gly |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ala | Lys | Thr | Gln | Ser | Asn | Pro | Glu | Asn | Thr | Val | Gly | Ile | Leu | Thr | Met |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Ala | Gly | Lys | Gly | Val | Arg | Val | Leu | Thr | Thr | Pro | Thr | Ser | Asp | Leu | Gly |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |



Lys Ile Leu Ala Cys Met His Gly Leu Asp Val Gly Gly Glu Ile Asn  
65 70 75 80  
Leu Thr Ala Ala Ile Gln Ile Ala Gln Leu Ala Leu Lys His Arg Gln  
85 90 95  
Asn Lys Asn Gln Arg Gln Arg Ile Ile Val Phe Ala Gly Ser Pro Ile  
100 105 110  
Lys Tyr Glu Lys Lys Ala Leu Glu Ile Val Gly Lys Arg Leu Lys Lys  
115 120 125  
Asn Ser Val Ser Leu Asp Ile Val Asn Phe Gly Glu Asp Asp Asp Glu  
130 135 140  
Glu Lys Pro Gln Lys Leu Glu Ala Leu Leu Thr Ala Val Asn Asn Asn  
145 150 155 160  
Asp Gly Ser His Ile Val His Val Pro Ser Gly Ala Asn Ala Leu Ser  
165 170 175  
Asp Val Leu Leu Ser Thr Pro Val Phe Thr Gly Asp Glu Gly Ala Ser  
180 185 190  
Gly Tyr Val Ser Ala Ala Ala Ala Ala Ala Gly Gly Asp Phe  
195 200 205  
Asp Phe Gly Val Asp Pro Asn Ile Asp Pro Glu Leu Ala Leu Ala Leu  
210 215 220  
Arg Val Ser Met Glu Glu Glu Arg Ala Arg Gln Gln Ala Ala Ala Lys  
225 230 235 240  
Lys Ala Ala Asp Glu Ala Cys Gln Lys Asp Lys Asp Gly Asp Thr Ala  
245 250 255  
Ser Ala Ser Gln Glu Thr Val Ala Arg Thr Thr Asp Lys Asn Ala Glu  
260 265 270  
Pro Met Asp Glu Asp Ser Ala Leu Leu Asp Gln Ala Ile Ala Met Ser  
275 280 285  
Xaa Gly Asp Val Asn Met Ser Glu Ala Ala Asp Glu Asp Gln Asp Leu  
290 295 300  
Ala Leu Ala Leu Gln Met Ser Met Ser Gly Glu Glu Ser Ser Glu Ala  
305 310 315 320  
Thr Gly Ala Gly Asn Asn Leu Leu Gly Asn Gln Ala Phe Ile Ser Ser  
325 330 335  
Val Leu Ser Ser Leu Pro Gly Val Asp Pro Asn Asp Pro Ala Val Lys  
340 345 350  
Glu Leu Leu Ala Ser Leu Pro Asp Glu Ser Lys Arg His Glu Glu Glu  
355 360 365  
Glu Ser Ser Ser Lys Lys Gly Glu Asp Glu Lys Lys  
370 375 380

(2) INFORMATION FOR SEQ ID NO:2179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 371 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..371

(D) OTHER INFORMATION: / Ceres Seq. ID 1571948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2179:

Met Arg Asn Gly Asp Tyr Ser Pro Ser Arg Leu Gln Ala Gln Thr Glu  
1 5 10 15  
Ala Val Asn Leu Leu Cys Gly Ala Lys Thr Gln Ser Asn Pro Glu Asn  
20 25 30  
Thr Val Gly Ile Leu Thr Met Ala Gly Lys Gly Val Arg Val Leu Thr  
35 40 45  
Thr Pro Thr Ser Asp Leu Gly Lys Ile Leu Ala Cys Met His Gly Leu  
50 55 60  
Asp Val Gly Gly Glu Ile Asn Leu Thr Ala Ala Ile Gln Ile Ala Gln

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 65                                                              | 70  | 75  | 80  |
| Leu Ala Leu Lys His Arg Gln Asn Lys Asn Gln Arg Gln Arg Ile Ile |     |     |     |
|                                                                 | 85  | 90  | 95  |
| Val Phe Ala Gly Ser Pro Ile Lys Tyr Glu Lys Lys Ala Leu Glu Ile |     |     |     |
|                                                                 | 100 | 105 | 110 |
| Val Gly Lys Arg Leu Lys Lys Asn Ser Val Ser Leu Asp Ile Val Asn |     |     |     |
|                                                                 | 115 | 120 | 125 |
| Phe Gly Glu Asp Asp Asp Glu Glu Lys Pro Gln Lys Leu Glu Ala Leu |     |     |     |
|                                                                 | 130 | 135 | 140 |
| Leu Thr Ala Val Asn Asn Asn Asp Gly Ser His Ile Val His Val Pro |     |     |     |
|                                                                 | 145 | 150 | 155 |
| Ser Gly Ala Asn Ala Leu Ser Asp Val Leu Leu Ser Thr Pro Val Phe |     |     |     |
|                                                                 | 165 | 170 | 175 |
| Thr Gly Asp Glu Gly Ala Ser Gly Tyr Val Ser Ala Ala Ala Ala     |     |     |     |
|                                                                 | 180 | 185 | 190 |
| Ala Ala Ala Gly Gly Asp Phe Asp Phe Gly Val Asp Pro Asn Ile Asp |     |     |     |
|                                                                 | 195 | 200 | 205 |
| Pro Glu Leu Ala Leu Ala Leu Arg Val Ser Met Glu Glu Glu Arg Ala |     |     |     |
|                                                                 | 210 | 215 | 220 |
| Arg Gln Glu Ala Ala Ala Lys Lys Ala Ala Asp Glu Ala Cys Gln Lys |     |     |     |
|                                                                 | 225 | 230 | 235 |
| Asp Lys Asp Gly Asp Thr Ala Ser Ala Ser Gln Glu Thr Val Ala Arg |     |     |     |
|                                                                 | 245 | 250 | 255 |
| Thr Thr Asp Lys Asn Ala Glu Pro Met Asp Glu Asp Ser Ala Leu Leu |     |     |     |
|                                                                 | 260 | 265 | 270 |
| Asp Gln Ala Ile Ala Met Ser Xaa Gly Asp Val Asn Met Ser Glu Ala |     |     |     |
|                                                                 | 275 | 280 | 285 |
| Ala Asp Glu Asp Gln Asp Leu Ala Leu Ala Leu Gln Met Ser Met Ser |     |     |     |
|                                                                 | 290 | 295 | 300 |
| Gly Glu Glu Ser Ser Glu Ala Thr Gly Ala Gly Asn Asn Leu Leu Gly |     |     |     |
|                                                                 | 305 | 310 | 315 |
| Asn Gln Ala Phe Ile Ser Ser Val Leu Ser Ser Leu Pro Gly Val Asp |     |     |     |
|                                                                 | 325 | 330 | 335 |
| Pro Asn Asp Pro Ala Val Lys Glu Leu Ala Ser Leu Pro Asp Glu     |     |     |     |
|                                                                 | 340 | 345 | 350 |
| Ser Lys Arg His Glu Glu Glu Glu Ser Ser Ser Lys Lys Gly Glu Asp |     |     |     |
|                                                                 | 355 | 360 | 365 |
| Glu Lys Lys                                                     |     |     |     |
| 370                                                             |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2180:

|             |            |            |             |             |            |     |
|-------------|------------|------------|-------------|-------------|------------|-----|
| atacttgtaa  | aagctagagt | caacgcggtt | cagttctcaga | ccagacgaaa  | caacgatgct | 60  |
| taactctatc  | actttaacc  | ggaaaccacc | actcccggtc  | aactctctgtg | ggttttcagg | 120 |
| taatacactc  | tcgtcttttt | gtcgaagaac | tataacggaa  | ggtagttcga  | gcaaggctct | 180 |
| ttcgttttgg  | tacaaaaatg | ttggttcaat | gaagtgtggt  | cggagcaatt  | ggccggggcg | 240 |
| ttctgggact  | gcgtttgggc | atctagtcgg | ggctctctgg  | ggtctcagggt | gaaattcagg | 300 |
| tggtctctgg  | gggttaggtg | gttcaggcgg | tggtggtaat  | ggttggttcg  | gcggcggttg | 360 |
| tggtgatgga  | agcgacggaa | aaggaaagaa | cggtgtcaet  | ctctcatagt  | accaggctct | 420 |
| ttctcacaac  | ttctctgttt | tgaccaaaag | tgtgaccgca  | gcacttttga  | acctcggttg | 480 |
| agatttgatc  | tgctcagctt | caatcaacaa | gacctcatcg  | ctggacaaga  | agaggacact | 540 |
| cactttttacc | ttcttgggct | tagggctagt | cggtccaaca  | ttgcattttt  | ggtattttga | 600 |

|            |            |             |            |            |             |      |
|------------|------------|-------------|------------|------------|-------------|------|
| tttgagcaaa | gttgtgacag | cttctggatt  | atcaggcgca | gttataccag | tttactgga   | 660  |
| tcagtttgtt | tttgcctcta | ttttgtgtgg  | agttttctta | tcagcagttg | tgacacttga  | 720  |
| aggaaaacca | tcaaatgtca | taccgaagct  | acaacaggag | tggactgggt | caatgatagc  | 780  |
| aaattggcag | ctatggatac | catttcagtt  | tcttaacttc | agattttgtc | cacagaacta  | 840  |
| ccaggtactt | gcttcaaacg | tagtggcttt  | ggcttggaa  | gtgattttat | cattcaaaagc | 900  |
| tcacaaagaa | gttgttgcaa | agtagacatg  | tttcttaact | ggagcctaga | ggtgggttgc  | 960  |
| ggattgttat | cggcagagtt | ttgggggaaac | gttcttgtct | gctgatgcaa | atgtttgtgtg | 1020 |
| tttcgaaaca | attatttggg | aacctgtcac  | ttgacatitt | cttagagttg | aaacaagctt  | 1080 |
| ttctcaagc  | acttcaata  | tttcccatc   | atcaatgttt | catatattta | ttgKtctctc  | 1140 |

(2) INFORMATION FOR SEQ ID NO:2181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..289
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2181:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Asn | Ser | Ile | Thr | Leu | Thr | Arg | Lys | Pro | Pro | Leu | Pro | Phe | Asn |
| 1   |     | 5   |     |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Val | Gly | Phe | Ser | Gly | Asn | His | Ser | Ser | Ser | Phe | Cys | Arg | Arg | Thr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Thr | Glu | Gly | Ser | Ser | Ser | Lys | Ala | Leu | Ser | Phe | Gly | Tyr | Lys | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Gly | Ser | Leu | Lys | Cys | Gly | Arg | Ser | Asn | Trp | Pro | Gly | Arg | Ser | Gly |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Thr | Ala | Phe | Gly | His | Leu | Val | Arg | Val | Ser | Ala | Val | Ser | Gly | Gly | Asn |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Gly | Gly | Ser | Gly | Gly | Leu | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Asn | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Ser | Gly | Gly | Gly | Gly | Gly | Asp | Gly | Ser | Asp | Gly | Lys | Gly | Lys | Lys |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Arg | Ser | Leu | Leu | Ser | Trp | Tyr | Gln | Ala | Leu | Leu | Ser | Asn | Ser | Pro | Val |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Leu | Thr | Lys | Ala | Val | Thr | Ala | Ala | Leu | Leu | Asn | Leu | Val | Gly | Asp | Leu |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Ile | Cys | Gln | Leu | Thr | Ile | Asn | Lys | Thr | Ser | Ser | Leu | Asp | Lys | Lys | Arg |
| 145 |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Thr | Leu | Thr | Phe | Thr | Phe | Leu | Gly | Leu | Gly | Leu | Val | Gly | Pro | Thr | Leu |
|     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |     |
| His | Phe | Trp | Tyr | Leu | Tyr | Leu | Ser | Lys | Val | Val | Thr | Ala | Ser | Gly | Leu |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ser | Gly | Ala | Val | Ile | Arg | Leu | Leu | Leu | Asp | Gln | Phe | Val | Phe | Ala | Pro |
|     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Ile | Phe | Val | Gly | Val | Phe | Leu | Ser | Ala | Val | Val | Thr | Leu | Glu | Gly | Lys |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Pro | Ser | Asn | Val | Ile | Pro | Lys | Leu | Gln | Gln | Glu | Trp | Thr | Gly | Ala | Met |
| 225 |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Ile | Ala | Asn | Trp | Gln | Leu | Trp | Ile | Pro | Phe | Gln | Phe | Leu | Asn | Phe | Arg |
|     |     | 245 |     |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Phe | Val | Pro | Gln | Asn | Tyr | Gln | Val | Leu | Ala | Ser | Asn | Val | Val | Ala | Leu |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Ala | Trp | Asn | Val | Ile | Leu | Ser | Phe | Lys | Ala | His | Lys | Glu | Val | Val | Ala |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

Lys

(2) INFORMATION FOR SEQ ID NO:2182:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 731 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..731  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2182:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| attttccaca  | acttggaagt | cgaaatccat | ttcgaatttt | ggttagcagc | gatttcaaat | 60  |
| tcacaaacgt  | agaattatgg | cgggagtgaa | tcaggcgtgt | atcttctgtg | agatcgtgcg | 120 |
| aaatccaacc  | actactcgtc | tccttcacac | cgatgagaaa | gtccatcgct | ttcaagacat | 180 |
| caagcctgca  | gccagagggc | actattttgt | gattccaaaa | gaacatatcc | ctactgtgaa | 240 |
| tgacctttag  | agaagagatg | aagactactc | acttgtaaga | cacatgctta | gtgtgggaca | 300 |
| acaactgttg  | cagaaagatg | ctctccaaag | cattcataga | tttggttttc | accagccacc | 360 |
| gatttaacagt | gttgatcatc | tccatctcca | ctgttttgca | ttgccttatg | tgccagatgt | 420 |
| gaaagccatc  | aagtacaagt | ctttgggacc | tttgggtgga | tttatggaag | ccgagacact | 480 |
| gctagagaag  | ataaggCctc | ttctttcaca | gggtMactg  | aacccaactt | gtttaaccgc | 540 |
| attgcgttgc  | ttctctttgc | taaaactgtg | caatatctct | ttctattctt | tttctgtgca | 600 |
| aatctgtgaa  | caaatgccaa | atattattag | agattttgta | tatgaagaaa | ggatgtgtca | 660 |
| agtaattata  | tgtaatttct | gccattgtcc | aatagttaac | acttaacacc | aatctcattg | 720 |
| tttccatgct  | t          |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2183:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 209 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..209  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2183:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Gly | Val | Asn | Gln | Ala | Cys | Ile | Phe | Cys | Glu | Ile | Val | Arg | Asn |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Pro | Thr | Thr | Thr | Arg | Leu | Leu | His | Thr | Asp | Glu | Lys | Val | Ile | Ala | Phe |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gln | Asp | Ile | Lys | Pro | Ala | Ala | Gln | Arg | His | Tyr | Leu | Val | Ile | Pro | Lys |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Glu | His | Ile | Pro | Thr | Val | Asn | Asp | Leu | Gln | Arg | Arg | Asp | Glu | Asp | Tyr |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ser | Leu | Val | Arg | His | Met | Leu | Ser | Val | Gly | Gln | Gln | Leu | Leu | Gln | Lys |  |
|     |     |     | 65  |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Asp | Ala | Pro | Gln | Ser | Ile | His | Arg | Phe | Gly | Phe | His | Gln | Pro | Pro | Phe |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Asn | Ser | Val | Asp | His | Leu | His | Leu | His | Cys | Phe | Ala | Leu | Pro | Tyr | Val |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Pro | Arg | Trp | Lys | Ala | Ile | Lys | Tyr | Lys | Ser | Leu | Gly | Pro | Leu | Gly | Gly |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Phe | Ile | Glu | Ala | Glu | Thr | Leu | Leu | Glu | Lys | Ile | Arg | Pro | Leu | Leu | Ser |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Lys | Val | Xaa | Leu | Asn | Pro | Thr | Cys | Leu | Thr | Ala | Leu | Arg | Cys | Phe | Ser |  |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     |     |  |
| Leu | Leu | Lys | Leu | Cys | Asn | Ile | Ser | Phe | Leu | Phe | Cys | Trp | Gln | Ile |     |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |     |     |     |  |
| Cys | Glu | Gln | Met | Pro | Asn | Ile | Ile | Arg | Asp | Phe | Val | Tyr | Glu | Arg | Arg |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |     |  |
| Met | Cys | Gln | Val | Ile | Ile | Cys | Asn | Phe | Cys | His | Cys | Pro | Ile | Val | Asn |  |

Thr 195 200 205

(2) INFORMATION FOR SEQ ID NO:2184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1571965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2184:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ser | Val | Gly | Gln | Gln | Leu | Leu | Lys | Asp | Ala | Pro | Gln | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | His | Arg | Phe | Gly | Phe | His | Gln | Pro | Pro | Phe | Asn | Ser | Val | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  | His |
| Leu | His | Leu | His | Cys | Phe | Ala | Leu | Pro | Tyr | Val | Pro | Arg | Trp | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     | Ala |
| Ile | Lys | Tyr | Lys | Ser | Leu | Gly | Pro | Leu | Gly | Gly | Phe | Ile | Glu | Ala |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     | Glu |
| Thr | Leu | Leu | Glu | Lys | Ile | Arg | Pro | Leu | Leu | Ser | Lys | Val | Xaa | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Pro | Thr | Cys | Leu | Thr | Ala | Leu | Arg | Cys | Phe | Ser | Leu | Leu | Lys | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  | Cys |
| Asn | Ile | Ser | Phe | Leu | Phe | Phe | Cys | Trp | Gln | Ile | Cys | Glu | Gln | Met |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 | Pro |
| Asn | Ile | Ile | Arg | Asp | Phe | Val | Tyr | Glu | Arg | Arg | Met | Cys | Gln | Val |
|     |     |     | 115 |     |     | 120 |     |     |     |     |     | 125 |     | Ile |
| Ile | Cys | Asn | Phe | Cys | His | Cys | Pro | Ile | Val | Asn | Thr |     |     |     |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1374
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2185:

|             |             |            |            |             |            |     |
|-------------|-------------|------------|------------|-------------|------------|-----|
| aacacaaaaga | caataaaaatt | aatcaaaaat | aaacaaagga | gagagacaga  | agaaacagag | 60  |
| agagtagtta  | attccggtgg  | ttttctgtct | atctactttc | atccaccttc  | atcccttccg | 120 |
| ccccaaaatt  | caattctctc  | ttcctttctc | tctctttctc | cttaaaaaact | ctaactttac | 180 |
| tcatctcact  | tccaaagtct  | caacctttct | tctctaattg | agatctgcac  | ttacttcaaa | 240 |
| tcacaaccac  | cttggtctct  | cattctcttc | gttctggggt | caatctcatt  | cttcaaatcc | 300 |
| attctcaccc  | tctcagatc   | tttctacatc | tacttctctc | gaccatccaa  | aaacctccgc | 360 |
| cgatacgggt  | catgggcaat  | catcaaccga | ccaacagacg | gaatcggtaa  | agctttcgcc | 420 |
| tttcagttag  | cccagaaaag  | tcttaacctt | atactcgttg | ctcgtaacc   | agacaagctc | 480 |
| aaagatgtct  | ctgattccat  | cagatctaa  | tatagtcaaa | ctcagatctt  | gacogttgtg | 540 |
| atggatgtct  | ctggagatat  | tgatgaaggt | gtgaaacgga | ttaaggagag  | tattgaagga | 600 |
| ttgatgtgtg  | ggattttgat  | taataatgtc | ggcatgtctt | atccttatgc  | taagtatttt | 660 |
| catgaggttg  | atgaagagtt  | gatcaataac | ttgattaaga | tcaatgttga  | aggaactaat | 720 |
| aaagttaact  | aaagtctgtt  | gcttaaatat | cttaagagga | agaaaggtgc  | tattattact | 780 |
| atgggtcttg  | gtgctgtctc  | tcttatctct | tcttatctct | tttactctgt  | tattgctgtg | 840 |
| gtcaaaacgt  | acgtggatca  | gttcaaaaag | tgtctacatg | ttgagtataa  | gaagagtggt | 900 |
| attgatgttc  | aatgccaggt  | tccctgttat | gttgcaacaa | agatgacaaa  | aataagaaga | 960 |

gcaccccttct tagttgcac accagagggg tacgcaaagg cagcacTgcg tttttagggc 1020  
tatgaagcgc aatgcacacc gtactggcct cagcgtctca tgggtgcagt tgtctctgca 1080  
ttgccgaaa ggcgtttttga atcatttaac atcaagagat gcctccagat ccggaagaag 1140  
ggctctccaaa aagactccat gaagaaagaa tgaatcttcc aggttttaag tactaccaag 1200  
aatttctctc ttctgaagtt gttggtttct tgaaaagcct ctgttctgaa tcttttgtaa 1260  
gactttgact ctttagtttt ctaagttttt tataatttaa gattaaaaac cctaacgtac 1320  
acgaataatt tacttctctt gtttctattt ataatattaa gcagtggtgt attc

(2) INFORMATION FOR SEQ ID NO:2186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..318

(D) OTHER INFORMATION: / Ceres Seq. ID 1571988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2186:

Met Glu Ile Cys Thr Tyr Phe Lys Ser Gln Pro Thr Trp Leu Leu Ile  
1 5 10 15  
Leu Phe Val Leu Gly Ser Ile Ser Ile Phe Lys Phe Ile Phe Thr Leu  
20 25 30  
Leu Arg Ser Phe Tyr Ile Tyr Phe Leu Arg Pro Ser Lys Asn Leu Arg  
35 40 45  
Arg Tyr Gly Ser Trp Ala Ile Ile Thr Gly Pro Thr Asp Gly Ile Gly  
50 55 60  
Lys Ala Phe Ala Phe Gln Leu Ala Gln Lys Gly Leu Asn Leu Ile Leu  
65 70 75 80  
Val Ala Arg Asn Pro Asp Lys Leu Lys Asp Val Ser Asp Ser Ile Arg  
85 90 95  
Ser Lys Tyr Ser Gln Thr Gln Ile Leu Thr Val Val Met Asp Phe Ser  
100 105 110  
Gly Asp Ile Asp Glu Gly Val Lys Arg Ile Lys Glu Ser Ile Glu Gly  
115 120 125  
Leu Asp Val Gly Ile Leu Ile Asn Asn Ala Gly Met Ser Tyr Pro Tyr  
130 135 140  
Ala Lys Tyr Phe His Glu Val Asp Glu Glu Leu Ile Asn Asn Leu Ile  
145 150 155 160  
Lys Ile Asn Val Glu Gly Thr Thr Lys Val Thr Gln Ala Val Leu Pro  
165 170 175  
Asn Met Leu Lys Arg Lys Lys Gly Ala Ile Ile Asn Met Gly Ser Gly  
180 185 190  
Ala Ala Ala Leu Ile Pro Ser Tyr Pro Phe Tyr Ser Val Tyr Ala Gly  
195 200 205  
Ala Lys Thr Tyr Val Asp Gln Phe Thr Lys Cys Leu His Val Glu Tyr  
210 215 220  
Lys Lys Ser Gly Ile Asp Val Gln Cys Gln Val Pro Leu Tyr Val Ala  
225 230 235 240  
Thr Lys Met Thr Lys Ile Arg Arg Ala Ser Phe Leu Val Ala Ser Pro  
245 250 255  
Glu Gly Tyr Ala Lys Ala Ala Leu Arg Phe Val Gly Tyr Glu Ala Gln  
260 265 270  
Cys Thr Pro Tyr Trp Pro His Ala Leu Met Gly Ala Val Val Ser Ala  
275 280 285  
Leu Pro Glu Ser Val Phe Glu Ser Phe Asn Ile Lys Arg Cys Leu Gln  
290 295 300  
Ile Arg Lys Lys Gly Leu Gln Lys Asp Ser Met Lys Lys Glu  
305 310 315

(2) INFORMATION FOR SEQ ID NO:2187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..210  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571989  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2187:  
Met Asp Phe Ser Gly Asp Ile Asp Glu Gly Val Lys Arg Ile Lys Glu  
1 5 10 15  
Ser Ile Glu Gly Leu Asp Val Gly Ile Leu Ile Asn Asn Ala Gly Met  
20 25 30  
Ser Tyr Pro Tyr Ala Lys Tyr Phe His Glu Val Asp Glu Glu Leu Ile  
35 40 45  
Asn Asn Leu Ile Lys Ile Asn Val Glu Gly Thr Thr Lys Val Thr Gln  
50 55 60  
Ala Val Leu Pro Asn Met Leu Lys Arg Lys Lys Gly Ala Ile Ile Asn  
65 70 75 80  
Met Gly Ser Gly Ala Ala Leu Ile Pro Ser Tyr Pro Phe Tyr Ser  
85 90 95  
Val Tyr Ala Gly Ala Lys Thr Tyr Val Asp Gln Phe Thr Lys Cys Leu  
100 105 110  
His Val Glu Tyr Lys Lys Ser Gly Ile Asp Val Gln Cys Gln Val Pro  
115 120 125  
Leu Tyr Val Ala Thr Lys Met Thr Lys Ile Arg Arg Ala Ser Phe Leu  
130 135 140  
Val Ala Ser Pro Glu Gly Tyr Ala Lys Ala Ala Leu Arg Phe Val Gly  
145 150 155 160  
Tyr Glu Ala Gln Cys Thr Pro Tyr Trp Pro His Ala Leu Met Gly Ala  
165 170 175  
Val Val Ser Ala Leu Pro Glu Ser Val Phe Glu Ser Phe Asn Ile Lys  
180 185 190  
Arg Cys Leu Gln Ile Arg Lys Lys Gly Leu Gln Lys Asp Ser Met Lys  
195 200 205  
Lys Glu  
210

(2) INFORMATION FOR SEQ ID NO:2188:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..179  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2188:

Met Ser Tyr Pro Tyr Ala Lys Tyr Phe His Glu Val Asp Glu Glu Leu  
1 5 10 15  
Ile Asn Asn Leu Ile Lys Ile Asn Val Glu Gly Thr Thr Lys Val Thr  
20 25 30  
Gln Ala Val Leu Pro Asn Met Leu Lys Arg Lys Lys Gly Ala Ile Ile  
35 40 45  
Asn Met Gly Ser Gly Ala Ala Ala Leu Ile Pro Ser Tyr Pro Phe Tyr  
50 55 60  
Ser Val Tyr Ala Gly Ala Lys Thr Tyr Val Asp Gln Phe Thr Lys Cys  
65 70 75 80  
Leu His Val Glu Tyr Lys Lys Ser Gly Ile Asp Val Gln Cys Gln Val

|                                                                 |     |  |     |  |     |  |
|-----------------------------------------------------------------|-----|--|-----|--|-----|--|
|                                                                 | 85  |  | 90  |  | 95  |  |
| Pro Leu Tyr Val Ala Thr Lys Met Thr Lys Ile Arg Arg Ala Ser Phe |     |  |     |  |     |  |
|                                                                 | 100 |  | 105 |  | 110 |  |
| Leu Val Ala Ser Pro Glu Gly Tyr Ala Lys Ala Ala Leu Arg Phe Val |     |  |     |  |     |  |
|                                                                 | 115 |  | 120 |  | 125 |  |
| Gly Tyr Glu Ala Gln Cys Thr Pro Tyr Trp Pro His Ala Leu Met Gly |     |  |     |  |     |  |
|                                                                 | 130 |  | 135 |  | 140 |  |
| Ala Val Val Ser Ala Leu Pro Glu Ser Val Phe Glu Ser Phe Asn Ile |     |  |     |  |     |  |
|                                                                 | 145 |  | 150 |  | 155 |  |
| Lys Arg Cys Leu Gln Ile Arg Lys Lys Gly Leu Gln Lys Asp Ser Met |     |  |     |  |     |  |
|                                                                 | 165 |  | 170 |  | 175 |  |
| Lys Lys Glu                                                     |     |  |     |  |     |  |

(2) INFORMATION FOR SEQ ID NO:2189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 917 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..917
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2189:

|             |             |            |            |             |            |     |
|-------------|-------------|------------|------------|-------------|------------|-----|
| attctcaactt | actctttttt  | ttttttttgt | ttcttgttta | gaagaagcaa  | tggccacttc | 60  |
| agcaatccaa  | cactcttctt  | ttgccggcca | aacggctcta | aagccatcca  | acgacctcct | 120 |
| tgcgaagtc   | ggagcctcta  | atggtggcgg | cgcggttata | atgcgcgcta  | ccgtcaagtc | 180 |
| taccctcag   | agcatctggt  | atggaccaga | cgcctcccaa | tacctaggac  | cattctcgga | 240 |
| aaacacacca  | tcatacctaa  | ctggagaata | ccctggagac | tacggctggg  | acaccctgg  | 300 |
| ttcttcagcc  | gattccagaaa | cattcgcaaa | gaatcgtgag | ctcgaagtga  | tcacacagta | 360 |
| atgggcaatg  | ttgggagctt  | taggctgcac | cttccctgaa | attctctcaa  | aaaacggagt | 420 |
| caaatccgtt  | gaagccgtgt  | ggttcaaggc | aggatctcaa | atcttctcag  | aaggaggact | 480 |
| tgactacctc  | ggaaacccta  | acttgatcca | cgccgaaagc | atattagcta  | tatggcgctg | 540 |
| tcaagttgtg  | ctaattgggat | tcattgaagg | gtacagaaac | ggaggtggtc  | ctcttgggga | 600 |
| agggcctgac  | ccgcttttacc | cgggcggggc | cttcgaccgc | ttgaacttag  | cgtaggatcc | 660 |
| agaagcgttt  | tcggagttga  | aagtgaagga | gcttaaaaaa | ggctgctctg  | ctatgtttct | 720 |
| aatgtttgga  | ttctttgttc  | aagccatagt | taccggtaaa | ggctcgatcg  | aaaatctgtt | 780 |
| cgatcacatt  | gcagaccctg  | tggctaacca | tgcttgGGct | tacgccaacca | actctgtccc | 840 |
| cggaaaaatg  | agtttgatcg  | gataatttat | gtaaattata | tcttttaaac  | attttcaatt | 900 |
| gcattaaagt  | tatcccc     |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..217
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2190:

|                                                                 |    |
|-----------------------------------------------------------------|----|
| Phe Ser Leu Thr Ser Phe Leu Phe Leu Cys Ser Cys Leu Glu Glu Ala |    |
| 1                                                               | 5  |
|                                                                 | 10 |
| Met Ala Thr Ser Ala Ile Gln His Ser Ser Phe Ala Gly Gln Thr Ala |    |
|                                                                 | 20 |
|                                                                 | 25 |
| Leu Lys Pro Ser Asn Asp Leu Leu Arg Lys Val Gly Ala Ser Asn Gly |    |
|                                                                 | 35 |
|                                                                 | 40 |
| Gly Gly Arg Val Ile Met Arg Arg Thr Val Lys Ser Thr Pro Gln Ser |    |
|                                                                 | 50 |
|                                                                 | 55 |
|                                                                 | 60 |



Ile Trp Tyr Gly Pro Asp Arg Pro Lys Tyr Leu Gly Pro Phe Ser Glu  
65 70 75 80  
Asn Thr Pro Ser Tyr Leu Thr Gly Glu Tyr Pro Gly Asp Tyr Gly Trp  
85 90 95  
Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr Phe Ala Lys Asn Arg  
100 105 110  
Glu Leu Gly Val Ile His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly  
115 120 125  
Cys Thr Phe Pro Glu Ile Leu Ser Lys Asn Gly Val Lys Phe Gly Glu  
130 135 140  
Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe Ser Glu Gly Gly Leu  
145 150 155 160  
Asp Tyr Leu Gly Asn Pro Asn Leu Ile His Ala Gln Ser Ile Leu Ala  
165 170 175  
Ile Trp Ala Cys Gln Val Val Leu Met Gly Phe Ile Glu Gly Tyr Arg  
180 185 190  
Ile Gly Gly Gly Pro Leu Gly Glu Gly Leu Asp Pro Leu Tyr Pro Gly  
195 200 205  
Gly Ala Phe Asp Pro Leu Asn Leu Ala  
210 215

(2) INFORMATION FOR SEQ ID NO:2191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..201

(D) OTHER INFORMATION: / Ceres Seq. ID 1572001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2191:

Met Ala Thr Ser Ala Ile Gln His Ser Ser Phe Ala Gly Gln Thr Ala  
1 5 10 15  
Leu Lys Pro Ser Asn Asp Leu Leu Arg Lys Val Gly Ala Ser Asn Gly  
20 25 30  
Gly Gly Arg Val Ile Met Arg Arg Thr Val Lys Ser Thr Pro Gln Ser  
35 40 45  
Ile Trp Tyr Gly Pro Asp Arg Pro Lys Tyr Leu Gly Pro Phe Ser Glu  
50 55 60  
Asn Thr Pro Ser Tyr Leu Thr Gly Glu Tyr Pro Gly Asp Tyr Gly Trp  
65 70 75 80  
Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr Phe Ala Lys Asn Arg  
85 90 95  
Glu Leu Glu Val Ile His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly  
100 105 110  
Cys Thr Phe Pro Glu Ile Leu Ser Lys Asn Gly Val Lys Phe Gly Glu  
115 120 125  
Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe Ser Glu Gly Gly Leu  
130 135 140  
Asp Tyr Leu Gly Asn Pro Asn Leu Ile His Ala Gln Ser Ile Leu Ala  
145 150 155 160  
Ile Trp Ala Cys Gln Val Val Leu Met Gly Phe Ile Glu Gly Tyr Arg  
165 170 175  
Ile Gly Gly Gly Pro Leu Gly Glu Gly Leu Asp Pro Leu Tyr Pro Gly  
180 185 190  
Gly Ala Phe Asp Pro Leu Asn Leu Ala  
195 200

(2) INFORMATION FOR SEQ ID NO:2192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..164  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572002  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2192:  
Met Arg Arg Thr Val Lys Ser Thr Pro Gln Ser Ile Trp Tyr Gly Pro  
1 5 10 15  
Asp Arg Pro Lys Tyr Leu Gly Pro Phe Ser Glu Asn Thr Pro Ser Tyr  
20 25 30  
Leu Thr Gly Glu Tyr Pro Gly Asp Tyr Gly Trp Asp Thr Ala Gly Leu  
35 40 45  
Ser Ala Asp Pro Glu Thr Phe Ala Lys Asn Arg Glu Leu Glu Val Ile  
50 55 60  
His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly Cys Thr Phe Pro Glu  
65 70 75 80  
Ile Leu Ser Lys Asn Gly Val Lys Phe Gly Glu Ala Val Trp Phe Lys  
85 90 95  
Ala Gly Ser Gln Ile Phe Ser Glu Gly Gly Leu Asp Tyr Leu Gly Asn  
100 105 110  
Pro Asn Leu Ile His Ala Gln Ser Ile Leu Ala Ile Trp Ala Cys Gln  
115 120 125  
Val Val Leu Met Gly Phe Ile Glu Gly Tyr Arg Ile Gly Gly Gly Pro  
130 135 140  
Leu Gly Glu Gly Leu Asp Pro Leu Tyr Pro Gly Ala Phe Asp Pro  
145 150 155 160  
Leu Asn Leu Ala

(2) INFORMATION FOR SEQ ID NO:2193:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 932 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..932  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2193:

attacctctc tctcaattcac ctctcgctaa gttgtcggtta gcCgttaggg ttccgatcta 60  
atcatggcgg acctgtgttt gaaggagggt aactgtggcc ggccctgaaa gatccgaag 120  
ttggacaaag cttgcgaagg atcgaaatcg tccctggaac atctcaagct aggaacacgtg 180  
gaagatgatg agtatctctcg acagtatgtt ttgtttcact acgaattcca taaatccgag 240  
ggtttcacgg ttgattggga gaaatatgac tacatgttcc atataaggcc gtggaaaaat 300  
tcaccaccta tcagcgatat acgaaccaat gctgatgtga tccgtgatgt gacactcttt 360  
gcatttgaga aacacaatga agctcatgga tctaaacttg tgtttgtcga gcatgtctca 420  
gctaatttca aattttccaa tggctctcct tgctgggtta cattctgggc taccgatattg 480  
gcctcatctg ctctcacatc gcagatctat caagtcgaac ttggcgctcg cggaaaacag 540  
tttgaatttc ccatcttcag ggtcaagcct aaggacgaag agatggatga tgttgaagtg 600  
aaaccacocct ctccatgcc ttatgatgac tatgataaac caccggttgt ctttgttcga 660  
gcgtctcctg aagatggtgt ccccttctgc ttgtatcgaa ctggagctct ttatgatctc 720  
tatcggtctg gttttgaagg aaaaagtata tataaccattc ctttggtagc aaagagatat 780  
gatgttagtc actgactgaa aaatcaaaat aggccttgat taatatata cctctggaat 840  
tttcaacttc ttctattctc taaaatgtac tagcttctct tctagagatc tatgaacaca 900  
aatagaattg atattcaaaa atccatttgt tt

(2) INFORMATION FOR SEQ ID NO:2194:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..224
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1572024
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2194:

Met Ala Asp Ser Val Leu Lys Glu Val Asn Cys Gly Arg Pro Glu Lys  
1 5 10 15  
Ile Pro Lys Leu Asp Lys Ala Cys Glu Gly Ser Lys Ser Ser Trp Lys  
20 25 30  
His Leu Lys Leu Gly Asn Val Glu Asp Asp Glu Tyr Leu Arg Gln Tyr  
35 40 45  
Cys Leu Phe His Tyr Glu Phe His Lys Ser Glu Gly Phe Thr Val Asp  
50 55 60  
Trp Glu Lys Tyr Asp Tyr Met Phe His Ile Arg Pro Leu Glu Asn Ser  
65 70 75 80  
Pro Pro Ile Ser Asp Ile Arg Thr Asn Ala Asp Val Ile Arg Asp Val  
85 90 95  
Thr Leu Phe Ala Ile Glu Lys His Asn Glu Ala His Gly Ser Lys Leu  
100 105 110  
Val Phe Val Glu His Val Ser Ala Asn Phe Lys Phe Ala Asn Gly Leu  
115 120 125  
Leu Cys Trp Leu Thr Phe Trp Ala Thr Asp Met Ala Ser Ser Ala Pro  
130 135 140  
Thr Ser Gln Ile Tyr Gln Val Glu Leu Trp Arg Arg Gly Lys Gln Phe  
145 150 155 160  
Glu Ile Pro Ile Phe Arg Val Lys Pro Lys Asp Glu Glu Met Asp Asp  
165 170 175  
Val Glu Val Lys Pro Pro Ser Pro Met Pro Tyr Asp Asp Tyr Asp Lys  
180 185 190  
Pro Pro Val Val Phe Val Arg Ala Ala Pro Glu Asp Gly Val Pro Phe  
195 200 205  
Val Phe Asp Arg Thr Gly Ala Leu Tyr Asp Leu Tyr Arg Ser Gly Leu  
210 215 220

(2) INFORMATION FOR SEQ ID NO:2195:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 154 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572025
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2195:

Met Phe His Ile Arg Pro Leu Glu Asn Ser Pro Pro Ile Ser Asp Ile  
1 5 10 15  
Arg Thr Asn Ala Asp Val Ile Arg Asp Val Thr Leu Phe Ala Ile Glu  
20 25 30  
Lys His Asn Glu Ala His Gly Ser Lys Leu Val Phe Val Glu His Val  
35 40 45  
Ser Ala Asn Phe Lys Phe Ala Asn Gly Leu Leu Cys Trp Leu Thr Phe  
50 55 60  
Trp Ala Thr Asp Met Ala Ser Ser Ala Pro Thr Ser Gln Ile Tyr Gln

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 65                                                              | 70  | 75  | 80  |
| Val Glu Leu Trp Arg Arg Gly Lys Gln Phe Glu Ile Pro Ile Phe Arg |     |     |     |
|                                                                 | 85  | 90  | 95  |
| Val Lys Pro Lys Asp Glu Glu Met Asp Asp Val Glu Val Lys Pro Pro |     |     |     |
|                                                                 | 100 | 105 | 110 |
| Ser Pro Met Pro Tyr Asp Asp Tyr Asp Lys Pro Pro Val Val Phe Val |     |     |     |
|                                                                 | 115 | 120 | 125 |
| Arg Ala Ala Pro Glu Asp Gly Val Pro Phe Val Phe Asp Arg Thr Gly |     |     |     |
|                                                                 | 130 | 135 | 140 |
| Ala Leu Tyr Asp Leu Tyr Arg Ser Gly Leu                         |     |     |     |
| 145                                                             | 150 |     |     |

(2) INFORMATION FOR SEQ ID NO:2196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..633
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2196:

|            |            |            |             |             |             |     |
|------------|------------|------------|-------------|-------------|-------------|-----|
| tcgaaaaaac | atcacccggg | aatctgacgg | cggcttagta  | cggccggcta  | ctgcacaaaag | 60  |
| gactgtgttc | ttcttaggct | tgatacttgc | cttgggaaga  | atataacaat  | catttttggg  | 120 |
| gtagctaaaa | cgctaagctc | tatogtcata | tcattatcat  | taataacttat | ttgatatcta  | 180 |
| aatatcataa | aaatggccgc | tcgttcactc | tcgggtgcgc  | ttaaatctct  | ttgCtcgcc   | 240 |
| gcattccgaa | gtctgtcttg | ttccattgtc | ttaaaggagga | gttacgttgc  | tacatcgag   | 300 |
| aatgtaacag | cagcaggatt | gagtaaggga | ggttccacca  | gagttatggt  | ggggaagatg  | 360 |
| gaacagagag | gtttagatca | agagccagag | tctgcttggg  | gaccagatcc  | agttactgga  | 420 |
| tactatagac | cttccaatcg | tgccgctgaa | attgatccag  | ctgagctcag  | agaattgctt  | 480 |
| ttgaaaaaca | aagcaaatgc | tttctgagga | ttttgattgg  | ttggttgact  | tggttccagt  | 540 |
| ggaagggtgt | cgtaggcgac | tattatgatt | atgtgtgttt  | atgtttgtct  | tgtatcaact  | 600 |
| attaagtata | aataaagatc | acattaaact | gtc         |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2197:

|                                                                 |     |    |    |  |  |  |  |  |  |
|-----------------------------------------------------------------|-----|----|----|--|--|--|--|--|--|
| Met Ala Ala Arg Ser Leu Ser Gly Ala Val Lys Ser Leu Cys Ser Ala |     |    |    |  |  |  |  |  |  |
| 1                                                               | 5   | 10 | 15 |  |  |  |  |  |  |
| Ala Ser Gly Ser Leu Ser Cys Ser Ile Val Leu Arg Arg Ser Tyr Val |     |    |    |  |  |  |  |  |  |
|                                                                 | 20  | 25 | 30 |  |  |  |  |  |  |
| Ala Thr Ser Gln Asn Val Thr Ala Ala Gly Leu Ser Lys Gly Gly Ser |     |    |    |  |  |  |  |  |  |
|                                                                 | 35  | 40 | 45 |  |  |  |  |  |  |
| Thr Arg Val Met Val Gly Lys Met Glu Gln Arg Gly Leu Asp Gln Glu |     |    |    |  |  |  |  |  |  |
|                                                                 | 50  | 55 | 60 |  |  |  |  |  |  |
| Ala Glu Ser Ala Trp Gly Pro Asp Pro Val Thr Gly Tyr Tyr Arg Pro |     |    |    |  |  |  |  |  |  |
|                                                                 | 65  | 70 | 75 |  |  |  |  |  |  |
| Ser Asn Arg Ala Ala Glu Ile Asp Pro Ala Glu Leu Arg Glu Leu Leu |     |    |    |  |  |  |  |  |  |
|                                                                 | 85  | 90 | 95 |  |  |  |  |  |  |
| Leu Lys Asn Lys Ala Lys Ser Phe                                 |     |    |    |  |  |  |  |  |  |
|                                                                 | 100 |    |    |  |  |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:2198:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..53  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572028  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2198:  
Met Val Gly Lys Met Glu Gln Arg Gly Leu Asp Gln Glu Ala Glu Ser  
1 5 10 15  
Ala Trp Gly Pro Asp Pro Val Thr Gly Tyr Tyr Arg Pro Ser Asn Arg  
20 25 30  
Ala Ala Glu Ile Asp Pro Ala Glu Leu Arg Glu Leu Leu Lys Asn  
35 40 45  
Lys Ala Lys Ser Phe  
50

(2) INFORMATION FOR SEQ ID NO:2199:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 790 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..790  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572029  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2199:  
agaccaccaa gaaaacaaag acctatcgat catgaagatc agacttagca taaccatcat 60  
acttttatca tacacagttgg ctacgggtggc cggacaacaa tgcggtcgctc aaggcgggtgg 120  
tcgaacttgt cccggtaaca tctgctgcag tcagtagcgtt tactgtggta ccaccggga 180  
ckrcrtgtct ccgaccaaca actgtcagag caattgttgg ggaagtgggc ctagcgggacc 240  
aggggagagc gcgtcgaaac tacgcgccac ctaccatttc tataatccgg cgcagaataa 300  
ttgggatttg agagccgtga gtgcttattg ctccacgtgg gatgctgata agccgtacgc 360  
atggcggagc aagtatggct ggaccgcctt ctgcggggccg gcaggacctc gtgggtcaagc 420  
ttcttgcggc aagtgtttaa ggggtgaagaa cacaagaaca aatgctgcag taactgtgag 480  
aatagtggac caatgcagca acggagagctt ggatttggat gtacgaatgt tcaatcfaat 540  
agacaccgat ggttttggct atcaacaagg ccattctcatt gttgactacc aatttgtctga 600  
ctgtggcaat gagctcattg ggcagcctga ttccagaaac atgcttgttt cggccattga 660  
tcgctgttga tattatgtta tgattttgag gtcaaatatc atcggctcac ataaaaataa 720  
taaaagaccg tatatatgta ttgtcagagg atatatgttt cgtatcaata aggaaatttt 780  
aaatattatt

(2) INFORMATION FOR SEQ ID NO:2200:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 222 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..222  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572030  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2200:  
Asp His Gln Glu Asn Lys Asp Leu Ser Ile Met Lys Ile Arg Leu Ser  
1 5 10 15  
Ile Thr Ile Ile Leu Leu Ser Tyr Thr Val Ala Thr Val Ala Gly Gln  
20 25 30

Gln Cys Gly Arg Gln Gly Gly Gly Arg Thr Cys Pro Gly Asn Ile Cys  
35 40 45  
Cys Ser Gln Tyr Gly Tyr Cys Gly Thr Thr Ala Asp Xaa Cys Ser Pro  
50 55 60  
Thr Asn Asn Cys Gln Ser Asn Cys Trp Gly Ser Gly Pro Ser Gly Pro  
65 70 75 80  
Gly Glu Ser Ala Ser Asn Val Arg Ala Thr Tyr His Phe Tyr Asn Pro  
85 90 95  
Ala Gln Asn Asn Trp Asp Leu Arg Ala Val Ser Ala Tyr Cys Ser Thr  
100 105 110  
Trp Asp Ala Asp Lys Pro Tyr Ala Trp Arg Ser Lys Tyr Gly Trp Thr  
115 120 125  
Ala Phe Cys Gly Pro Ala Gly Pro Arg Gly Gln Ala Ser Cys Gly Lys  
130 135 140  
Cys Leu Arg Val Lys Asn Thr Arg Thr Asn Ala Ala Val Thr Val Arg  
145 150 155 160  
Ile Val Asp Gln Cys Ser Asn Gly Gly Leu Asp Val Ala Met  
165 170 175  
Phe Asn Gln Ile Asp Thr Asp Gly Phe Gly Tyr Gln Gln Gly His Leu  
180 185 190  
Ile Val Asp Tyr Gln Phe Val Asp Cys Gly Asn Glu Leu Ile Gly Gln  
195 200 205  
Pro Asp Ser Arg Asn Met Leu Val Ser Ala Ile Asp Arg Val  
210 215 220

(2) INFORMATION FOR SEQ ID NO:2201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1572031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2201:

Met Lys Ile Arg Leu Ser Ile Thr Ile Ile Leu Leu Ser Tyr Thr Val  
1 5 10 15  
Ala Thr Val Ala Gly Gln Gln Cys Gly Arg Gln Gly Gly Gly Arg Thr  
20 25 30  
Cys Pro Gly Asn Ile Cys Cys Ser Gln Tyr Gly Tyr Cys Gly Thr Thr  
35 40 45  
Ala Asp Xaa Cys Ser Pro Thr Asn Asn Cys Gln Ser Asn Cys Trp Gly  
50 55 60  
Ser Gly Pro Ser Gly Pro Gly Glu Ser Ala Ser Asn Val Arg Ala Thr  
65 70 75 80  
Tyr His Phe Tyr Asn Pro Ala Gln Asn Asn Trp Asp Leu Arg Ala Val  
85 90 95  
Ser Ala Tyr Cys Ser Thr Trp Asp Ala Asp Lys Pro Tyr Ala Trp Arg  
100 105 110  
Ser Lys Tyr Gly Trp Thr Ala Phe Cys Gly Pro Ala Gly Pro Arg Gly  
115 120 125  
Gln Ala Ser Cys Gly Lys Cys Leu Arg Val Lys Asn Thr Arg Thr Asn  
130 135 140  
Ala Ala Val Thr Val Arg Ile Val Asp Gln Cys Ser Asn Gly Gly Leu  
145 150 155 160  
Asp Leu Asp Val Ala Met Phe Asn Gln Ile Asp Thr Asp Gly Phe Gly  
165 170 175  
Tyr Gln Gln Gly His Leu Ile Val Asp Tyr Gln Phe Val Asp Cys Gly  
180 185 190  
Asn Glu Leu Ile Gly Gln Pro Asp Ser Arg Asn Met Leu Val Ser Ala

195  
Ile Asp Arg Val  
210

200

205

(2) INFORMATION FOR SEQ ID NO:2202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..719
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2202:

|          |       |         |       |          |         |        |       |        |       |         |        |       |     |
|----------|-------|---------|-------|----------|---------|--------|-------|--------|-------|---------|--------|-------|-----|
| atatattt | gtga  | attagtc | gga   | tatatata | aa      | tacgcg | gttc  | ga     | tattc | caaa    | ttaga  | atagt | 60  |
| catatag  | tca   | cgcggt  | ttata | aacaatt  | cgg     | gtata  | aaatt | gtaagt | caca  | cagaaaa | aaga   |       | 120 |
| aagaaac  | gaa   | acgaa   | acgaa | ttatg    | gattt   | gaagaa | agca  | tcctt  | gtttt | tattc   | ctctct |       | 180 |
| ttctct   | gtctc | cacctg  | caac  | tgcaac   | accca   | ctttg  | ctcac | gcggt  | ctcgc | gatctt  | caac   |       | 240 |
| aagttt   | agcc  | ttcgtt  | gatc  | caaac    | accatga | tgatc  | ctccg | tttca  | agaag | tagaatt | gaa    |       | 300 |
| gccagac  | cggt  | gacgt   | aatcg | aagcca   | atttt   | accgaa | aat   | acagtc | ggtt  | ttaagaa | agg    |       | 360 |
| cggcgga  | gga   | ggagc   | agag  | gtggag   | ggcg    | cttcg  | gcgga | ggagg  | gcga  | gtttc   | gcg    |       | 420 |
| aggaggg  | agat  | tctag   | cagag | gcggtg   | ggag    | aagtt  | ctagc | agagg  | cgga  | gaggg   | agtc   |       | 480 |
| tagcaga  | gga   | ggagga  | atac  | gtccg    | attcc   | gattt  | atggc | gggtg  | gaacg | accgc   | asygg  |       | 540 |
| tcatcat  | tca   | agcgc   | ggcg  | gggaa    | actgc   | tagtg  | gttgg | ttaggt | ctat  | cgattt  | ttagc  |       | 600 |
| cgggttt  | aggt  | ttggtt  | ttttt | aaagct   | ttcta   | tattt  | gattt | accggt | ttag  | gttaaat | gtt    |       | 660 |
| tgatgc   | cggt  | tttgc   | ttcc  | actg     | gtttgc  | tcctc  | ggatt | ttatc  | agaag | tttgtt  | ag     |       |     |

(2) INFORMATION FOR SEQ ID NO:2203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2203:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Leu | Lys | Lys | Ala | Ser | Leu | Phe | Leu | Phe | Leu | Leu | Leu | Cys | Leu |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     |     | 15  |     |
| His | Leu | Gln | Leu | Gln | His | His | Phe | Ala | His | Ala | Val | Ser | Arg | Ser | Ser |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     |     | 30  |     |
| Thr | Ser | Leu | Ala | Phe | Val | Asp | Pro | Asn | His | Asp | Asp | Leu | Pro | Phe | Gln |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     |     | 45  |     |
| Glu | Val | Glu | Leu | Lys | Pro | Asp | Gly | Asp | Val | Ile | Glu | Ala | Asn | Leu | Pro |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Lys | Leu | Thr | Val | Val | Val | Lys | Lys | Gly | Gly | Gly | Gly | Gly | Gly | Arg | Gly |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Gly | Gly | Gly | Phe | Gly | Gly | Gly | Arg | Ser | Phe | Gly | Gly | Gly | Gly | Gly | Ser |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     | 95  |     |
| Ser | Ser | Arg | Gly | Gly | Gly | Ser | Ser | Ser | Arg | Gly | Gly | Gly | Gly | Ser |     |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     |     | 110 |     |
| Ser | Ser | Arg | Gly | Gly | Gly | Ile | Arg | Pro | Ile | Pro | Ile | Tyr | Gly | Gly | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     | 125 |     |
| Thr | His | Arg | Xaa | Gly | His | His | Ser | Ser | Gly | Gly | Arg | Glu | Thr | Ala | Ser |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     |     |     | 140 |     |
| Gly | Trp | Leu | Gly | Leu | Ser | Ile | Leu | Ala | Gly | Leu | Gly | Leu | Val | Phe |     |
|     |     |     | 145 |     |     |     | 150 |     |     |     |     |     |     | 155 |     |

(2) INFORMATION FOR SEQ ID NO:2204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1411 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1411  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2204:

|             |            |             |            |             |             |      |
|-------------|------------|-------------|------------|-------------|-------------|------|
| ttctaaagta  | acgcgataaa | tctaatgcatt | tcccacgatt | tgtgtttgtc  | cctctgacga  | 60   |
| aaaatcctcg  | gatctgttgc | attctotcca  | aagcttgaat | cagaagaag   | cttttgaaga  | 120  |
| tcagcctaaa  | agtgatctct | cataactgct  | taaaagattg | ttgaaactcg  | aagatgtctt  | 180  |
| tggccgagat  | aaacaagaat | gaagtgcaga  | ttgtatttgg | ggctcttatt  | gctgacctta  | 240  |
| cacagttttt  | gaccagctgg | agccctttct  | tctccggatt | ccatctgaat  | gttgtcaaa   | 300  |
| atcatgagct  | caaggaggaa | ctcaacatcc  | cagaaggctt | tgacgtagat  | gtctactcta  | 360  |
| agactgacat  | ggaaaagggt | gtggcgcat   | ccaattccac | catgttctct  | ggctattctt  | 420  |
| gcagatatatt | cggttatctc | gtatctaaaa  | agaagtacat | tgtctctatt  | gatgatgatt  | 480  |
| gtgtcccCtg  | ctaaagatcc | gaagggttcc  | ctagtggatg | ctgttactca  | gcacgtgac   | 540  |
| aaccttgaaa  | accagccacc | gcctctcttc  | ttcaacaccc | tttatgatcc  | ttactgcgag  | 600  |
| ggagctggatt | ttgtccgttg | atacccttcc  | agcctcagaa | gtgggtgcc   | ttgtgtcgca  | 660  |
| tttgtgtggc  | tttggcttaa | tctagctgat  | cttgatgctc | caacacaa    | gtctcaagca  | 720  |
| gagaaaagga  | acactgcata | tgttgatgcg  | gttatgactg | tcccgcccaa  | ggctatgcta  | 780  |
| cccataacgc  | gaatcaacat | tgccttttaac | cgcgagttgg | tgggtccagc  | tttgggtcct  | 840  |
| gcactcagat  | tggctggaga | aggaaaagtg  | agatgggaaa | cacttgaaga  | tggtttgggtg | 900  |
| ggagatgttc  | tgaacaacat | ctctgatcat  | ttgggttatg | gtgtgaaaac  | cggactgcct  | 960  |
| tatgtgtgga  | gaacagagag | aggagatgca  | gtggagagtt | tgaagaaaga  | atgggaagga  | 1020 |
| atgaagctga  | tggagaaaag | tgttccattt  | tgcattcat  | tgaaattgcc  | cgagaactgcg | 1080 |
| cttaaaagttg | aagattgtgt | gattgagctt  | gtcaaaacgg | tgaagagaga  | gttaggttca  | 1140 |
| gatgatctcg  | cctttacgca | agctgctgat  | gctatggtta | agtggtgtcca | gctctggaa   | 1200 |
| tctgttaatt  | ctagcgcctg | aagttgaaca  | atctcttgag | gttaggtgtcc | tttatcactt  | 1260 |
| ctaagcatat  | tatcatgtct | cagagattta  | ccaagtcgt  | tttcttctct  | ttagatcat   | 1320 |
| catgtttatt  | ttctcttttt | atctaaatta  | taagcatgtg | ttttgagac   | actcaataat  | 1380 |
| gtaacctgat  | gaaccccatc | tgcttggact  | c          |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..290  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2205:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Thr | Leu | Arg | Leu | Thr | Trp | Lys | Arg | Leu | Trp | Ala | His | Pro | Ile |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Pro | Pro | Cys | Ser | Leu | Ala | Ile | Leu | Ala | Asp | Ile | Ser | Val | Ile | Ser | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Leu | Lys | Arg | Ser | Thr | Leu | Ser | Leu | Leu | Met | Met | Ile | Val | Ser | Pro | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Lys | Asp | Pro | Lys | Gly | Phe | Leu | Val | Asp | Ala | Val | Thr | Gln | His | Val | Ile |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Asn | Leu | Glu | Asn | Pro | Ala | Thr | Pro | Leu | Phe | Phe | Asn | Thr | Leu | Tyr | Asp |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Tyr | Cys | Glu | Gly | Ala | Asp | Phe | Val | Arg | Gly | Tyr | Pro | Phe | Ser | Leu |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Arg | Ser | Gly | Val | Pro | Cys | Ala | Ala | Ser | Cys | Gly | Leu | Trp | Leu | Asn | Leu |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ala | Asp | Leu | Asp | Ala | Pro | Thr | Gln | Ala | Leu | Lys | Thr | Glu | Lys | Arg | Asn |



115 120 125  
Thr Ala Tyr Val Asp Ala Val Met Thr Val Pro Ala Lys Ala Met Leu  
130 135 140  
Pro Ile Ser Gly Ile Asn Ile Ala Phe Asn Arg Glu Leu Val Gly Pro  
145 150 155  
Ala Leu Val Pro Ala Leu Arg Leu Ala Gly Glu Lys Val Arg Trp  
165 170 175  
Glu Thr Leu Glu Asp Val Trp Cys Gly Met Cys Leu Lys His Ile Ser  
180 185 190  
Asp His Leu Gly Tyr Gly Val Lys Thr Gly Leu Pro Tyr Val Trp Arg  
195 200 205  
Asn Glu Arg Gly Asp Ala Val Glu Ser Leu Arg Lys Lys Trp Glu Gly  
210 215 220  
Met Lys Leu Met Glu Lys Ser Val Pro Phe Phe Asp Ser Leu Lys Leu  
225 230 235  
Pro Glu Thr Ala Leu Lys Val Glu Asp Cys Val Ile Glu Leu Ala Lys  
245 250 255  
Ala Val Lys Glu Gln Leu Gly Ser Asp Asp Pro Ala Phe Thr Gln Ala  
260 265 270  
Ala Asp Ala Met Val Lys Trp Val Gln Leu Trp Asn Ser Val Asn Ser  
275 280 285  
Ser Ala  
290

(2) INFORMATION FOR SEQ ID NO:2206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..249

(D) OTHER INFORMATION: / Ceres Seq. ID 1572048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2206:

Met Met Ile Val Ser Pro Ala Lys Asp Pro Lys Gly Phe Leu Val Asp  
1 5 10 15  
Ala Val Thr Gln His Val Ile Asn Leu Glu Asn Pro Ala Thr Pro Leu  
20 25 30  
Phe Phe Asn Thr Leu Tyr Asp Pro Tyr Cys Glu Gly Ala Asp Phe Val  
35 40 45  
Arg Gly Tyr Pro Phe Ser Leu Arg Ser Gly Val Pro Cys Ala Ala Ser  
50 55 60  
Cys Gly Leu Trp Leu Asn Leu Ala Asp Leu Asp Ala Pro Thr Gln Ala  
65 70 75 80  
Leu Lys Thr Glu Lys Arg Asn Thr Ala Tyr Val Asp Ala Val Met Thr  
85 90 95  
Val Pro Ala Lys Ala Met Leu Pro Ile Ser Gly Ile Asn Ile Ala Phe  
100 105 110  
Asn Arg Glu Leu Val Gly Pro Ala Leu Val Pro Ala Leu Arg Leu Ala  
115 120 125  
Gly Glu Gly Lys Val Arg Trp Glu Thr Leu Glu Asp Val Trp Cys Gly  
130 135 140  
Met Cys Leu Lys His Ile Ser Asp His Leu Gly Tyr Gly Val Lys Thr  
145 150 155 160  
Gly Leu Pro Tyr Val Trp Arg Asn Glu Arg Gly Asp Ala Val Glu Ser  
165 170 175  
Leu Arg Lys Lys Trp Glu Gly Met Lys Leu Met Glu Lys Ser Val Pro  
180 185 190  
Phe Phe Asp Ser Leu Lys Leu Pro Glu Thr Ala Leu Lys Val Glu Asp  
195 200 205

Cys Val Ile Glu Leu Ala Lys Ala Val Lys Glu Gln Leu Gly Ser Asp  
210 215 220  
Asp Pro Ala Phe Thr Gln Ala Ala Asp Ala Met Val Lys Trp Val Gln  
225 230 235 240  
Leu Trp Asn Ser Val Asn Ser Ser Ala  
245

(2) INFORMATION FOR SEQ ID NO:2207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..248
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572049
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2207:

Met Ile Val Ser Pro Ala Lys Asp Pro Lys Gly Phe Leu Val Asp Ala  
1 5 10 15  
Val Thr Gln His Val Ile Asn Leu Glu Asn Pro Ala Thr Pro Leu Phe  
20 25 30  
Phe Asn Thr Leu Tyr Asp Pro Tyr Cys Glu Gly Ala Asp Phe Val Arg  
35 40 45  
Gly Tyr Pro Phe Ser Leu Arg Ser Gly Val Pro Cys Ala Ala Ser Cys  
50 55 60  
Gly Leu Trp Leu Asn Leu Ala Asp Leu Asp Ala Pro Thr Gln Ala Leu  
65 70 75 80  
Lys Thr Glu Lys Arg Asn Thr Ala Tyr Val Asp Ala Val Met Thr Val  
85 90 95  
Pro Ala Lys Ala Met Leu Pro Ile Ser Gly Ile Asn Ile Ala Phe Asn  
100 105 110  
Arg Glu Leu Val Gly Pro Ala Leu Val Pro Ala Leu Arg Leu Ala Gly  
115 120 125  
Glu Gly Lys Val Arg Trp Glu Thr Leu Glu Asp Val Trp Cys Gly Met  
130 135 140  
Cys Leu Lys His Ile Ser Asp His Leu Gly Tyr Gly Val Lys Thr Gly  
145 150 155 160  
Leu Pro Tyr Val Trp Arg Asn Glu Arg Gly Asp Ala Val Glu Ser Leu  
165 170 175  
Arg Lys Lys Trp Glu Gly Met Lys Leu Met Glu Lys Ser Val Pro Phe  
180 185 190  
Phe Asp Ser Leu Lys Leu Pro Glu Thr Ala Leu Lys Val Glu Asp Cys  
195 200 205  
Val Ile Glu Leu Ala Lys Ala Val Lys Glu Gln Leu Gly Ser Asp Asp  
210 215 220  
Pro Ala Phe Thr Gln Ala Ala Asp Ala Met Val Lys Trp Val Gln Leu  
225 230 235 240  
Trp Asn Ser Val Asn Ser Ser Ala  
245

(2) INFORMATION FOR SEQ ID NO:2208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..652
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2208:

|             |             |             |            |             |             |     |
|-------------|-------------|-------------|------------|-------------|-------------|-----|
| attttttcttt | tcatttcatt  | tctgattgtc  | tttctcagaa | tccttagaac  | acactctgat  | 60  |
| taacgaatca  | aagatogatt  | tgggattgtg  | atcgatcgag | gaagaagatg  | acggaggcga  | 120 |
| tgataaggaa  | gaagccaggaa | atggcgagtg  | tgaaggatat | gccgttgcct  | caggatggtc  | 180 |
| caccacccgg  | tggattcgca  | ccggctccgat | atgctcgccg | gatctctaac  | acgggtccaa  | 240 |
| gcgccatggc  | tattttcttt  | accgtttcag  | gtgcttttgc | tggggggatg  | taccaagtgc  | 300 |
| gtcaggggcaa | caaaatccgc  | agggcgctga  | aggaagagaa | atacgtctgc  | cgtagagcga  | 360 |
| ttctaccAat  | tcttcaagct  | gaagaagatg  | aaaggtttgt | gtctgagtgg  | aagaagtatc  | 420 |
| tagaatacga  | ggcgagtggt  | atgaaggatg  | ttcctggatg | gaaagtcggt  | gaaaacgtgt  | 480 |
| acaattctgg  | tcgctggatg  | cctccagcta  | ctggagagct | tcgtctctgat | gtctcggtaaa | 540 |
| ttatcaatgg  | ctccttttga  | tgatgatgaa  | tgaatgtttg | tttaagcatt  | ttagaacctt  | 600 |
| gatgtttctt  | gtctctcttt  | ttccatcgta  | taataagaga | attgatacat  | ac          |     |

(2) INFORMATION FOR SEQ ID NO:2209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2209:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Glu | Ala | Met | Ile | Arg | Lys | Lys | Pro | Gly | Met | Ala | Ser | Val | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Met | Pro | Leu | Leu | Gln | Asp | Gly | Pro | Pro | Gly | Gly | Phe | Ala | Pro |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Arg | Tyr | Ala | Arg | Arg | Ile | Ser | Asn | Thr | Gly | Pro | Ser | Ala | Met | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ile | Phe | Leu | Thr | Val | Ser | Gly | Ala | Phe | Ala | Trp | Gly | Met | Tyr | Gln | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Gln | Gly | Asn | Lys | Ile | Arg | Arg | Ala | Leu | Lys | Glu | Glu | Lys | Tyr | Ala |
|     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Arg | Arg | Ala | Ile | Leu | Pro | Ile | Leu | Gln | Ala | Glu | Glu | Asp | Glu | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Phe | Val | Ser | Glu | Trp | Lys | Lys | Tyr | Leu | Glu | Tyr | Glu | Ala | Asp | Val | Met |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Asp | Val | Pro | Gly | Trp | Lys | Val | Gly | Glu | Asn | Val | Tyr | Asn | Ser | Gly |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Arg | Trp | Met | Pro | Pro | Ala | Thr | Gly | Glu | Leu | Arg | Pro | Asp | Val | Trp |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2210:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Arg | Lys | Lys | Pro | Gly | Met | Ala | Ser | Val | Lys | Asp | Met | Pro | Leu |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Leu | Gln | Asp | Gly | Pro | Pro | Pro | Gly | Gly | Phe | Ala | Pro | Val | Arg | Tyr | Ala |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Arg | Ile | Ser | Asn | Thr | Gly | Pro | Ser | Ala | Met | Ala | Ile | Phe | Leu | Thr |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Val | Ser | Gly | Ala | Phe | Ala | Trp | Gly | Met | Tyr | Gln | Val | Gln | Gly | Asn |     |

50 55 60  
Lys Ile Arg Arg Ala Leu Lys Glu Glu Lys Tyr Ala Ala Arg Arg Ala  
65 70 75 80  
Ile Leu Pro Ile Leu Gln Ala Glu Glu Asp Glu Arg Phe Val Ser Glu  
85 90 95  
Trp Lys Lys Tyr Leu Glu Tyr Glu Ala Asp Val Met Lys Asp Val Pro  
100 105 110  
Gly Trp Lys Val Gly Glu Asn Val Tyr Asn Ser Gly Arg Trp Met Pro  
115 120 125  
Pro Ala Thr Gly Glu Leu Arg Pro Asp Val Trp  
130 135

(2) INFORMATION FOR SEQ ID NO:2211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2211:

Met Ala Ser Val Lys Asp Met Pro Leu Leu Gln Asp Gly Pro Pro Pro  
1 5 10 15  
Gly Gly Phe Ala Pro Val Arg Tyr Ala Arg Arg Ile Ser Asn Thr Gly  
20 25 30  
Pro Ser Ala Met Ala Ile Phe Leu Thr Val Ser Gly Ala Phe Ala Trp  
35 40 45  
Gly Met Tyr Gln Val Gly Gln Gly Asn Lys Ile Arg Arg Ala Leu Lys  
50 55 60  
Glu Glu Lys Tyr Ala Ala Arg Arg Ala Ile Leu Pro Ile Leu Gln Ala  
65 70 75 80  
Glu Glu Asp Glu Arg Phe Val Ser Glu Trp Lys Lys Tyr Leu Glu Tyr  
85 90 95  
Glu Ala Asp Val Met Lys Asp Val Pro Gly Trp Lys Val Gly Glu Asn  
100 105 110  
Val Tyr Asn Ser Gly Arg Trp Met Pro Pro Ala Thr Gly Glu Leu Arg  
115 120 125  
Pro Asp Val Trp  
130

(2) INFORMATION FOR SEQ ID NO:2212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..600
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2212:

atataaaccc tctcgGcgt gccattgaaa ctctttcaag gagagagctg ctactctgca 60  
accatgtcga agcgaggaag aggaggaacc tctggttaaca agttcaggat gtcactgggt 120  
cttcagtggt cagccactgt gaactgtgct gacaacaccc gagctaagaa cctttacatc 180  
atttcggtta aaggaatcaa gggtcgtctt aaccgtttgc catcagcttg tgttggtgat 240  
atggttatgg ctactgttaa gaaaggttaag cctgatctcc gtaagaaggt gctctcctgt 300  
gtcattgtta ggcagaggaa gctctggcgc cgaaaggacg gtgtcttcac gtatttcgaa 360  
gataatgtgt gtgtcattgt caatccaacg ggtgatatga aaggatctgc tatcactgga 420  
ccaatcgtaa aggagtgtgc tgatctgtgg ccaagaatcg caagtgtctgc gaacgccatc 480

gtttaagcaa gcttgagatc tctatgtttt gtgttgaacg tttagcatta tctctatttg 540  
ggattgtttt tttgttttct cttagacttt tgttatgcct taaagctgat tctagttctc 600

(2) INFORMATION FOR SEQ ID NO:2213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2213:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Lys | Arg | Gly | Arg | Gly | Gly | Thr | Ser | Gly | Asn | Lys | Phe | Arg | Met |
| 1   |     |     |     | 5   |     |     |     |     |     |     |     |     |     | 10  | 15  |
| Ser | Leu | Gly | Leu | Pro | Val | Ala | Ala | Thr | Val | Asn | Cys | Ala | Asp | Asn | Thr |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Gly | Ala | Lys | Asn | Leu | Tyr | Ile | Ile | Ser | Val | Lys | Gly | Ile | Lys | Gly | Arg |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Leu | Asn | Arg | Leu | Pro | Ser | Ala | Cys | Val | Gly | Asp | Met | Val | Met | Ala | Thr |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Val | Lys | Lys | Gly | Lys | Pro | Asp | Leu | Arg | Lys | Lys | Val | Leu | Pro | Ala | Val |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     | 80  |     |
| Ile | Val | Arg | Gln | Arg | Lys | Pro | Trp | Arg | Arg | Lys | Asp | Gly | Val | Phe | Met |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Tyr | Phe | Glu | Asp | Asn | Ala | Gly | Val | Ile | Val | Asn | Pro | Lys | Gly | Asp | Met |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Gly | Ser | Ala | Ile | Thr | Gly | Pro | Ile | Gly | Lys | Glu | Cys | Ala | Asp | Leu |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Trp | Pro | Arg | Ile | Ala | Ser | Ala | Ala | Asn | Ala | Ile | Val |     |     |     |     |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572084

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2214:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | Gly | Leu | Pro | Val | Ala | Ala | Thr | Val | Asn | Cys | Ala | Asp | Asn |
| 1   |     |     |     | 5   |     |     |     |     |     |     |     |     |     | 10  | 15  |
| Thr | Gly | Ala | Lys | Asn | Leu | Tyr | Ile | Ile | Ser | Val | Lys | Gly | Ile | Lys | Gly |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Leu | Asn | Arg | Leu | Pro | Ser | Ala | Cys | Val | Gly | Asp | Met | Val | Met | Ala |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Thr | Val | Lys | Lys | Gly | Lys | Pro | Asp | Leu | Arg | Lys | Lys | Val | Leu | Pro | Ala |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Val | Ile | Val | Arg | Gln | Arg | Lys | Pro | Trp | Arg | Arg | Lys | Asp | Gly | Val | Phe |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     | 80  |     |
| Met | Tyr | Phe | Glu | Asp | Asn | Ala | Gly | Val | Ile | Val | Asn | Pro | Lys | Gly | Asp |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Met | Lys | Gly | Ser | Ala | Ile | Thr | Gly | Pro | Ile | Gly | Lys | Glu | Cys | Ala | Asp |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Trp | Pro | Arg | Ile | Ala | Ser | Ala | Ala | Asn | Ala | Ile | Val |     |     |     |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..81

(D) OTHER INFORMATION: / Ceres Seq. ID 1572085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2215:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Val | Met | Ala | Thr | Val | Lys | Lys | Gly | Lys | Pro | Asp | Leu | Arg | Lys | Lys |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Val | Leu | Pro | Ala | Val | Ile | Val | Arg | Gln | Arg | Lys | Pro | Trp | Arg | Arg | Lys |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asp | Gly | Val | Phe | Met | Tyr | Phe | Glu | Asp | Asn | Ala | Gly | Val | Ile | Val | Asn |  |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Pro | Lys | Gly | Asp | Met | Lys | Gly | Ser | Ala | Ile | Thr | Gly | Pro | Ile | Gly | Lys |  |
|     |     |     |     | 50  |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Glu | Cys | Ala | Asp | Leu | Trp | Pro | Arg | Ile | Ala | Ser | Ala | Ala | Asn | Ala | Ile |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Val |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..519

(D) OTHER INFORMATION: / Ceres Seq. ID 1572094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2216:

|             |             |            |             |            |             |     |
|-------------|-------------|------------|-------------|------------|-------------|-----|
| acatccaaaca | acaaaaaacac | aagcgtagaa | ascaaaaactc | aactaatgtt | gttatcaccc  | 60  |
| aaaagagaag  | agcaaacacac | atggCtttcg | ctttgaggtt  | cttcacatgc | tttgttttga  | 120 |
| cagtggtcat  | cgttgcatca  | gtggatgcag | caataacatg  | tggcacagt  | gcaagtagct  | 180 |
| tgagtcacatg | tctaggctac  | ctatcgaaag | gtgggggtgt  | gccacctccg | tgctgtgcag  | 240 |
| gagtcacaaa  | gttgaacggt  | atggctcaaa | ccacacccga  | ccgccaccaa | gcattgcagat | 300 |
| gcttacagtc  | cqctgcaaaa  | ggggttaate | caagtcNtag  | cctctggcct | tcctggaaaag | 360 |
| tgccgtgttta | gcatacccct  | atcccCatct | ccacgagcac  | caactgcgcc | accatcaagt  | 420 |
| acgggtgggga | ataacgcacat | catttgccgt | aagagtattg  | tttcgtatac | gtaaaataag  | 480 |
| acgcctatct  | aagctgatat  | ttaacctgtc | tttgtttgt   |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1572095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2217:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Gln | Gln | Gln | Lys | His | Lys | Arg | Arg | Lys | Gln | Asn | Ser | Thr | Asn | Cys |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     | 15  |     |     |     |  |
| Val | Ile | Thr | Gln | Lys | Arg | Arg | Ala | Asn | Thr | Met | Ala | Phe | Ala | Leu | Arg |  |
|     |     |     |     | 20  |     |     | 25  |     |     |     |     | 30  |     |     |     |  |

Phe Phe Thr Cys Phe Val Leu Thr Val Phe Ile Val Ala Ser Val Asp  
35 40 45  
Ala Ala Ile Thr Cys Gly Thr Val Ala Ser Ser Leu Ser Pro Cys Leu  
50 55 60  
Gly Tyr Leu Ser Lys Gly Gly Val Val Pro Pro Cys Cys Ala Gly  
65 70 75 80  
Val Lys Lys Leu Asn Gly Met Ala Gln Thr Thr Pro Asp Arg Gln Gln  
85 90 95  
Ala Cys Arg Cys Leu Gln Ser Ala Ala Lys Gly Val Asn Pro Ser Xaa  
100 105 110  
Ser Leu Trp Trp Ser Trp Lys Val Arg Cys  
115 120

(2) INFORMATION FOR SEQ ID NO:2218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2218:

Met Ala Phe Ala Leu Arg Phe Phe Thr Cys Phe Val Leu Thr Val Phe  
1 5 10 15  
Ile Val Ala Ser Val Asp Ala Ala Ile Thr Cys Gly Thr Val Ala Ser  
20 25 30  
Ser Leu Ser Pro Cys Leu Gly Tyr Leu Ser Lys Gly Gly Val Val Pro  
35 40 45  
Pro Pro Cys Cys Ala Gly Val Lys Lys Leu Asn Gly Met Ala Gln Thr  
50 55 60  
Thr Pro Asp Arg Gln Gln Ala Cys Arg Cys Leu Gln Ser Ala Ala Lys  
65 70 75 80  
Gly Val Asn Pro Ser Xaa Ser Leu Trp Pro Ser Trp Lys Val Arg Cys  
85 90 95

(2) INFORMATION FOR SEQ ID NO:2219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..808
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2219:

|             |             |            |             |             |            |     |
|-------------|-------------|------------|-------------|-------------|------------|-----|
| atcaacccaaa | acaaaaacata | aaaaacaagt | ggaagcttta  | aaacgagagg  | gatagagcaa | 60  |
| aaatggcgac  | gtcgggaacg  | tacgtgacgg | aagttccgct  | aaaaggatcg  | gccgagaaat | 120 |
| actacaagag  | gtggaagaac  | gagaaccatg | tcttccctga  | tgctatcgcg  | caccacatcc | 180 |
| aaaatgttac  | cgttcaacga  | ggcgaacatg | actctcacgg  | gtctatcagg  | agttggaact | 240 |
| acacatggga  | tggaaaaggag | gaggtgttca | aggagagaag  | agagatagac  | gatgagacca | 300 |
| aaacgttgac  | gttaagagga  | cttgagggtc | acgtgatgga  | gcagctcaaa  | gtgtacgacg | 360 |
| tcgtctacca  | attcattccc  | aaactctgag | atacctgcac  | cgcgcaaaatc | actttaatat | 420 |
| gggagaagcg  | caacgatgat  | tccccgaac  | caagcggcta  | catgaaattc  | gtcaagagct | 480 |
| tggttgctga  | catgggaaac  | cacgttagcc | CcAAAAAAAAA | AAAAAAAAaaa | ctaatcatc  | 540 |
| attcccacag  | tcgtcgtcat  | catcatcatc | atcatcatca  | tcatcatcat  | catcatcatc | 600 |
| atcatcatca  | tcattcatcat | catcatcatc | atcactatct  | cgaatttataa | gttaagatgt | 660 |

tttcagtata ataaatgggg tcttgtggat cgttcatttc tatgtgtaaa cggtttggtt 720  
ctgtatgatg ctccgatata ttgttatggt catgatcata tgcggggttc gatataatga 780  
ttcttaagat taatttaacta cacatttc

(2) INFORMATION FOR SEQ ID NO:2220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..195
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2220:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Thr | Ser | Gly | Thr | Tyr | Val | Thr | Glu | Val | Pro | Leu | Lys | Gly | Ser |     |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |     |
| Ala | Glu | Lys | Tyr | Lys | Arg | Trp | Lys | Asn | Glu | Asn | His | Val | Phe | Pro |     |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |     |
| Asp | Ala | Ile | Gly | His | His | Ile | Gln | Asn | Val | Thr | Val | His | Glu | Gly | Glu |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| His | Asp | Ser | His | Gly | Ser | Ile | Arg | Ser | Trp | Asn | Tyr | Thr | Trp | Asp | Gly |     |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Lys | Glu | Glu | Val | Phe | Lys | Glu | Arg | Arg | Glu | Ile | Asp | Asp | Glu | Thr | Lys |     |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     |
| Thr | Leu | Thr | Leu | Arg | Gly | Leu | Glu | Gly | His | Val | Met | Glu | Gln | Leu | Lys |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Val | Tyr | Asp | Val | Val | Tyr | Gln | Phe | Ile | Pro | Lys | Ser | Glu | Asp | Thr | Cys |     |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Ile | Gly | Lys | Ile | Thr | Leu | Ile | Trp | Glu | Lys | Arg | Asn | Asp | Asp | Ser | Pro |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Glu | Pro | Ser | Gly | Tyr | Met | Lys | Phe | Val | Lys | Ser | Leu | Val | Ala | Asp | Met |     |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Asn | His | Val | Ser | Pro | Lys | Lys | Lys | Lys | Lys | Lys | Leu | Asn | His | His |     |
|     |     |     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     | 160 |     |
| Ser | His | Ser | Arg | Arg | His | His | His | His | His | His | His | His | His | His | His |     |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| His | His | His | His | His | His | His | His | His | His | His | His | His | His | His | His | Tyr |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Leu | Asp | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 195 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2221:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Gln | Leu | Lys | Val | Tyr | Asp | Val | Val | Tyr | Gln | Phe | Ile | Pro | Lys |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Ser | Glu | Asp | Thr | Cys | Ile | Gly | Lys | Ile | Thr | Leu | Ile | Trp | Glu | Lys | Arg |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asn | Asp | Asp | Ser | Pro | Glu | Pro | Ser | Gly | Tyr | Met | Lys | Phe | Val | Lys | Ser |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu | Val | Ala | Asp | Met | Gly | Asn | His | Val | Ser | Pro | Lys | Lys | Lys | Lys | Lys |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |  |



Lys Leu Asn His His Ser His Ser Arg Arg His His His His His His  
65 70 75 80  
His His His His His His His His His His His His His His His  
85 90 95  
His His His His Tyr Leu Asp Leu  
100

(2) INFORMATION FOR SEQ ID NO:2222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1201

(D) OTHER INFORMATION: / Ceres Seq. ID 1572120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2222:

ctacatgcc gtcgcctgtt accgtccggt gctattctcc ttcacaaatct cacatttttc 60  
gtaccgggta gaagatgaga atcacgcaga tctgtttatg tctggtaata gtggcattgt 120  
cttcaagctc ccatgtctcg tccgatcaga tcttccacgc tcactagttt ggaacattca 180  
gcagaaacaa tctgtgaacca aagtacaaga ttgagttcct tcttgaagat tcaccttttc 240  
accgggtgta taactctggaa tcaatgggta tgttggtata gcattggaat cggtttttat 300  
gtactctacc gaaagaggaa aaagcgacga gtggatggac ttctagtcag caaaaattata 360  
gtactgtgat gatggaaaca cagcaactgg tgaagctaaa gactcctgat gaattgcttc 420  
aaccacttag tgaataatgt ctttttaggc aagagggttg gtggtcttat gagttttggc 480  
atcagaagta tgtgcggcag Ccacacgttg aggatgaaaa caagattgtt caagagtatt 540  
ttttgggtac ttttgaccga gaggcaActg cggcggttaa tcaaaactgtt tctgatgctt 600  
caactgatgc atctcagagg tatcactctc atgtatacac caatgggacc acctggtatc 660  
ttacagatgc acctcgcgaa gtctgaggtga ggtttgtatg cgcagaaaaa agggcaatgg 720  
tcacttcaat cactgaatta tcaacttgca agtacgcact gactgttcag tgcaccaact 780  
tgtgcaagca tvscctgttc cagctagaga aaccagtgtc acacacgac cactgcaatg 840  
cgatcccagtc ggaagaagac gcaacaagaa acaaggaaga acaagcagta gacgaattac 900  
ctaagatgat agctgattct tgaataccgc ctaagtgaat accctaagag taagagttaa 960  
cagcgactgt atatacaaga actagcatat ctccattttc agtggttacc gctgtagtga 1020  
tcatgttttc aattggggtc gcttgcgtgt aggatgatga tactctctct gtaatttttt 1080  
gcatacttaa aatagcattt caatagaagg tactgataaa ccactgttga agcaaaagact 1140  
gcaagcttca tgaatacatat atgtttccgt ttcactaatg aatttgttcc aagtgtaggg 1200

(2) INFORMATION FOR SEQ ID NO:2223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..282

(D) OTHER INFORMATION: / Ceres Seq. ID 1572121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2223:

Met Arg Ile Thr Gln Ile Leu Leu Cys Leu Val Ile Val Ala Leu Ser  
1 5 10 15  
Ser Ser Ser His Val Trp Ser Asp Gln Ile Phe Pro Ala His Leu Val  
20 25 30  
Gly Thr Phe Ser Arg Asn Asn Arg Glu Pro Lys Tyr Lys Ile Glu Phe  
35 40 45  
Leu Pro Glu Asp Ser Pro Phe His Pro Gly Asp Asn Leu Glu Ser Met  
50 55 60  
Val Met Leu Asp Lys His Gly Asn Arg Phe Leu Cys Tyr Leu Pro Lys  
65 70 75 80

Glu Glu Lys Ala Thr Ser Gly Trp Thr Ser Ser Gln Gln Asn Ile Ser  
85 90 95  
Thr Val Met Met Glu Thr Gln Gln Leu Val Lys Leu Lys Thr Pro Asp  
100 105 110  
Glu Leu Leu Gln Pro Leu Ser Glu Lys Cys Leu Phe Arg Gln Glu Gly  
115 120 125  
Trp Trp Ser Tyr Glu Phe Cys His Gln Lys Tyr Val Arg Gln Leu His  
130 135 140  
Val Glu Asp Glu Asn Lys Ile Val Gln Glu Phe Phe Leu Gly Thr Phe  
145 150 155 160  
Asp Pro Glu Ala Thr Ala Ala Phe Asn Gln Thr Val Ser Asp Ala Ser  
165 170 175  
Thr Asp Ala Ser Gln Arg Tyr His Ser His Val Tyr Thr Asn Gly Thr  
180 185 190  
Thr Cys Asp Leu Thr Gly Ser Pro Arg Glu Val Glu Val Arg Phe Val  
195 200 205  
Cys Ala Glu Thr Arg Ala Met Val Thr Ser Ile Thr Glu Leu Ser Thr  
210 215 220  
Cys Lys Tyr Ala Leu Thr Val Gln Cys Pro Thr Leu Cys Lys His Xaa  
225 230 235 240  
Leu Phe Gln Leu Glu Lys Pro Val Ser His Thr Ile His Cys Asn Ala  
245 250 255  
Ile Pro Val Glu Glu Asp Ala Thr Arg Asn Lys Glu Glu Gln Ala Val  
260 265 270  
Asp Glu Ser Pro Lys Met Ile Ala Asp Ser  
275 280

(2) INFORMATION FOR SEQ ID NO:2224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1572122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2224:

Met Val Met Leu Asp Lys His Gly Asn Arg Phe Leu Cys Tyr Leu Pro  
1 5 10 15  
Lys Glu Glu Lys Ala Thr Ser Gly Trp Thr Ser Ser Gln Gln Asn Ile  
20 25 30  
Ser Thr Val Met Met Glu Thr Gln Gln Leu Val Lys Leu Lys Thr Pro  
35 40 45  
Asp Glu Leu Leu Gln Pro Leu Ser Glu Lys Cys Leu Phe Arg Gln Glu  
50 55 60  
Gly Trp Trp Ser Tyr Glu Phe Cys His Gln Lys Tyr Val Arg Gln Leu  
65 70 75 80  
His Val Glu Asp Glu Asn Lys Ile Val Gln Glu Phe Phe Leu Gly Thr  
85 90 95  
Phe Asp Pro Glu Ala Thr Ala Ala Phe Asn Gln Thr Val Ser Asp Ala  
100 105 110  
Ser Thr Asp Ala Ser Gln Arg Tyr His Ser His Val Tyr Thr Asn Gly  
115 120 125  
Thr Thr Cys Asp Leu Thr Gly Ser Pro Arg Glu Val Glu Val Arg Phe  
130 135 140  
Val Cys Ala Glu Thr Arg Ala Met Val Thr Ser Ile Thr Glu Leu Ser  
145 150 155 160  
Thr Cys Lys Tyr Ala Leu Thr Val Gln Cys Pro Thr Leu Cys Lys His  
165 170 175  
Xaa Leu Phe Gln Leu Glu Lys Pro Val Ser His Thr Ile His Cys Asn

180 185 190  
Ala Ile Pro Val Glu Glu Asp Ala Thr Arg Asn Lys Glu Glu Gln Ala  
195 200 205  
Val Asp Glu Ser Pro Lys Met Ile Ala Asp Ser  
210 215

(2) INFORMATION FOR SEQ ID NO:2225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1572123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2225:

Met Leu Asp Lys His Gly Asn Arg Phe Leu Cys Tyr Leu Pro Lys Glu  
1 5 10 15  
Glu Lys Ala Thr Ser Gly Trp Thr Ser Ser Gln Gln Asn Ile Ser Thr  
20 25 30  
Val Met Met Glu Thr Gln Gln Leu Val Lys Leu Lys Thr Pro Asp Glu  
35 40 45  
Leu Leu Gln Pro Leu Ser Glu Lys Cys Leu Phe Arg Gln Glu Gly Trp  
50 55 60  
Trp Ser Tyr Glu Phe Cys His Gln Lys Tyr Val Arg Gln Leu His Val  
65 70 75 80  
Glu Asp Glu Asn Lys Ile Val Gln Glu Phe Phe Leu Gly Thr Phe Asp  
85 90 95  
Pro Glu Ala Thr Ala Phe Asn Gln Thr Val Ser Asp Ala Ser Thr  
100 105 110  
Asp Ala Ser Gln Arg Tyr His Ser His Val Tyr Thr Asn Gly Thr Thr  
115 120 125  
Cys Asp Leu Thr Gly Ser Pro Arg Glu Val Glu Val Arg Phe Val Cys  
130 135 140  
Ala Glu Thr Arg Ala Met Val Thr Ser Ile Thr Glu Leu Ser Thr Cys  
145 150 155 160  
Lys Tyr Ala Leu Thr Val Gln Cys Pro Thr Leu Cys Lys His Xaa Leu  
165 170 175  
Phe Gln Leu Glu Lys Pro Val Ser His Thr Ile His Cys Asn Ala Ile  
180 185 190  
Pro Val Glu Glu Asp Ala Thr Arg Asn Lys Glu Glu Gln Ala Val Asp  
195 200 205  
Glu Ser Pro Lys Met Ile Ala Asp Ser  
210 215

(2) INFORMATION FOR SEQ ID NO:2226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1662 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1662

(D) OTHER INFORMATION: / Ceres Seq. ID 1572139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2226:

aaacctgtat ttatcaatt accacattt gtctaaagcaa aatggattta ttactcatat 60  
ccttaaacac tatcataatc gccgcctaca tgcaaaatct acgacgtcgg ggaatccaaca 120  
taccgcgggg accaccaacg cgatttcttg tcggaaacct tcatcaactg aaaccattat 180  
ggacgcagtc ttctcccgag tggtaacaga ettatggccc catoatatcg gtgtggttag 240

|             |             |             |             |            |            |      |
|-------------|-------------|-------------|-------------|------------|------------|------|
| gatcacagct  | agctgtgttg  | gtctcgagct  | ctgacttagc  | caaacaagt  | ttgagagaca | 300  |
| aagactacca  | actctgtaac  | cgacacagaa  | cgcgaaggat  | gactcagaac | ggcagcgatc | 360  |
| ttatttggct  | tgactacgga  | gcacattatg  | tgaaaaatgag | aaaactctgt | acactcgagc | 420  |
| tcctttcttt  | gaaaagcata  | gagtggttca  | ggctgatgag  | agagatggaa | gtaagtcca  | 480  |
| tggtttaagct | gattttcaat  | gacttcatga  | gcgatgatca  | gaaacccagt | gtgttgagga | 540  |
| actatctaga  | tctctgtgct  | ttgaacattg  | tttcaagatt  | agttatcggg | aaaacattcg | 600  |
| aaccccaaaga | tgggaagagag | tttagatcaa  | ttgtagaaga  | ggagactcgc | ttgcccggcg | 660  |
| caaccaagat  | gcttgattac  | accgtttggc  | ttaaacgtct  | ttcgtcatgg | ttcactagcg | 720  |
| caaaagcgctt | catgaagcac  | atggctcgga  | aaagaatttg  | gtttaaacga | gctgtaattg | 780  |
| atgaagtata  | tggaggaaga  | gatcaaaagt  | gttttgttca  | gagtcgttta | gagttgaaag | 840  |
| agaaggatga  | gctgaccgag  | gagactgtga  | tgggactggg  | ctggaacatg | ttaactcgag | 900  |
| gagctgacac  | aaccgcgata  | actattgaat  | gggcaatggc  | agagatgata | agatgccga  | 960  |
| cogtgaaaga  | aaaggtgaga  | gatgagcttg  | attccgttgg  | tggatccgga | cggttaatgt | 1020 |
| ctgatgcaga  | tatcccaaaa  | ctgcggttcc  | tgcgaatcgt  | actcaaaaga | gcctctcggc | 1080 |
| ttcaccctcc  | aacaccattg  | atgcttccac  | acaaggccag  | cgaatcagtt | caggtagggt | 1140 |
| ggtagcaaat  | tcttaaggga  | gccacggttt  | atgtcaacgt  | gcagcgcatg | gctcgagatc | 1200 |
| ctgcaaaact  | gagtaaccga  | gatgagttta  | gaccagagag  | gtttcttggt | gaggaacacg | 1260 |
| acgttaaaag  | tcaagacttt  | cggttctctc  | catttgggtc  | gggaagacgg | gtgtgtccag | 1320 |
| cogctcaact  | cagctcaatt  | atgatgacat  | tagcactagg  | tagtttggtt | cattgtttct | 1380 |
| catggacatc  | ctctacacct  | cgagaaacaca | ttgacatgac  | cgagaagcct | gattagtgtt | 1440 |
| gtttacatgaa | ggctccattg  | caggctctag  | cttcgtccag  | gctgccacaa | gagttatacc | 1500 |
| tttaactttt  | aactgagata  | gattatatta  | atcaacataa  | gataaagaga | gattctcaat | 1560 |
| tgcgaaaaac  | agatgtagct  | atggcaagat  | ttaggacatg  | gatgatgaaa | tgggtctgat | 1620 |
| aaacagaatg  | tagctattga  | tagtaataaa  | actaaatatt  | cc         |            |      |

(2) INFORMATION FOR SEQ ID NO:2227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..500

(D) OTHER INFORMATION: / Ceres Seq. ID 1572140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2227:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Cys | Ile | Leu | Ser | Ile | Thr | Thr | Leu | Cys | Leu | Ser | Lys | Met | Asp | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Leu | Ile | Ser | Leu | Thr | Thr | Ile | Ile | Ile | Ala | Ala | Tyr | Met | Gln | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Arg | Arg | Arg | Gly | Ser | Asn | Ile | Pro | Pro | Gly | Pro | Pro | Thr | Arg | Phe |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Val | Gly | Asn | Leu | His | Gln | Leu | Lys | Pro | Leu | Trp | Thr | Gln | Ser | Phe |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Glu | Trp | Ser | Gln | Thr | Tyr | Gly | Pro | Ile | Ile | Ser | Val | Trp | Leu | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |     |
| Ser | Gln | Leu | Ala | Val | Val | Val | Ser | Ser | Ser | Asp | Leu | Ala | Lys | Gln | Val |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Leu | Arg | Asp | Lys | Asp | Tyr | Gln | Leu | Cys | Asn | Arg | His | Arg | Thr | Ala | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Met | Thr | Gln | Asn | Gly | Ser | Asp | Leu | Ile | Trp | Ser | Asp | Tyr | Gly | Ala | His |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Tyr | Val | Lys | Met | Arg | Lys | Leu | Cys | Thr | Leu | Glu | Leu | Phe | Ser | Leu | Lys |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Ile | Glu | Cys | Phe | Arg | Ser | Met | Arg | Glu | Met | Glu | Val | Ser | Ser | Met |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |     |
| Val | Lys | Ser | Ile | Phe | Asn | Asp | Phe | Met | Ser | Asp | Asp | Gln | Lys | Pro | Val |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Val | Leu | Arg | Asn | Tyr | Leu | Asp | Ser | Val | Ala | Leu | Asn | Ile | Val | Ser | Arg |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Leu | Val | Ile | Gly | Lys | Thr | Phe | Glu | Pro | Lys | Asp | Gly | Arg | Glu | Phe | Arg |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Leu | Leu | Leu | Ile | Ser | Leu | Thr | Thr | Ile | Ile | Ile | Ala | Ala | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Gln | Asn | Leu | Arg | Arg | Arg | Gly | Ser | Asn | Ile | Pro | Pro | Gly | Pro | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Arg | Phe | Leu | Val | Gly | Asn | Leu | His | Gln | Leu | Lys | Pro | Leu | Trp | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Ser | Phe | Ser | Glu | Trp | Ser | Gln | Thr | Tyr | Gly | Pro | Ile | Ile | Ser | Val |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Trp | Leu | Gly | Ser | Gln | Leu | Ala | Val | Val | Val | Ser | Ser | Ser | Asp | Leu | Ala |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |

Lys Gln Val Leu Arg Asp Lys Asp Tyr Gln Leu Cys Asn Arg His Arg  
85 90 95  
Thr Ala Arg Met Thr Gln Asn Gly Ser Asp Leu Ile Trp Ser Asp Tyr  
100 105 110  
Gly Ala His Tyr Val Lys Met Arg Lys Leu Cys Thr Leu Glu Leu Phe  
115 120 125  
Ser Leu Lys Ser Ile Glu Cys Phe Arg Ser Met Arg Glu Met Glu Val  
130 135 140  
Ser Ser Met Val Lys Ser Ile Phe Asn Asp Phe Met Ser Asp Asp Gln  
145 150 155 160  
Lys Pro Val Val Leu Arg Asn Tyr Leu Asp Ser Val Ala Leu Asn Ile  
165 170 175  
Val Ser Arg Leu Val Ile Gly Lys Thr Phe Glu Pro Lys Asp Gly Arg  
180 185 190  
Glu Phe Arg Ser Ile Val Glu Arg Glu Thr Arg Leu Pro Gly Ala Thr  
195 200 205  
Lys Met Leu Asp Tyr Thr Val Trp Leu Lys Arg Leu Ser Ser Trp Phe  
210 215 220  
Thr Ser Asp Lys Ala Phe Met Lys His Met Ala Arg Lys Arg Asn Trp  
225 230 235 240  
Phe Lys Arg Ala Val Met Asp Glu Val Tyr Gly Gly Arg Asp Gln Lys  
245 250 255  
Cys Phe Val Gln Ser Leu Leu Glu Leu Lys Glu Lys Asp Glu Leu Thr  
260 265 270  
Glu Glu Thr Val Met Gly Leu Val Trp Asn Met Leu Thr Ala Gly Ala  
275 280 285  
Asp Thr Thr Ala Ile Thr Ile Glu Trp Ala Met Ala Glu Met Ile Arg  
290 295 300  
Cys Pro Thr Val Lys Glu Lys Val Gln Asp Glu Leu Asp Ser Val Val  
305 310 315 320  
Gly Ser Gly Arg Leu Met Ser Asp Ala Asp Ile Pro Lys Leu Pro Phe  
325 330 335  
Leu Gln Cys Val Leu Lys Glu Ala Leu Arg Leu His Pro Pro Thr Pro  
340 345 350  
Leu Met Leu Pro His Lys Ala Ser Glu Ser Val Gln Val Gly Gly Tyr  
355 360 365  
Lys Val Pro Lys Gly Ala Thr Val Tyr Val Asn Val Gln Ala Ile Ala  
370 375 380  
Arg Asp Pro Ala Asn Trp Ser Asn Pro Asp Glu Phe Arg Pro Glu Arg  
385 390 395 400  
Phe Leu Val Glu Glu Thr Asp Val Lys Gly Gln Asp Phe Arg Val Leu  
405 410 415  
Pro Phe Gly Ser Gly Arg Arg Val Cys Pro Ala Ala Gln Leu Ser Leu  
420 425 430  
Asn Met Met Thr Leu Ala Leu Gly Ser Leu Leu His Cys Phe Ser Trp  
435 440 445  
Thr Ser Ser Thr Pro Arg Glu His Ile Asp Met Thr Glu Lys Pro Gly  
450 455 460  
Leu Val Cys Tyr Met Lys Ala Pro Leu Gln Ala Leu Ala Ser Ser Arg  
465 470 475 480  
Leu Pro Gln Glu Leu Tyr Leu  
485

(2) INFORMATION FOR SEQ ID NO:2229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1572142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2229:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Asn | Leu | Arg | Arg | Arg | Gly | Ser | Asn | Ile | Pro | Pro | Gly | Pro | Pro |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Arg | Phe | Leu | Val | Gly | Asn | Leu | His | Gln | Leu | Lys | Pro | Leu | Trp | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Ser | Phe | Ser | Glu | Trp | Ser | Gln | Thr | Tyr | Gly | Pro | Ile | Ile | Ser | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Trp | Leu | Gly | Ser | Gln | Leu | Ala | Val | Val | Ser | Ser | Ser | Ser | Asp | Leu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Lys | Gln | Val | Leu | Arg | Asp | Lys | Asp | Tyr | Gln | Leu | Cys | Asn | Arg | His | Arg |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Ala | Arg | Met | Thr | Gln | Asn | Gly | Ser | Asp | Leu | Ile | Trp | Ser | Asp | Tyr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Ala | His | Tyr | Val | Lys | Met | Arg | Lys | Leu | Cys | Thr | Leu | Glu | Leu | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Leu | Lys | Ser | Ile | Glu | Cys | Phe | Arg | Ser | Met | Arg | Glu | Met | Glu | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Ser | Met | Val | Lys | Ser | Ile | Phe | Asn | Asp | Phe | Met | Ser | Ser | Asp | Gln |
|     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Lys | Pro | Val | Val | Leu | Arg | Asn | Tyr | Leu | Asp | Ser | Val | Ala | Leu | Asn | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Ser | Arg | Leu | Val | Ile | Gly | Lys | Thr | Phe | Glu | Pro | Lys | Asp | Gly | Arg |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Phe | Arg | Ser | Ile | Val | Glu | Arg | Glu | Thr | Arg | Leu | Pro | Gly | Ala | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Met | Leu | Asp | Tyr | Thr | Val | Trp | Leu | Lys | Arg | Leu | Ser | Ser | Trp | Phe |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Ser | Asp | Lys | Ala | Phe | Met | Lys | His | Met | Ala | Arg | Lys | Arg | Asn | Trp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Lys | Arg | Ala | Val | Met | Asp | Glu | Val | Tyr | Gly | Gly | Arg | Asp | Gln | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Cys | Phe | Val | Gln | Ser | Leu | Leu | Glu | Leu | Lys | Glu | Lys | Asp | Glu | Leu | Thr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Glu | Thr | Val | Met | Gly | Leu | Val | Trp | Asn | Met | Leu | Thr | Ala | Gly | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | Thr | Thr | Ala | Ile | Thr | Ile | Glu | Trp | Ala | Met | Ala | Glu | Met | Ile | Arg |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Cys | Pro | Thr | Val | Lys | Glu | Lys | Val | Gln | Asp | Glu | Leu | Asp | Ser | Val | Val |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gly | Ser | Gly | Arg | Leu | Met | Ser | Asp | Ala | Asp | Ile | Pro | Lys | Leu | Pro | Phe |
|     |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Leu | Gln | Cys | Val | Leu | Lys | Glu | Ala | Leu | Arg | Leu | His | Pro | Pro | Thr | Pro |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Met | Leu | Pro | His | Lys | Ala | Ser | Glu | Ser | Val | Gln | Val | Gly | Gly | Tyr |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Lys | Val | Pro | Lys | Gly | Ala | Thr | Val | Tyr | Val | Asn | Val | Gln | Ala | Ile | Ala |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Arg | Asp | Pro | Ala | Asn | Trp | Ser | Asn | Pro | Asp | Glu | Phe | Arg | Pro | Glu | Arg |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Phe | Leu | Val | Glu | Glu | Thr | Asp | Val | Lys | Gly | Gln | Asp | Phe | Arg | Val | Leu |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |     |
| Pro | Phe | Gly | Ser | Gly | Arg | Arg | Val | Cys | Pro | Ala | Ala | Gln | Leu | Ser | Leu |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Asn | Met | Met | Thr | Leu | Ala | Leu | Gly | Ser | Leu | Leu | His | Cys | Phe | Ser | Trp |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Thr | Ser | Ser | Thr | Pro | Arg | Glu | His | Ile | Asp | Met | Thr | Glu | Lys | Pro | Gly |
|     |     |     | 435 |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Leu | Val | Cys | Tyr | Met | Lys | Ala | Pro | Leu | Gln | Ala | Leu | Ala | Ser | Ser | Arg |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |

Leu Pro Gln Glu Leu Tyr Leu  
465 470

(2) INFORMATION FOR SEQ ID NO:2230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1390
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2230:

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| aggctccgtcg | cttctcttcc  | atttctcttc | attttctgatt | tgtattetta  | tttttttcca  | 60   |
| gtagctcctcg | ctctgtgaat  | tcttccgctc | acgatagatc  | tgcttatact  | ccttacattc  | 120  |
| aaccttagat  | ctgaacatg   | ggtgcaggtg | gaagaatgcc  | ggttctact   | tcttccaaga  | 180  |
| aatcggaac   | cgacacacaa  | aagcgtgtgc | cgtgcgagaa  | acgccttct   | tgcgtgggag  | 240  |
| atctgaagaa  | agcaatcccg  | cgcattgtt  | tcaaacgctc  | aatcccttc   | tctttctct   | 300  |
| accttatcag  | tgacatcatt  | atagcctcat | gcttctacta  | cgtgccacc   | aattacttct  | 360  |
| ctctctccc   | tcagcctctc  | tcttacttgg | cttggccact  | ctattgggce  | tgtcaagggt  | 420  |
| gtgtcctaac  | tggtatctgg  | gtcatagccc | acgaatgcgg  | tcaccaagca  | tcaagcgaat  | 480  |
| accaatggct  | ggatgacaca  | gttggtctta | tcttccattc  | cttctctctc  | gtcccttact  | 540  |
| tctctggaa   | gtatagtcat  | ggccgtcacc | attccaacac  | tggatccctc  | gaaagagatg  | 600  |
| aagttattgt  | ccccaaagcag | aaatcagcaa | tcaagtgtta  | cgggaaatac  | ctcaacaacc  | 660  |
| ctcttgagcg  | catcatgatg  | ttaaccgtcc | agttgtctct  | cgggtggccc  | tgttacttag  | 720  |
| cttttaacgt  | ctctggcaga  | cgttatgacg | ggttcgttgg  | ccatttcttc  | cccaacgctc  | 780  |
| ccatctacaa  | tgaccgagaa  | cgctccaga  | tatacctctc  | tgatcgcggt  | attctagccg  | 840  |
| tctgttttgg  | tctttaccgt  | tacgctgctg | cacaagggat  | ggcctcgatg  | attctgcctct | 900  |
| acggagtacc  | gcttctgata  | gtgaatgcgt | tctcgttctt  | gatcaactac  | tgcgacaca   | 960  |
| ctcacctctc  | gttgcctcac  | tacgattcat | cagagtgagg  | ctggctcagg  | ggagcttttg  | 1020 |
| ctaccgtaga  | cagagactac  | ggaatcttga | acaaggtgtt  | ccacaacatt  | acagacacac  | 1080 |
| acgtggctca  | tcactgttct  | tcgacaatgc | cgcattataa  | cgcgaatgaa  | gctacaagg   | 1140 |
| cgataaagcc  | aattcttgga  | gaccattacc | agttcgatgg  | aacaccgtgg  | tatgtggcga  | 1200 |
| tgtataggaa  | ggcaaaaggag | tgtatctatg | tagaaccgga  | cagggaagggt | gacaaaggag  | 1260 |
| gtgtgtactg  | gtacaacaat  | aagttatgat | gatgatgggt  | aagaaattgt  | cgacttttct  | 1320 |
| cttgtctgtt  | tgtcttttgt  | taagaagct  | atgcttcgtt  | ttaataatct  | tattgtccat  | 1380 |
| tttgttgtgc  |             |            |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..383
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2231:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ala | Gly | Gly | Arg | Met | Pro | Val | Pro | Thr | Ser | Ser | Lys | Lys | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Thr | Asp | Thr | Thr | Lys | Arg | Val | Pro | Cys | Glu | Lys | Pro | Pro | Phe | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Val | Gly | Asp | Leu | Lys | Lys | Ala | Ile | Pro | Pro | His | Cys | Phe | Lys | Arg | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Pro | Arg | Ser | Phe | Ser | Tyr | Leu | Ile | Ser | Asp | Ile | Ile | Ile | Ala | Ser |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Cys | Phe | Tyr | Tyr | Val | Ala | Thr | Asn | Tyr | Phe | Ser | Leu | Leu | Pro | Gln | Pro |
|     |     |     | 65  |     | 70  |     |     | 75  |     |     |     |     | 80  |     |     |
| Leu | Ser | Tyr | Leu | Ala | Trp | Pro | Leu | Tyr | Trp | Ala | Cys | Gln | Gly | Cys | Val |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Val | Pro | Thr | Ser | Ser | Lys | Lys | Ser | Glu | Thr | Asp | Thr | Thr | Lys |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Val | Pro | Cys | Glu | Lys | Pro | Pro | Phe | Ser | Val | Gly | Asp | Leu | Lys | Lys |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ile | Pro | Pro | His | Cys | Phe | Lys | Arg | Ser | Ile | Pro | Arg | Ser | Phe | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Leu | Ile | Ser | Asp | Ile | Ile | Ile | Ala | Ser | Cys | Phe | Tyr | Tyr | Val | Ala |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Thr | Asn | Tyr | Phe | Ser | Leu | Leu | Pro | Gln | Pro | Leu | Ser | Tyr | Leu | Ala | Trp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Leu | Tyr | Trp | Ala | Cys | Gln | Gly | Cys | Val | Leu | Thr | Gly | Ile | Trp | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

Ile Ala His Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Leu  
100 105 110  
Asp Asp Thr Val Gly Leu Ile Phe His Ser Phe Leu Leu Val Pro Tyr  
115 120 125  
Phe Ser Trp Lys Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser  
130 135 140  
Leu Glu Arg Asp Glu Val Phe Val Pro Lys Gln Lys Ser Ala Ile Lys  
145 150 155 160  
Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu Gly Arg Ile Met Met Leu  
165 170 175  
Thr Val Gln Phe Val Leu Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val  
180 185 190  
Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys His Phe Phe Pro Asn Ala  
195 200 205  
Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln Ile Tyr Leu Ser Asp Ala  
210 215 220  
Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr Arg Tyr Ala Ala Ala Gln  
225 230 235 240  
Gly Met Ala Ser Met Ile Cys Leu Tyr Gly Val Pro Leu Leu Ile Val  
245 250 255  
Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser  
260 265 270  
Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu  
275 280 285  
Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn  
290 295 300  
Ile Thr Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His  
305 310 315 320  
Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile Leu Gly Asp  
325 330 335  
His Tyr Gln Phe Asp Gly Thr Pro Trp Tyr Val Ala Met Tyr Arg Glu  
340 345 350  
Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu Gly Asp Lys Lys  
355 360 365  
Gly Val Tyr Trp Tyr Asn Asn Lys Leu  
370 375

(2) INFORMATION FOR SEQ ID NO:2233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1572150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2233:

Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu Tyr Leu Ala  
1 5 10 15  
Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys His Phe Phe  
20 25 30  
Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln Ile Tyr Leu  
35 40 45  
Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr Arg Tyr Ala  
50 55 60  
Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly Val Pro Leu  
65 70 75 80  
Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr  
85 90 95  
His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg

|                                                                 |                                         |                 |     |  |                 |     |
|-----------------------------------------------------------------|-----------------------------------------|-----------------|-----|--|-----------------|-----|
|                                                                 | 100                                     |                 | 105 |  | 110             |     |
| Gly Ala                                                         | Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile | Leu Asn Lys Val |     |  |                 |     |
|                                                                 | 115                                     | 120             |     |  | 125             |     |
| Phe His Asn Ile Thr Asp Thr His Val Ala His His                 |                                         |                 |     |  | Leu Phe Ser Thr |     |
|                                                                 | 130                                     | 135             |     |  | 140             |     |
| Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile |                                         |                 |     |  |                 |     |
|                                                                 | 145                                     | 150             |     |  | 155             | 160 |
| Leu Gly Asp His Tyr Gln Phe Asp Gly Thr Pro Trp Tyr Val Ala Met |                                         |                 |     |  |                 |     |
|                                                                 | 165                                     | 170             |     |  | 175             |     |
| Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu Gly |                                         |                 |     |  |                 |     |
|                                                                 | 180                                     | 185             |     |  | 190             |     |
| Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu                 |                                         |                 |     |  |                 |     |
|                                                                 | 195                                     | 200             |     |  |                 |     |

(2) INFORMATION FOR SEQ ID NO:2234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2234:

|             |            |             |            |            |             |      |
|-------------|------------|-------------|------------|------------|-------------|------|
| aaaaaaacca  | ataaaattgg | tcgcttcgca  | aaaactgaga | tttgagttct | tccttcggtg  | 60   |
| gaaagagcaa  | attttacttt | taagaaattt  | gaaaacaaag | tttcattaaa | cagatttggtg | 120  |
| ggatttttaa  | tttgaatttt | gatcagtgaa  | tcaacgataa | acgattcgtc | gttatggaag  | 180  |
| gagtttggtc  | acggttaggc | aggttcctga  | cacggtagcg | accggcaacg | gttttcaccg  | 240  |
| gtccgggtcg  | gaagtggaa  | aagaagtggg  | tacacgtctc | tcctccact  | aagaaagaca  | 300  |
| ataataatag  | ctctcccggt | tccgcccgtg  | ctgcagcttc | cgctggtta  | ggtggttcga  | 360  |
| attctgacgg  | cagtaattga | tcgcatttgc  | tgctgtataa | gtgggcacca | ttgtcccgga  | 420  |
| acggtaacgg  | gaatgaagat | ggtaaaagtg  | agagttaatt | tccgagcgag | gacacggtgg  | 480  |
| cgacgggtgc  | agaagatcct | ccgcggcgga  | gattcaaata | cgttccgata | gcagttactg  | 540  |
| aggaacagaa  | gaaggaaatt | acagaaaattg | aggacgatga | taagattgag | gaggaatgaca | 600  |
| agattgatga  | ggataataag | gtcgagcagg  | aagacaaggt | tgatgaggac | aaaactgtag  | 660  |
| aggagtgcag  | cgagaagaaa | gcggaagtgt  | aagtggaaat | ggaggaaaag | cctgatatca  | 720  |
| atgatgttcc  | aatggaagat | attcagcagg  | atgaagaaaa | aatagtacag | gatgatgaag  | 780  |
| aaaaagtagt  | gcgacaagat | ttgaacgaaa  | gcactgtgga | tttaggactg | accttaaatg  | 840  |
| caaacgatgc  | tgatgctgat | gcagaaaaacg | acccgaaaga | ggacaagcca | ttagaagaat  | 900  |
| gataaaactgc | gtgcattggt | ttgttctctc  | acctcaact  | ctcaatatca | attaggaaga  | 960  |
| aagacattac  | agaaagaaca | aagcagtcac  | tagatatgga | cgcagatcct | tgatttggtc  | 1020 |
| tgtaaccocca | tggcttattc | cttttgatgt  | taatgaaat  | gactcattga | ttcagactga  | 1080 |
| tcattcaatt  | cataggcaga | ttcttgctc   |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:2235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..242
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2235:

|                                                                 |    |    |  |  |    |  |
|-----------------------------------------------------------------|----|----|--|--|----|--|
| Met Glu Gly Val Gly Ala Arg Leu Gly Arg Ser Thr Arg Tyr Gly     |    |    |  |  |    |  |
|                                                                 | 5  | 10 |  |  | 15 |  |
| Pro Ala Thr Val Phe Thr Gly Pro Val Arg Lys Trp Lys Lys Lys Trp |    |    |  |  |    |  |
|                                                                 | 20 | 25 |  |  | 30 |  |
| Val His Val Ser Pro Ser Thr Lys Lys Asp Asn Asn Asn Ser Ser Ser |    |    |  |  |    |  |

|     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|
|     | 35  |     | 40  |     | 45  |
| Gly | Ser | Ala | Ala | Ala | Ala |
| 50  |     |     |     | 55  |     |
| Asp | Gly | Ser | Asn | Gly | Ser |
| 65  |     |     | 70  |     |     |
| Ser | Gln | Asn | Gly | Asn | Gly |
|     |     | 85  |     |     | 90  |
| Pro | Ser | Glu | Asp | Thr | Val |
|     |     | 100 |     | 105 |     |
| Arg | Phe | Lys | Tyr | Val | Pro |
|     | 115 |     |     | 120 |     |
| Ile | Thr | Glu | Ile | Glu | Asp |
| 130 |     |     | 135 |     | 140 |
| Asp | Glu | Asp | Asn | Lys | Val |
| 145 |     |     | 150 |     | 155 |
| Thr | Val | Glu | Glu | Ser | Ser |
|     |     | 165 |     |     | 170 |
| Glu | Glu | Lys | Pro | Asp | Ile |
|     |     | 180 |     | 185 |     |
| Asp | Glu | Glu | Lys | Ile | Val |
|     |     | 195 |     | 200 |     |
| Asp | Leu | Asn | Glu | Ser | Thr |
| 210 |     |     |     | 215 |     |
| Asp | Ala | Asp | Ala | Asp | Ala |
| 225 |     |     | 230 |     | 235 |
| Glu | Glu |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..850
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2236:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| ctgagctcag | cttcactttg  | ctcgacgtta | tcttcttcgt | tcagcgacaa | tgcgctcgat | 60  |
| tacgaacetc | gcctcttctc  | tctcttcaat | ctcgcttcac | tcccaagtgt | ctcaaagacc | 120 |
| taacaccatt | tctctccccc  | gcgcgaattc | agtattcgca | ttaccggcga | aatccgcacg | 180 |
| ccgcgctctc | ctatctatca  | ccgccacggt | atctgctcca | ccggaggagg | aggagatagt | 240 |
| tgaactgaag | aaatacgtea  | aatcgaggct | tcccgaggga | tttgctgctc | agaagattat | 300 |
| tggcactgga | cgacgttaag  | gcgcaatcgc | tagagtttgt | cttcaggaa  | gtactgggaa | 360 |
| ggttatcatc | aactatcgtg  | atgccaaagg | gtaccttcag | ggaaatccat | tgtggcttca | 420 |
| gtatgttaaa | gtaccattgg  | tgacttttag | atatgagaat | agctacgaca | tatttgtgaa | 480 |
| agcccatgga | ggcggctctc  | caggtccaag | tcaagcaatt | accttgggag | tcgcacgtgc | 540 |
| actcctgaag | gtaagtgcag  | accacagatc | gcctttgaag | aaggaaaggt | tgctcactag | 600 |
| agatgcgaga | gtgggttgaaa | gaaagaaggc | cgggctcaa  | aaggcgcgta | aagccccaca | 660 |
| attctccaag | cgttaagagt  | tttatatata | attgaatcaa | ctcttcaagt | agaactcctc | 720 |
| gcctccattt | ttttttaaaa  | cttttcttgt | ctattatcgg | tcttttgttt | catgttaagt | 780 |
| tttatgtgta | gacgaactaa  | tacaatctct | gttttgtttg | aatggaacgc | aaagttgata | 840 |
| tgGcttttgt |             |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 1572181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2237:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Ser | Ile | Thr | Asn | Leu | Ala | Ser | Ser | Leu | Ser | Ser | Leu | Ser | Phe |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser | Ser | Gln | Val | Ser | Gln | Arg | Pro | Asn | Thr | Ile | Ser | Phe | Pro | Arg | Ala |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asn | Ser | Val | Phe | Ala | Leu | Pro | Ala | Lys | Ser | Ala | Arg | Arg | Ala | Ser | Leu |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Ile | Thr | Ala | Thr | Val | Ser | Ala | Pro | Pro | Glu | Glu | Glu | Glu | Ile | Val |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Glu | Leu | Lys | Lys | Tyr | Val | Lys | Ser | Arg | Leu | Pro | Gly | Gly | Phe | Ala | Ala |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Gln | Lys | Ile | Ile | Gly | Thr | Gly | Arg | Arg | Lys | Cys | Ala | Ile | Ala | Arg | Val |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Val | Leu | Gln | Glu | Gly | Thr | Gly | Lys | Val | Ile | Ile | Asn | Tyr | Arg | Asp | Ala |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Lys | Glu | Tyr | Leu | Gln | Gly | Asn | Pro | Leu | Trp | Leu | Gln | Tyr | Val | Lys | Val |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Pro | Leu | Val | Thr | Leu | Gly | Tyr | Glu | Asn | Ser | Tyr | Asp | Ile | Phe | Val | Lys |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ala | His | Gly | Gly | Gly | Leu | Ser | Gly | Gln | Ala | Gln | Ala | Ile | Thr | Leu | Gly |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Val | Ala | Arg | Ala | Leu | Leu | Lys | Val | Ser | Ala | Asp | His | Arg | Ser | Pro | Leu |  |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Lys | Lys | Glu | Gly | Leu | Leu | Thr | Arg | Asp | Ala | Arg | Val | Val | Glu | Arg | Lys |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Lys | Ala | Gly | Leu | Lys | Lys | Ala | Arg | Lys | Ala | Pro | Gln | Phe | Ser | Lys | Arg |  |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2238:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 700 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..700

(D) OTHER INFORMATION: / Ceres Seq. ID 1572195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2238:

|             |            |             |             |             |            |     |
|-------------|------------|-------------|-------------|-------------|------------|-----|
| acttgtctctc | atattagttt | gttatacaac  | tcacttagaa  | taattgtagat | tacatttcag | 60  |
| ccaaattcatc | attcttgaga | gaaaaagaaat | cgaagatggc  | aacaaaatcc  | accggaggta | 120 |
| ccgagaaaac  | caagtcgata | gaagtgaaga  | agaaaactaat | caacgtgttg  | atcgtcgatg | 180 |
| atgatccatt  | aaaccgtaga | ctccacgaga  | tgatcatcaa  | aacgatcgga  | ggaatttctc | 240 |
| agactgcaaa  | gaatggcgag | gaggcagtg   | tcctccacgc  | tgacggcgAa  | gcattctttc | 300 |
| accttattct  | aatggataag | gaaatgcctg  | agaggggatg  | agtttcgaca  | actaagaagc | 360 |
| taagagaaat  | gaaagtgaac | tcaatgatcg  | ttggggtaac  | gtcagtagct  | gaccaagaag | 420 |
| aagagcgtaa  | ggctttttat | gaagctgggc  | tcaaccattg  | cttgaaaaaa  | cccttaacca | 480 |
| aggccaaagt  | cttcccgctc | attagccacc  | tcttcgatgc  | ttgatgggat  | aaggctcatt | 540 |
| aatgtatcta  | tattttcaat | catgaaatca  | cctacacgtg  | tatttgacac  | aaaaatctgc | 600 |
| atttgttgtg  | atatagggtt | tctcatatct  | atgtttgatt  | tattttctta  | tcgtccggag | 660 |
| taaaatcatg  | caagtcattt | ctttgggcta  | ataaaatatt  |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..142  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572196  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2239:  
Met Ala Thr Lys Ser Thr Gly Gly Thr Glu Lys Thr Lys Ser Ile Glu  
1 5 10 15  
Val Lys Lys Lys Leu Ile Asn Val Leu Ile Val Asp Asp Asp Pro Leu  
20 25 30  
Asn Arg Arg Leu His Glu Met Ile Ile Lys Thr Ile Gly Gly Ile Ser  
35 40 45  
Gln Thr Ala Lys Asn Gly Glu Glu Ala Val Ile Leu His Arg Asp Gly  
50 55 60  
Glu Ala Ser Phe Asp Leu Ile Leu Met Asp Lys Glu Met Pro Glu Arg  
65 70 75 80  
Asp Gly Val Ser Thr Thr Lys Lys Leu Arg Glu Met Lys Val Thr Ser  
85 90 95  
Met Ile Val Gly Val Thr Ser Val Ala Asp Gln Glu Glu Glu Arg Lys  
100 105 110  
Ala Phe Met Glu Ala Gly Leu Asn His Cys Leu Glu Lys Pro Leu Thr  
115 120 125  
Lys Ala Lys Ile Phe Pro Leu Ile Ser His Leu Phe Asp Ala  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2240:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 104 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..104  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572197  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2240:  
Met Ile Ile Lys Thr Ile Gly Gly Ile Ser Gln Thr Ala Lys Asn Gly  
1 5 10 15  
Glu Glu Ala Val Ile Leu His Arg Asp Gly Glu Ala Ser Phe Asp Leu  
20 25 30  
Ile Leu Met Asp Lys Glu Met Pro Glu Arg Asp Gly Val Ser Thr Thr  
35 40 45  
Lys Lys Leu Arg Glu Met Lys Val Thr Ser Met Ile Val Gly Val Thr  
50 55 60  
Ser Val Ala Asp Gln Glu Glu Glu Arg Lys Ala Phe Met Glu Ala Gly  
65 70 75 80  
Leu Asn His Cys Leu Glu Lys Pro Leu Thr Lys Ala Lys Ile Phe Pro  
85 90 95  
Leu Ile Ser His Leu Phe Asp Ala  
100

(2) INFORMATION FOR SEQ ID NO:2241:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 982 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -

(B) LOCATION: 1..982

(D) OTHER INFORMATION: / Ceres Seq. ID 1572201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2241:

|             |             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| agaacacaaa  | caaaaaacaca | ttgtaacatt  | agttaaagca  | taaagctctt  | ttatgtcgaa  | 60  |
| taataataat  | ctctcgacca  | ccgtgaatca  | agaaacgacg  | acgtctctgt  | aagttctcaat | 120 |
| cacattgcct  | actgatcaat  | ctctcacaac  | ctcaccagga  | tcatctctct  | ctccttcaac  | 180 |
| gagaccttcc  | gggtgatcac  | cggcgagaag  | aacggcgact  | ggattattccg | gcaagcactc  | 240 |
| tatttttcagg | gggattcgac  | tacgtaacgg  | aaaatgggta  | tcggagatta  | gagagccacg  | 300 |
| taaaacgaca  | agaatttggc  | tcgggactta  | tcgggtaccg  | gagatggctg  | ccgccgttta  | 360 |
| cgaagtggct  | cgcttagctt  | taaaaggacc  | aggccgtttt  | gaattttcct  | ggGtttagct  | 420 |
| ttgacttacg  | tggtccgggt  | ttcaaaactct | gctgcggata  | taagagcgcc  | tgctagttaga | 480 |
| gcagcgagga  | ggaagcaacc  | ggatcagggt  | ggggatgaga  | Aggtattgga  | accggttcaa  | 540 |
| cccgcaaaag  | aggaagaatt  | agaagaagtg  | tcgtgtaact  | cgtgttcggt  | ggagtttatg  | 600 |
| gatgaggaag  | cgatgttgaa  | tatgccgact  | ttgttgacgg  | agatggctga  | agggatgttg  | 660 |
| atgagttcac  | cgagaatgat  | gatacatccg  | acgatggaaag | atgattcgcc  | ggagaatcac  | 720 |
| gaaggagata  | atcttttgag  | ttataaatga  | atccattgaa  | gctgctctct  | ttttttattgt | 780 |
| tttcggctcg  | aatgagattt  | tcctccctttt | ttttctcttt  | tggttcgctg  | ttatggaag   | 840 |
| tcaaataggt  | tattaatatg  | atctattaat  | atttttgaaa  | cataatgagt  | ttgaatttga  | 900 |
| atttttccat  | ttttatataa  | atatggttta  | tatgagggaa  | aaatagatac  | atatcgaaga  | 960 |
| tataagaatt  | gtttttctgc  | tt          |             |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2242:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1572202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2243:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Asn | Asn | Asn | Asn | Ser | Pro | Thr | Thr | Val | Asn | Gln | Glu | Thr | Thr |
| 1   |     | 5   |     |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Thr | Ser | Arg | Glu | Val | Ser | Ile | Thr | Leu | Pro | Thr | Asp | Gln | Ser | Pro | Gln |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ser | Pro | Gly | Ser | Ser | Ser | Ser | Pro | Ser | Pro | Arg | Pro | Ser | Gly | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Pro | Ala | Arg | Arg | Thr | Ala | Thr | Gly | Leu | Ser | Gly | Lys | His | Ser | Ile |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Arg | Gly | Ile | Arg | Leu | Arg | Asn | Gly | Lys | Trp | Val | Ser | Glu | Ile | Arg |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| Glu | Pro | Arg | Lys | Thr | Thr | Arg | Ile | Trp | Leu | Gly | Thr | Tyr | Pro | Val | Pro |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Met | Ala | Ala | Ala | Ala | Tyr | Asp | Val | Ala | Ala | Leu | Ala | Leu | Lys | Gly |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Pro | Gly | Arg | Phe | Glu | Phe | Ser | Thr | Val |     |     |     |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1572203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2243:

Met Lys Gln Pro Asp Gln Gly Gly Asp Glu Lys Val Leu Glu Pro Val

|                                                                 |                                                     |    |    |
|-----------------------------------------------------------------|-----------------------------------------------------|----|----|
| 1                                                               | 5                                                   | 10 | 15 |
| Gln Pro Gly                                                     | Lys Glu Glu Glu Leu Glu Glu Val Ser Cys Asn Ser Cys |    |    |
|                                                                 | 20                                                  | 25 | 30 |
| Ser Leu Glu Phe Met Asp Glu Glu Ala Met Leu Asn Met Pro Thr Leu |                                                     |    |    |
|                                                                 | 35                                                  | 40 | 45 |
| Leu Thr Glu Met Ala Glu Gly Met Leu Met Ser Pro Pro Arg Met Met |                                                     |    |    |
|                                                                 | 50                                                  | 55 | 60 |
| Ile His Pro Thr Met Glu Asp Asp Ser Pro Glu Asn His Glu Gly Asp |                                                     |    |    |
|                                                                 | 65                                                  | 70 | 75 |
| Asn Leu Trp Ser Tyr Lys                                         |                                                     |    | 80 |
|                                                                 | 85                                                  |    |    |

(2) INFORMATION FOR SEQ ID NO:2244:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 932 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..932

(D) OTHER INFORMATION: / Ceres Seq. ID 1572204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2244:

|            |            |            |             |             |             |     |
|------------|------------|------------|-------------|-------------|-------------|-----|
| aactgtttga | tttctgagga | gaatccatgt | tttccattcg  | aagaaaactc  | taactttctc  | 60  |
| gttgaagcgt | tgagctctct | acctctttat | ctccggagat  | gtataataac  | atgggacctc  | 120 |
| aaccggggat | gccaaagac  | ccaggaaacc | ctgagccctg  | tccatttggt  | aatcctttca  | 180 |
| ctggagctgg | ctcgggtttt | atccgtgggt | gtttggggag  | gtatggggag  | agaattttag  | 240 |
| gatcgartc  | tgagtatgtt | cagagcaata | taagccggta  | cttctctgat  | cgcgaatact  | 300 |
| atttccaagt | gaatgatcaa | tatgtgagga | ataaactgaa  | gggtgttctg  | tttcttttcc  | 360 |
| tacacggggg | acaatggacc | agaatatctg | aaccagttgg  | tggtaggctc  | tcatacaaac  | 420 |
| ctccaatata | tgatatcaat | gctccCagac | ttgtacattc  | ccatttatggc | atttgggtacc | 480 |
| tacgtttttc | ttgctgggtc | ttcattggga | agtttacacc  | ggaagcctttg |             | 540 |
| aattggctgt | ttgtgaaagg | attggttggt | tggtttttgc  | aagttaagtct | cctgaaagta  | 600 |
| acacttctat | caacttgtag | tgagagggca | ccattactag  | ataattgtggc | atacggaggg  | 660 |
| tatgcttttg | ctggtctctg | tcttgogggc | tttgccaaaa  | taatgtgggg  | atactcgtac  | 720 |
| tacgctgtga | tgccatggac | ttgtctatgc | actgggattt  | tcttgggtgaa | gacgatgaaa  | 780 |
| cgtgtttctg | ttgctgaagt | aagaagttac | gattcggagca | aacatcacta  | ccttctctctg | 840 |
| tttttagcct | tggtccagtt | cccacttttg | atatggcttg  | gtaacattag  | tgittaatttg | 900 |
| cttctttgaa | atgaaaaaag | acgtttttgt | gt          |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1572205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2245:

|                                                                 |    |    |    |
|-----------------------------------------------------------------|----|----|----|
| Met Ile Ser Met Leu Pro Asp Leu Tyr Ile Pro Phe Met Ala Phe Gly |    |    |    |
| 1                                                               | 5  | 10 | 15 |
| Thr Tyr Val Val Leu Ala Gly Leu Ser Leu Gly Leu Asn Gly Lys Phe |    |    |    |
|                                                                 | 20 | 25 | 30 |
| Thr Pro Glu Ala Leu Asn Trp Leu Phe Val Lys Gly Leu Val Gly Trp |    |    |    |
|                                                                 | 35 | 40 | 45 |
| Phe Leu Gln Val Met Leu Leu Lys Val Thr Leu Leu Ser Leu Gly Ser |    |    |    |
|                                                                 | 50 | 55 | 60 |
| Gly Glu Ala Pro Leu Leu Asp Ile Val Ala Tyr Gly Gly Tyr Ala Phe |    |    |    |
|                                                                 | 65 | 70 | 75 |
|                                                                 |    |    | 80 |



Ala Gly Leu Cys Leu Ala Gly Phe Ala Lys Ile Met Trp Gly Tyr Ser  
85 90 95  
Tyr Tyr Ala Leu Met Pro Trp Thr Cys Leu Cys Thr Gly Ile Phe Leu  
100 105 110  
Val Lys Thr Met Lys Arg Val Leu Phe Ala Glu Val Arg Ser Tyr Asp  
115 120 125  
Ser Ser Lys His His Tyr Leu Leu Phe Leu Ala Leu Val Gln Phe  
130 135 140  
Pro Leu Leu Ile Trp Leu Gly Asn Ile Ser Val Asn Trp Leu Leu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2246:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 156 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1572206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2246:

Met Leu Pro Asp Leu Tyr Ile Pro Phe Met Ala Phe Gly Thr Tyr Val  
1 5 10 15  
Val Leu Ala Gly Leu Ser Leu Gly Leu Asn Gly Lys Phe Thr Pro Glu  
20 25 30  
Ala Leu Asn Trp Leu Phe Val Lys Gly Leu Val Gly Trp Phe Leu Gln  
35 40 45  
Val Met Leu Leu Lys Val Thr Leu Leu Ser Leu Gly Ser Gly Glu Ala  
50 55 60  
Pro Leu Leu Asp Ile Val Ala Tyr Gly Gly Tyr Ala Phe Ala Gly Leu  
65 70 75 80  
Cys Leu Ala Gly Phe Ala Lys Ile Met Trp Gly Tyr Ser Tyr Tyr Ala  
85 90 95  
Leu Met Pro Trp Thr Cys Leu Cys Thr Gly Ile Phe Leu Val Lys Thr  
100 105 110  
Met Lys Arg Val Leu Phe Ala Glu Val Arg Ser Tyr Asp Ser Ser Lys  
115 120 125  
His His Tyr Leu Leu Leu Phe Leu Ala Leu Val Gln Phe Pro Leu Leu  
130 135 140  
Ile Trp Leu Gly Asn Ile Ser Val Asn Trp Leu Leu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2247:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 147 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1572207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2247:

Met Ala Phe Gly Thr Tyr Val Val Leu Ala Gly Leu Ser Leu Gly Leu  
1 5 10 15  
Asn Gly Lys Phe Thr Pro Glu Ala Leu Asn Trp Leu Phe Val Lys Gly  
20 25 30  
Leu Val Gly Trp Phe Leu Gln Val Met Leu Leu Lys Val Thr Leu Leu  
35 40 45  
Ser Leu Gly Ser Gly Glu Ala Pro Leu Leu Asp Ile Val Ala Tyr Gly

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 50                                                              | 55  | 60  |
| Gly Tyr Ala Phe Ala Gly Leu Cys Leu Ala Gly Phe Ala Lys Ile Met |     |     |
| 65                                                              | 70  | 75  |
| Trp Gly Tyr Ser Tyr Tyr Ala Leu Met Pro Trp Thr Cys Leu Cys Thr |     |     |
|                                                                 | 85  | 90  |
| Gly Ile Phe Leu Val Lys Thr Met Lys Arg Val Leu Phe Ala Glu Val |     |     |
|                                                                 | 100 | 105 |
| Arg Ser Tyr Asp Ser Ser Lys His His Tyr Leu Leu Leu Phe Leu Ala |     |     |
|                                                                 | 115 | 120 |
| Leu Val Gln Phe Pro Leu Leu Ile Trp Leu Gly Asn Ile Ser Val Asn |     |     |
|                                                                 | 130 | 135 |
| Trp Leu Leu                                                     |     | 140 |
| 145                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:2248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1209
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2248:

|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| aaaaatctct | ttactaccag  | caagttgttt  | tcttgctaac  | ttcaaaacttc | tctttctctt  | 60   |
| gttctctctc | aagtcttgat  | cttatttacc  | gttaactttg  | tgaacaaaaa  | tcgaatcaaa  | 120  |
| cacacatgga | gcgcgccacg  | ctcaagcatc  | atcatactca  | agccgaccaa  | gaagcggcca  | 180  |
| acaacaacaa | caacaagtc   | ggctctgggt  | gttacacgtg  | tcgccagacc  | agcacgaggt  | 240  |
| ggacacgcag | gacggagcaa  | atcaaaaatcc | tcaaagaact  | ttactacaac  | aatgcaatcc  | 300  |
| ggtcaccaac | agccgatcag  | atccagaaga  | tcaactgcaag | gctgagacag  | ttcggaaaaa  | 360  |
| ttgagggcaa | gaagctcttt  | tactgtttcc  | agaaccataa  | ggctcgtgag  | cgtcagaaga  | 420  |
| agagattcaa | cggaacaaac  | atgaccacac  | catcttcac   | accacaactc  | gttatgatgg  | 480  |
| cggctaacga | tcattatcat  | cctctacttc  | accatcatca  | cgggtgtccc  | atgcagagac  | 540  |
| ctgctaattc | cgctcaacgtt | aaacttaacc  | aagaccatca  | tctctatcat  | cataacaagc  | 600  |
| catatccag  | cttcaataac  | gggaatttaa  | atcatgcaag  | ctcaggtact  | gaatgtggtg  | 660  |
| ttgttaatgc | ttctaattgc  | tacatgagta  | gccatgtcta  | tggatctatg  | gaacaagact  | 720  |
| gttctatgaa | ttacaacaac  | gtaggtggag  | gatggggcaa  | catggatcat  | cattactcat  | 780  |
| ctgcacctta | caacttcttc  | gatagagcaa  | agcctctgtt  | tggcttagaa  | gggtcatcaag | 840  |
| aagaagaaga | atgtggtggc  | gatgcttacc  | tggaaacatc  | acgtacgctt  | cctctctctc  | 900  |
| ctatgcacgg | tgaagatcac  | atcaacgggtg | gtagtgggtc  | catctggaag  | ttatggccaat | 960  |
| cggaagtctg | cccttcgcgt  | tctcttgagc  | tacgtctgaa  | ctagctctta  | cgccggtgtc  | 1020 |
| gctcggtatt | aaagctcttt  | cctctctctc  | tctctttcgt  | actcgtatgt  | tcacaactat  | 1080 |
| gcttcgctag | tgattaatga  | tgcagttggt  | atattagtag  | ttaaactagt  | atctctcgtt  | 1140 |
| atgtgtaatt | tgtaattact  | agctaagtag  | cgtctaggtt  | ttaatgttaa  | ttgacaaccg  | 1200 |
| ttttatctc  |             |             |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..292
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2249:

|                                                                 |    |
|-----------------------------------------------------------------|----|
| Met Glu Pro Pro Gln His Gln His His His His Gln Ala Asp Gln Glu |    |
| 1                                                               | 5  |
| Ser Gly Asn Asn Asn Asn Lys Ser Gly Ser Gly Gly Tyr Thr Cys     |    |
|                                                                 | 10 |
|                                                                 | 15 |

**Q**uestions & Answers

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: lin

FEATURE:

(B) LOCATION: 1..187

SEQUENCE DESCRIPTION:

5 10

[illegible]

Ser Ser Ala Pro Tyr Asn Phe Phe Asp Arg Ala Lys Pro Leu Phe Gly  
115 120 125  
Leu Glu Gly His Gln Glu Glu Cys Gly Gly Asp Ala Tyr Leu  
130 135 140  
Glu His Arg Arg Thr Leu Pro Leu Phe Pro Met His Gly Glu Asp His  
145 150 155 160  
Ile Asn Gly Gly Ser Gly Ala Ile Trp Lys Tyr Gly Gln Ser Glu Val  
165 170 175  
Arg Pro Cys Ala Ser Leu Glu Leu Arg Leu Asn  
180 185

(2) INFORMATION FOR SEQ ID NO:2251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1572243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2251:

Met Met Ala Ala Asn Asp His Tyr His Pro Leu Leu His His His His  
1 5 10 15  
Gly Val Pro Met Gln Arg Pro Ala Asn Ser Val Asn Val Lys Leu Asn  
20 25 30  
Gln Asp His His Leu Tyr His His Asn Lys Pro Tyr Pro Ser Phe Asn  
35 40 45  
Asn Gly Asn Leu Asn His Ala Ser Ser Gly Thr Glu Cys Gly Val Val  
50 55 60  
Asn Ala Ser Asn Gly Tyr Met Ser Ser His Val Tyr Gly Ser Met Glu  
65 70 75 80  
Gln Asp Cys Ser Met Asn Tyr Asn Asn Val Gly Gly Gly Trp Ala Asn  
85 90 95  
Met Asp His His Tyr Ser Ser Ala Pro Tyr Asn Phe Phe Asp Arg Ala  
100 105 110  
Lys Pro Leu Phe Gly Leu Glu Gly His Gln Glu Glu Glu Cys Gly  
115 120 125  
Gly Asp Ala Tyr Leu Glu His Arg Arg Thr Leu Pro Leu Phe Pro Met  
130 135 140  
His Gly Glu Asp His Ile Asn Gly Gly Ser Gly Ala Ile Trp Lys Tyr  
145 150 155 160  
Gly Gln Ser Glu Val Arg Pro Cys Ala Ser Leu Glu Leu Arg Leu Asn  
165 170 175

(2) INFORMATION FOR SEQ ID NO:2252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 667 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..667

(D) OTHER INFORMATION: / Ceres Seq. ID 1572244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2252:

acaacttccc cattttctgc ttctttttgt tcaactccaa tcacacaatt cacaaccat 60  
tgagaaacca ataaaaaac ctcaatcaaa aaaaaaaaaa aaaaaagatg aaatctcaa 120  
tttagtaag gagaaaaaag ccatttgaa taacttgaaa aggttttggg ttgcagaag 180

|            |             |             |             |             |            |     |
|------------|-------------|-------------|-------------|-------------|------------|-----|
| aaaatgaagg | agaaggcgga  | gagtggtgga  | ggagtaggat  | acgtgagagc  | agatcagata | 240 |
| gattttaaga | gtctgggacga | gcaattgcaag | agacacttaa  | gtaaaagcatg | gacgatggag | 300 |
| aagaggaaga | gtttgagtag  | tggtgaagat  | aacgtcaata  | acacccgaca  | taaccagaac | 360 |
| aacttcggac | atcgacagct  | tgtgtttcag  | aggccgcttc  | Cttggtggtg  | gatatagcaa | 420 |
| caacaacaac | agcagcaaga  | acgacataat  | taggtcgacc  | gaggttgaga  | agtcgaggag | 480 |
| agagtgggag | attgatcctt  | ctaagcttat  | aatcaaaaagt | gtgattgcta  | gaggtacttt | 540 |
| tggtacggtt | cacogtgaa   | tctacgatg   | tcaagatg    | gccgtaaaac  | tactagactg | 600 |
| gggagaagag | gggcacaggt  | cagacgcaga  | gatagCttcg  | cttagagctg  | ctttcactca | 660 |
| agaagtt    |             |             |             |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1572245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2253:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Glu | Lys | Ala | Glu | Ser | Gly | Gly | Val | Gly | Tyr | Val | Arg | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Asp | Gln | Ile | Asp | Leu | Lys | Ser | Leu | Asp | Glu | Gln | Leu | Gln | Arg | His |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  | Leu |
| Ser | Lys | Ala | Trp | Thr | Met | Glu | Lys | Arg | Lys | Ser | Leu | Ser | Asp | Gly |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  | Glu |
| Asp | Asn | Val | Asn | Asn | Thr | Arg | His | Asn | Gln | Asn | Asn | Phe | Gly | His |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  | Arg |
| Gln | Leu | Val | Phe | Gln | Arg | Pro | Leu | Pro | Trp | Trp | Trp | Ile |     |     |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1572246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2254:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Lys | Ile | Thr | Ser | Ile | Thr | Pro | Asp | Ile | Thr | Arg | Thr | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  | Ser |
| Asp | Ile | Asp | Ser | Leu | Cys | Phe | Arg | Gly | Arg | Phe | Leu | Gly | Gly | Tyr |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |
| Ser | Asn | Asn | Asn | Asn | Ser | Ser | Lys | Asn | Asp | Ile | Ile | Arg | Ser | Thr |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  | Glu |
| Val | Glu | Lys | Ser | Arg | Arg | Glu | Trp | Glu | Ile | Asp | Pro | Ser | Lys | Leu |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  | Ile |
| Ile | Lys | Ser | Val | Ile | Ala | Arg | Gly | Thr | Phe | Gly | Thr | Val | His | Arg |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  | Gly |
| Ile | Tyr | Asp | Gly | Gln | Asp | Val | Ala | Val | Lys | Leu | Leu | Asp | Trp | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  | Glu |
| Glu | Gly | His | Arg | Ser | Asp | Ala | Glu | Ile | Ala | Ser | Leu | Arg | Ala | Phe |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |
| Thr | Gln | Glu | Val |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 619 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..619

(D) OTHER INFORMATION: / Ceres Seq. ID 1572298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2255:

```
atttcggcg acgtgtgaatt atgtggctgg cgacgttato ttccctctat ttgtggcttt 60
cttcaccttc tctacctaat tacaggaacc gtagGtttcc aaagattaaa gCttcgctct 120
ttaattaccc tctagcgagc aaaatcatgg tcagaaattt accgttttct mcaagtgaag 180
attttctaaa gagagagttt tcagcttttg gagagatagc tgaagtgaag cttatcaaa 240
atgaggcaat gcagagatca aaagggttat cttttattca attcacgtct caagatgatg 300
cttttcttgc catagagacc atggaccgtc ggatgtacaa tggaagaatg atttatatag 360
acattgcgaa acccggtaaa cgtgattttc aaggactacc gaggacttct ggtccccctg 420
agaagtcgga tgtgccagaa gaagccgcta atgatgaggt tgcgtattgc tggattatgt 480
tgttagtatc aagctcacca aactgtaact gaacttgcac aaatcagatg tcaaattatg 540
cttcattata ggaatttgat caatgtgaag aatgtgtgtt actgataaac aattattgac 600
acggttccag ttacagctc
```

(2) INFORMATION FOR SEQ ID NO:2256:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1572299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2256:

```
Met Trp Ser Ala Thr Leu Ser Phe Pro Ser Phe Val Ala Ser Ser
1 5 10 15
Ser Leu Pro Asn Tyr Arg Asn Arg Arg Phe Pro Lys Ile Lys Ala Ser
20 25 30
Leu Phe Asn Tyr Pro Leu Ala Ser Lys Ile Met Val Arg Asn Leu Pro
35 40 45
Phe Ser Xaa Ser Glu Asp Phe Leu Lys Arg Glu Phe Ser Ala Phe Gly
50 55 60
Glu Ile Ala Glu Val Lys Leu Ile Lys Asp Glu Ala Met Gln Arg Ser
65 70 75 80
Lys Gly Tyr Ala Phe Ile Gln Phe Thr Ser Gln Asp Asp Ala Phe Leu
85 90 95
Ala Ile Glu Thr Met Asp Arg Arg Met Tyr Asn Gly Arg Met Ile Tyr
100 105 110
Ile Asp Ile Ala Lys Pro Gly Lys Arg Asp Phe Gln Gly Leu Pro Arg
115 120 125
Thr Ser Gly Pro Pro Glu Lys Ser Asp Val Pro Glu Glu Ala Ala Asn
130 135 140
Asp Glu Val Ala Asp Cys Trp Tyr
145 150
```

(2) INFORMATION FOR SEQ ID NO:2257:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..110  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572300  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2257:  
Met Val Arg Asn Leu Pro Phe Ser Xaa Ser Glu Asp Phe Leu Lys Arg  
1 5 10 15  
Glu Phe Ser Ala Phe Gly Glu Ile Ala Glu Val Lys Leu Ile Lys Asp  
20 25 30  
Glu Ala Met Gln Arg Ser Lys Gly Tyr Ala Phe Ile Gln Phe Thr Ser  
35 40 45  
Gln Asp Asp Ala Phe Leu Ala Ile Glu Thr Met Asp Arg Arg Met Tyr  
50 55 60  
Asn Gly Arg Met Ile Tyr Ile Asp Ile Ala Lys Pro Gly Lys Arg Asp  
65 70 75 80  
Phe Gln Gly Leu Pro Arg Thr Ser Gly Pro Pro Glu Lys Ser Asp Val  
85 90 95  
Pro Glu Glu Ala Ala Asn Asp Glu Val Ala Asp Cys Trp Tyr  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2258:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..76  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2258:

Met Gln Arg Ser Lys Gly Tyr Ala Phe Ile Gln Phe Thr Ser Gln Asp  
1 5 10 15  
Asp Ala Phe Leu Ala Ile Glu Thr Met Asp Arg Arg Met Tyr Asn Gly  
20 25 30  
Arg Met Ile Tyr Ile Asp Ile Ala Lys Pro Gly Lys Arg Asp Phe Gln  
35 40 45  
Gly Leu Pro Arg Thr Ser Gly Pro Pro Glu Lys Ser Asp Val Pro Glu  
50 55 60  
Glu Ala Ala Asn Asp Glu Val Ala Asp Cys Trp Tyr  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2259:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1386 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1386  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2259:

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| actggtggtga | atatgctg   | cgtttcgcaa | gtatcaccgg | gaattgc    | aaagcagagg  | 60  |
| accatgtacg  | gagacgtac  | aaactggaat | gaagatgagt | atagagaatc | aattttgaag  | 120 |
| gagcgagaga  | tagagacacg | caccgtcttc | agaacccgct | gggctcctcc | ggcgagaatc  | 180 |
| cttaataccg  | acgcatttgt | tgtagcctcc | agcgatggaa | ctttagcttt | ccattcaactg | 240 |
| aactcgcttg  | tgtctcaatc | ggcgagtttt | ggctactcga | aaggccaaga | tgttatgggtg | 300 |
| gctgaacctg  | agagagtgtg | tagggcacac | gaaggtcctg | cttatgatgt | taagtctcat  | 360 |
| gggtgaagacg | aagatgcttt | gctacttagt | tgtggtgatg | atggtagagt | taggggatgg  | 420 |
| aaatggagag  | aatttgcgtg | atcagatgtg | tctcttcatt | tgaagagaa  | tcattctgaag | 480 |
| ccattgcttg  | aactgattaa | tccacaacac | aaaggtccct | ggggtgcgct | ttcacagatg  | 540 |

|                                                                     |      |
|---------------------------------------------------------------------|------|
| cctgagatca atgccatgtc tgttgatcct cagtcaggaa gtgtatttac agcagctgggt  | 600  |
| gattcttgcg catattgttg ggacgtggag agtgcgtaaga ttaaaatgac ctttaaaaggt | 660  |
| catccagcat atttgcatac tgtatgttct cgtagttctg caagtccagat attgcacgggt | 720  |
| tcagaggatg ggaactgcgag aatctgggat tgcataaacg gaaaaatgtgt taaagtaatt | 780  |
| ggttccacag ataaaaagtc ccgccttcgc gttagtctta tggcccttga tgggagtgaa   | 840  |
| agctgggttg tttgtggaca gggcaaaaaa ttagtcttat ggaatcttcc ccgctcagaa   | 900  |
| tgcgtacaaa caataccocat ccctgcacat gtacaggatg tgaatgttga tgaataagcaa | 960  |
| attttgactg taggagcaga accacttcta agacgtttcg acttaaatgg agctttgctt   | 1020 |
| tctcaaaetc actgtgctcc ttgttcagta ttttccattt ccttgcatcc agcaggagta   | 1080 |
| gttgctgtgg gaggttatgg aggtattgtt gatgtcatct ctcaatttgg aagccatctc   | 1140 |
| tgcaaatctt gtacgaatgc attgtaaaac tccttacagt ttcttggattt ggcctgatcac | 1200 |
| octaaagagg taaccgaattg tgtcagtcag attattgcag aggttaagaa accottttctt | 1260 |
| tgtttttctt aggatcttgc tccactactaa agaccaatta gttgtttgggt taagtgtaat | 1320 |
| tggttgttgg ttcgtagtct gctatcaaat ttgaaccatt aaaatgcacat tggaccgggt  | 1380 |

(2) INFORMATION FOR SEQ ID NO:2260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 388 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..388

(D) OTHER INFORMATION: / Ceres Seq. ID 1572339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2260:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Gly | Asn | Ile | Ala | Gly | Val | Ser | Gln | Val | Ser | Pro | Gly | Ile | Ala |
| 1   |     | 5   |     |     |     | 10  |     |     |     |     |     |     | 15  |     |
| Lys | Lys | Gln | Arg | Thr | Met | Tyr | Gly | Asp | Ala | Thr | Asn | Trp | Asn | Glu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     | Asp |
| Glu | Tyr | Arg | Glu | Ser | Ile | Leu | Lys | Glu | Arg | Glu | Ile | Glu | Thr | Arg |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     | Thr |
| Val | Phe | Arg | Thr | Ala | Trp | Ala | Pro | Pro | Ala | Arg | Ile | Ser | Asn | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     | Asp |
| Ala | Phe | Val | Val | Ala | Ser | Ser | Asp | Gly | Thr | Leu | Ala | Phe | His | Ser |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | Leu |
| Asn | Ser | Leu | Val | Ser | Gln | Ser | Ala | Ser | Phe | Gly | Tyr | Ser | Lys | Gly |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  | Gln |
| Asp | Val | Met | Val | Ala | Glu | Pro | Glu | Arg | Val | Val | Arg | Ala | His | Glu |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     | Gly |
| Pro | Ala | Tyr | Asp | Val | Lys | Phe | Tyr | Gly | Glu | Asp | Glu | Asp | Ala | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     | Leu |
| Leu | Ser | Cys | Gly | Asp | Asp | Gly | Arg | Val | Arg | Gly | Trp | Lys | Trp | Arg |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     | Glu |
| Phe | Ala | Glu | Ser | Asp | Val | Ser | Leu | His | Leu | Lys | Glu | Asn | His | Leu |
|     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     | Lys |
| Pro | Leu | Leu | Glu | Leu | Ile | Asn | Pro | Gln | His | Lys | Gly | Pro | Trp | Gly |
|     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 | Ala |
| Leu | Ser | Pro | Met | Pro | Glu | Ile | Asn | Ala | Met | Ser | Val | Asp | Pro | Gln |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 | Ser |
| Gly | Ser | Val | Phe | Thr | Ala | Ala | Gly | Asp | Ser | Cys | Ala | Tyr | Cys | Trp |
|     |     | 195 |     |     |     |     | 200 |     |     |     | 205 |     |     | Asp |
| Val | Glu | Ser | Gly | Lys | Ile | Lys | Met | Thr | Phe | Lys | Gly | His | Ser | Asp |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     | Tyr |
| Leu | His | Thr | Val | Val | Ser | Arg | Ser | Ser | Ala | Ser | Gln | Ile | Leu | Thr |
|     |     | 225 |     |     |     | 230 |     |     | 235 |     |     |     |     | Gly |
| Ser | Glu | Asp | Gly | Thr | Ala | Arg | Ile | Trp | Asp | Cys | Lys | Thr | Gly | Lys |
|     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 | Cys |
| Val | Lys | Val | Ile | Gly | Ser | Gln | Asp | Lys | Lys | Ser | Arg | Leu | Arg | Val |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     |     | Ser |



Ser Met Ala Leu Asp Gly Ser Glu Ser Trp Leu Val Cys Gly Gln Gly  
275 280 285  
Lys Asn Leu Ala Leu Trp Asn Leu Pro Ala Ser Glu Cys Val Gln Thr  
290 295 300  
Ile Pro Ile Pro Ala His Val Gln Asp Val Met Phe Asp Glu Lys Gln  
305 310 315 320  
Ile Leu Thr Val Gly Ala Glu Pro Leu Leu Arg Arg Phe Asp Leu Asn  
325 330 335  
Gly Ala Leu Leu Ser Gln Ile His Cys Ala Pro Cys Ser Val Phe Ser  
340 345 350  
Ile Ser Leu His Pro Ala Gly Val Val Ala Val Gly Gly Tyr Gly Gly  
355 360 365  
Ile Val Asp Val Ile Ser Gln Phe Gly Ser His Leu Cys Thr Phe Arg  
370 375 380  
Ser Ser Ser Leu  
385

(2) INFORMATION FOR SEQ ID NO:2261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..367
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2261:

Met Tyr Gly Asp Ala Thr Asn Trp Asn Glu Asp Glu Tyr Arg Glu Ser  
1 5 10 15  
Ile Leu Lys Glu Arg Glu Ile Glu Thr Arg Thr Val Phe Arg Thr Ala  
20 25 30  
Trp Ala Pro Pro Ala Arg Ile Ser Asn Pro Asp Ala Phe Val Val Ala  
35 40 45  
Ser Ser Asp Gly Thr Leu Ala Phe His Ser Leu Asn Ser Leu Val Ser  
50 55 60  
Gln Ser Ala Ser Phe Gly Tyr Ser Lys Gly Gln Asp Val Met Val Ala  
65 70 75 80  
Glu Pro Glu Arg Val Val Arg Ala His Glu Gly Pro Ala Tyr Asp Val  
85 90 95  
Lys Phe Tyr Gly Glu Asp Glu Asp Ala Leu Leu Ser Cys Gly Asp  
100 105 110  
Asp Gly Arg Val Arg Gly Trp Lys Trp Arg Glu Phe Ala Glu Ser Asp  
115 120 125  
Val Ser Leu His Leu Lys Glu Asn His Leu Lys Pro Leu Leu Glu Leu  
130 135 140  
Ile Asn Pro Gln His Lys Gly Pro Trp Gly Ala Leu Ser Pro Met Pro  
145 150 155 160  
Glu Ile Asn Ala Met Ser Val Asp Pro Gln Ser Gly Ser Val Phe Thr  
165 170 175  
Ala Ala Gly Asp Ser Cys Ala Tyr Cys Trp Asp Val Glu Ser Gly Lys  
180 185 190  
Ile Lys Met Thr Phe Lys Gly His Ser Asp Tyr Leu His Thr Val Val  
195 200 205  
Ser Arg Ser Ser Ala Ser Gln Ile Leu Thr Gly Ser Glu Asp Gly Thr  
210 215 220  
Ala Arg Ile Trp Asp Cys Lys Thr Gly Lys Cys Val Lys Val Ile Gly  
225 230 235 240  
Ser Gln Asp Lys Lys Ser Arg Leu Arg Val Ser Ser Met Ala Leu Asp  
245 250 255  
Gly Ser Glu Ser Trp Leu Val Cys Gly Gln Gly Lys Asn Leu Ala Leu

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Net | Val | Ala | Glu | Pro | Glu | Arg | Val | Val | Arg | Ala | His | Glu | Gly | Pro | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Tyr | Asp | Val | Lys | Phe | Tyr | Gly | Glu | Asp | Glu | Asp | Ala | Leu | Leu | Leu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Gly | Asp | Asp | Gly | Arg | Val | Arg | Gly | Trp | Lys | Trp | Arg | Glu | Phe | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Glu | Ser | Asp | Val | Ser | Leu | His | Leu | Lys | Glu | Asn | His | Leu | Lys | Pro | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Glu | Leu | Ile | Asn | Pro | Gln | His | Lys | Gly | Pro | Trp | Gly | Ala | Leu | Ser |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Met | Pro | Glu | Ile | Asn | Ala | Met | Ser | Val | Asp | Pro | Gln | Ser | Gly | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Phe | Thr | Ala | Ala | Gly | Asp | Ser | Cys | Ala | Tyr | Cys | Trp | Asp | Val | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Gly | Lys | Ile | Lys | Met | Thr | Phe | Lys | Gly | His | Ser | Asp | Trp | Leu | His |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Thr | Val | Val | Ser | Arg | Ser | Ser | Ala | Ser | Gln | Ile | Leu | Thr | Gly | Ser | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Gly | Thr | Ala | Arg | Ile | Trp | Asp | Cys | Lys | Thr | Gly | Lys | Cys | Val | Lys |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Val | Ile | Gly | Ser | Gln | Asp | Lys | Lys | Ser | Arg | Leu | Arg | Val | Ser | Ser | Met |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ala | Leu | Asp | Gly | Ser | Glu | Ser | Trp | Leu | Val | Cys | Gly | Gln | Gly | Lys | Asn |
|     | 180 |     |     |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Leu | Ala | Leu | Trp | Asn | Leu | Pro | Ala | Ser | Glu | Cys | Val | Gln | Thr | Ile | Pro |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ile | Pro | Ala | His | Val | Gln | Asp | Val | Met | Phe | Asp | Glu | Lys | Gln | Ile | Leu |
|     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Thr | Val | Gly | Ala | Glu | Pro | Leu | Leu | Arg | Phe | Asp | Leu | Asn | Gly | Ala |     |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Leu | Leu | Ser | Gln | Ile | His | Cys | Ala | Pro | Cys | Ser | Val | Phe | Ser | Ile | Ser |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Leu | His | Pro | Ala | Gly | Val | Val | Ala | Val | Gly | Gly | Tyr | Gly | Gly | Ile | Val |
|     | 260 |     |     |     |     |     |     | 265 |     |     |     | 270 |     |     |     |
| Asp | Val | Ile | Ser | Gln | Phe | Gly | Ser | His | Leu | Cys | Thr | Phe | Arg | Ser | Ser |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |

Ser Leu  
290

(2) INFORMATION FOR SEQ ID NO:2263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2263:

|            |            |             |            |            |             |      |
|------------|------------|-------------|------------|------------|-------------|------|
| aacaacatct | ttcacacaac | aattcacaca  | atctctcggt | tttttttggt | tatcatcaaa  | 60   |
| agtttttaac | taaattacgt | atcaaaattcc | gagcaagatg | actattcttg | ttgaacattt  | 120  |
| tgttctcgat | tcaagagtg  | atgaaaagaa  | agtgatagag | gagagggata | atgaattgggt | 180  |
| gttgatgga  | ggttttggt  | ttccaaaatc  | aaaggaaact | gatgcattcg | atgctcctga  | 240  |
| tatgaatttc | ttgggccatt | ccttcaggga  | ttatgagaat | gatgaaagcg | agagacaaca  | 300  |
| agggtgtgag | gaattttaca | ggatgcaaca  | cattcaccag | acctatgact | ttgtgaagaa  | 360  |
| gatgagaaa  | gagtatggaa | aacttaacaa  | gatggaaatg | agtatatggg | aatgtttgtg  | 420  |
| gttattgaac | aatgtgtgtg | atgaaagcga  | tccggatcct | gatgagcctc | aaattcaaca  | 480  |
| ccttctccaa | acgcgtgaag | ccattcgaag  | ggactatccc | gacgaagatt | ggctccatct  | 540  |
| cactgcacct | atccatgatc | ttggcaaggt  | tctcctctgt | ccagaattcg | gtggtctctc  | 600  |
| ccagtggtgt | gtcgtggcg  | atacatttcc  | agttggatgt | accttcgact | cagccaatat  | 660  |
| tcaccacaag | tatttcaaa  | gaacacatga  | tatcaacaac | ccaaagtaca | acacaaaaaa  | 720  |
| tggagtttac | actgaaggat | gtggtttaga  | caatgttctc | atgtcatggg | gtcatgacga  | 780  |
| ctacatgtat | ttggtggcta | agaagaatgg  | cacgaccttc | cctcacgctg | ctctctctcat | 840  |
| tattcgatat | cattcctttt | atccatttga  | caaggcagga | gcctacacac | acttgatgaa  | 900  |
| cgatgaggac | agagatgac  | tcaagtggtc  | ccatgtcttc | aataaatatg | acctatacac  | 960  |
| taagagcaaa | gttctggtag | atgtcgaaac  | agtgaagcct | tactacattt | caactcatca  | 1020 |
| caagtatttt | ccggcgaaac | taaaatgggt  | agataaagct | acgtatcaat | tacttaacta  | 1080 |
| tcttttatga | ggagaacgag | atcgaaggtt  | aacgagtttt | ctattgtata | caacggaaga  | 1140 |
| taaatctatc | tataaaaaa  | gttggtgtgt  | tcatttgtaa | tttttcccc  | catcagttta  | 1200 |
| aaagttatgt | tgt        |             |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:2264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..317
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2264:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Ile | Leu | Val | Glu | His | Phe | Val | Pro | Asp | Ser | Arg | Val | Asp | Glu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Lys | Val | Ile | Glu | Glu | Arg | Asp | Asn | Glu | Leu | Val | Leu | Asp | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Val | Val | Pro | Lys | Ser | Lys | Glu | Thr | Asp | Ala | Phe | Asp | Ala | Pro | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Met | Asn | Phe | Leu | Gly | His | Ser | Phe | Arg | Asp | Tyr | Glu | Asn | Asp | Glu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Arg | Gln | Gln | Gly | Val | Glu | Glu | Phe | Tyr | Arg | Met | Gln | His | Ile | His |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Thr | Tyr | Asp | Phe | Val | Lys | Lys | Met | Arg | Lys | Glu | Tyr | Gly | Lys | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asn | Lys | Met | Glu | Met | Ser | Ile | Trp | Glu | Cys | Cys | Glu | Leu | Leu | Asn | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Asp | Glu | Ser | Asp | Pro | Asp | Leu | Asp | Glu | Pro | Gln | Ile | Gln | His |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Leu | Gln | Thr | Ala | Glu | Ala | Ile | Arg | Arg | Asp | Tyr | Pro | Asp | Glu | Asp |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Trp | Leu | His | Leu | Thr | Ala | Leu | Ile | His | Asp | Leu | Gly | Lys | Val | Leu | Leu |
|     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Pro | Glu | Phe | Gly | Gly | Leu | Pro | Gln | Trp | Ala | Val | Val | Gly | Asp | Thr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Pro | Val | Gly | Cys | Thr | Phe | Asp | Ser | Ala | Asn | Ile | His | His | Lys | Tyr |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Phe | Lys | Gly | Asn | His | Asp | Ile | Asn | Asn | Pro | Lys | Tyr | Asn | Thr | Lys | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Val | Tyr | Thr | Glu | Gly | Cys | Gly | Leu | Asp | Asn | Val | Leu | Met | Ser | Trp |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | His | Asp | Asp | Tyr | Met | Tyr | Leu | Val | Ala | Lys | Lys | Asn | Gly | Thr | Thr |
|     |     | 225 |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |
| Leu | Pro | His | Ala | Gly | Leu | Phe | Ile | Ile | Arg | Tyr | His | Ser | Phe | Tyr | Pro |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | His | Lys | Ala | Gly | Ala | Tyr | Thr | His | Leu | Met | Asn | Asp | Glu | Asp | Arg |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | Asp | Leu | Lys | Trp | Leu | His | Val | Phe | Asn | Lys | Tyr | Asp | Leu | Tyr | Ser |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Lys | Ser | Lys | Val | Leu | Val | Asp | Val | Glu | Gln | Val | Lys | Pro | Tyr | Tyr | Ile |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ser | Leu | Ile | Asn | Lys | Tyr | Phe | Pro | Ala | Lys | Leu | Lys | Trp |     |     |     |
|     |     | 305 |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 269 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..269

(D) OTHER INFORMATION: / Ceres Seq. ID 1572351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2265:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Phe | Leu | Gly | His | Ser | Phe | Arg | Asp | Tyr | Glu | Asn | Asp | Glu | Ser |
|     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Arg | Gln | Gln | Gly | Val | Glu | Glu | Phe | Tyr | Arg | Met | Gln | His | Ile | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Thr | Tyr | Asp | Phe | Val | Lys | Lys | Met | Arg | Lys | Glu | Tyr | Gly | Lys | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Asn | Lys | Met | Glu | Met | Ser | Ile | Trp | Glu | Cys | Cys | Glu | Leu | Leu | Asn | Asn |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Val | Asp | Glu | Ser | Asp | Pro | Asp | Leu | Asp | Glu | Pro | Gln | Ile | Gln | His |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Leu | Gln | Thr | Ala | Glu | Ala | Ile | Arg | Arg | Asp | Tyr | Pro | Asp | Glu | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Trp | Leu | His | Leu | Thr | Ala | Leu | Ile | His | Asp | Leu | Gly | Lys | Val | Leu | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Pro | Glu | Phe | Gly | Gly | Leu | Pro | Gln | Trp | Ala | Val | Val | Gly | Asp | Thr |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Phe | Pro | Val | Gly | Cys | Thr | Phe | Asp | Ser | Ala | Asn | Ile | His | His | Lys | Tyr |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Lys | Gly | Asn | His | Asp | Ile | Asn | Asn | Pro | Lys | Tyr | Asn | Thr | Lys | Asn |
|     |     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Val | Tyr | Thr | Glu | Gly | Cys | Gly | Leu | Asp | Asn | Val | Leu | Met | Ser | Trp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Gly | His | Asp | Asp | Tyr | Met | Tyr | Leu | Val | Ala | Lys | Lys | Asn | Gly | Thr | Thr |

180 185 190  
Leu Pro His Ala Gly Leu Phe Ile Arg Tyr His Ser Phe Tyr Pro  
195 200 205  
Leu His Lys Ala Gly Ala Tyr Thr His Leu Met Asn Asp Glu Asp Arg  
210 215 220  
Asp Asp Leu Lys Trp Leu His Val Phe Asn Lys Tyr Asp Leu Tyr Ser  
225 230 235 240  
Lys Ser Lys Val Leu Val Asp Val Glu Gln Val Lys Pro Tyr Tyr Ile  
245 250 255  
Ser Leu Ile Asn Lys Tyr Phe Pro Ala Lys Leu Lys Trp  
260 265

(2) INFORMATION FOR SEQ ID NO:2266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..242

(D) OTHER INFORMATION: / Ceres Seq. ID 1572352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2266:

Met Gln His Ile His Gln Thr Tyr Asp Phe Val Lys Lys Met Arg Lys  
1 5 10 15  
Glu Tyr Gly Lys Leu Asn Lys Met Glu Met Ser Ile Trp Glu Cys Cys  
20 25 30  
Glu Leu Leu Asn Asn Val Val Asp Glu Ser Asp Pro Asp Leu Asp Glu  
35 40 45  
Pro Gln Ile Gln His Leu Leu Gln Thr Ala Glu Ala Ile Arg Arg Asp  
50 55 60  
Tyr Pro Asp Glu Asp Trp Leu His Leu Thr Ala Leu Ile His Asp Leu  
65 70 75 80  
Gly Lys Val Leu Leu Pro Glu Phe Gly Gly Leu Pro Gln Trp Ala  
85 90 95  
Val Val Gly Asp Thr Phe Pro Val Gly Cys Thr Phe Asp Ser Ala Asn  
100 105 110  
Ile His His Lys Tyr Phe Lys Gly Asn His Asp Ile Asn Asn Pro Lys  
115 120 125  
Tyr Asn Thr Lys Asn Gly Val Tyr Thr Glu Gly Cys Gly Leu Asp Asn  
130 135 140  
Val Leu Met Ser Trp Gly His Asp Asp Tyr Met Tyr Leu Val Ala Lys  
145 150 155 160  
Lys Asn Gly Thr Thr Leu Pro His Ala Gly Leu Phe Ile Ile Arg Tyr  
165 170 175  
His Ser Phe Tyr Pro Leu His Lys Ala Gly Ala Tyr Thr His Leu Met  
180 185 190  
Asn Asp Glu Asp Arg Asp Asp Leu Lys Trp Leu His Val Phe Asn Lys  
195 200 205  
Tyr Asp Leu Tyr Ser Lys Ser Lys Val Leu Val Asp Val Glu Gln Val  
210 215 220  
Lys Pro Tyr Tyr Ile Ser Leu Ile Asn Lys Tyr Phe Pro Ala Lys Leu  
225 230 235 240  
Lys Trp

(2) INFORMATION FOR SEQ ID NO:2267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 629 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..629

(D) OTHER INFORMATION: / Ceres Seq. ID 1572364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2267:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| atccgatttt | attgttttga | taagttcgtg | tcgtcttcgt | ctctctaacc | caattctgtg  | 60  |
| gtgtctgaag | aaagcagaat | caaaAtccat | gtctttcaga | ggacttagca | ggccaaatgc  | 120 |
| aatatctgga | atgggtgttg | cgatgagag  | caaaaccaca | ttcttagagc | ttcaaaaggaa | 180 |
| aaaaactcat | cgctatgttg | ctttcaagat | tgatgaatcc | aaaaaagaag | ttgttgttga  | 240 |
| gaaaaactga | aacctacag  | agagctacga | tgatttctta | gcttcacttc | ctgataatga  | 300 |
| ctgcagatac | gctgtttatg | acttcgattt | cgttacttot | gagaattgtc | aaaagagcaa  | 360 |
| aatcttcttc | tttcttgtt  | ctccttcgac | ttctccagtt | cgggcgaagg | tgctttactc  | 420 |
| gacttctaaa | gaccagctaa | gtaaggagct | tcaagggatt | cactatgaga | ttcaagctac  | 480 |
| tgatcctact | gaggttgatc | ttgaagtgtt | acgcgaacga | gcgaactgag | agcaagcaag  | 540 |
| attgctatgt | ctattcaaaa | cttatggtaa | tgtaatgaat | aattcgtatt | ctctgtggat  | 600 |
| tgattttgtg | aaacacagtt | tcattgttcc |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1572365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2268:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Asp | Phe | Ile | Cys | Leu | Ile | Ser | Ser | Cys | Arg | Leu | Arg | Leu | Ser | Asn |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |  |
| Pro | Ile | Leu | Trp | Cys | Leu | Lys | Lys | Ala | Glu | Ser | Lys | Ser | Met | Ser | Phe |  |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     |     | 30  |  |
| Arg | Gly | Leu | Ser | Arg | Pro | Asn | Ala | Ile | Ser | Gly | Met | Gly | Val | Ala | Asp |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |  |
| Glu | Ser | Lys | Thr | Thr | Phe | Leu | Glu | Leu | Gln | Arg | Lys | Lys | Thr | His | Arg |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |  |
| Tyr | Val | Val | Phe | Lys | Ile | Asp | Glu | Ser | Lys | Lys | Glu | Val | Val | Val | Glu |  |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |  |
| Lys | Thr | Gly | Asn | Pro | Thr | Glu | Ser | Tyr | Asp | Asp | Phe | Leu | Ala | Ser | Leu |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     |     | 95  |  |
| Pro | Asp | Asn | Asp | Cys | Arg | Tyr | Ala | Val | Tyr | Asp | Phe | Asp | Phe | Val | Thr |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |
| Ser | Glu | Asn | Cys | Gln | Lys | Ser | Lys | Ile | Phe | Phe | Phe | Ser | Trp | Ser | Pro |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |
| Ser | Thr | Ser | Pro | Val | Arg | Ala | Lys | Val | Leu | Tyr | Ser | Thr | Ser | Lys | Asp |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |  |
| Gln | Leu | Ser | Lys | Glu | Leu | Gln | Gly | Ile | His | Tyr | Glu | Ile | Gln | Ala | Thr |  |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |  |
| Asp | Pro | Thr | Glu | Val | Asp | Leu | Glu | Val | Leu | Arg | Glu | Arg | Ala | Asn |     |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |

(2) INFORMATION FOR SEQ ID NO:2269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1572366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2269:

Met Ser Phe Arg Gly Leu Ser Arg Pro Asn Ala Ile Ser Gly Met Gly  
1 5 10 15  
Val Ala Asp Glu Ser Lys Thr Thr Phe Leu Glu Leu Gln Arg Lys Lys  
20 25 30  
Thr His Arg Tyr Val Val Phe Lys Ile Asp Glu Ser Lys Lys Glu Val  
35 40 45  
Val Val Glu Lys Thr Gly Asn Pro Thr Glu Ser Tyr Asp Asp Phe Leu  
50 55 60  
Ala Ser Leu Pro Asp Asn Asp Cys Arg Tyr Ala Val Tyr Asp Phe Asp  
65 70 75 80  
Phe Val Thr Ser Glu Asn Cys Gln Lys Ser Lys Ile Phe Phe Phe Ser  
85 90 95  
Trp Ser Pro Ser Thr Ser Pro Val Arg Ala Lys Val Leu Tyr Ser Thr  
100 105 110  
Ser Lys Asp Gln Leu Ser Lys Glu Leu Gln Gly Ile His Tyr Glu Ile  
115 120 125  
Gln Ala Thr Asp Pro Thr Glu Val Asp Leu Glu Val Leu Arg Glu Arg  
130 135 140  
Ala Asn  
145

(2) INFORMATION FOR SEQ ID NO:2270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1572367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2270:

Met Gly Val Ala Asp Glu Ser Lys Thr Thr Phe Leu Glu Leu Gln Arg  
1 5 10 15  
Lys Lys Thr His Arg Tyr Val Val Phe Lys Ile Asp Glu Ser Lys Lys  
20 25 30  
Glu Val Val Val Glu Lys Thr Gly Asn Pro Thr Glu Ser Tyr Asp Asp  
35 40 45  
Phe Leu Ala Ser Leu Pro Asp Asn Asp Cys Arg Tyr Ala Val Tyr Asp  
50 55 60  
Phe Asp Phe Val Thr Ser Glu Asn Cys Gln Lys Ser Lys Ile Phe Phe  
65 70 75 80  
Phe Ser Trp Ser Pro Ser Thr Ser Pro Val Arg Ala Lys Val Leu Tyr  
85 90 95  
Ser Thr Ser Lys Asp Gln Leu Ser Lys Glu Leu Gln Gly Ile His Tyr  
100 105 110  
Glu Ile Gln Ala Thr Asp Pro Thr Glu Val Asp Leu Glu Val Leu Arg  
115 120 125  
Glu Arg Ala Asn  
130

(2) INFORMATION FOR SEQ ID NO:2271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..798

(D) OTHER INFORMATION: / Ceres Seq. ID 1572368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2271:

|             |            |             |            |            |             |     |
|-------------|------------|-------------|------------|------------|-------------|-----|
| ttgtcaaaag  | ctgattcttc | gccttatggc  | atcgattttg | caccttcgaa | cgcccaaccc  | 60  |
| acggggaagat | tcactaatgg | tcgaaccatt  | tccgatattg | tggtggaagc | cttaggagca  | 120 |
| aaatcaccac  | caccaccata | tcttgaacca  | aaactaggag | ctaacacaa  | tctcaattgga | 180 |
| atcaactatg  | cttctgggtc | tgctggaatc  | ttggacgaca | ctgactctct | ggttcatcgg  | 240 |
| ggcgagttcc  | gctgagagaa | caagtgaagta | attttgagaa | gagtagagaa | tatatgttaa  | 300 |
| gcgtgattgg  | tgaaaatggt | acaaaagaga  | tgttgaagaa | tgcaatgttc | acaatcacaa  | 360 |
| ttggatcaaa  | tgaatttttg | aattatattc  | aacctcaat  | acctttcttc | tctcaagaca  | 420 |
| agctccccc   | tgaatgtcct | acaagattcc  | atggctctcc | atttTaaaca | cacatcttaa  | 480 |
| gcgattgcac  | cagctaggag | tgaaggaagt  | cgtggtgggt | ggagtagggc | cacctgggtg  | 540 |
| cataactctt  | gctcgagcgt | tgaatttwat  | accagccgga | aaatgctccg | aacaAgTcaa  | 600 |
| ccaagtgtac  | CgaggtTata | acatgaAgct  | tataactct  | cttaagacat | tgaacaatga  | 660 |
| gttaagatcc  | gaagattaca | acactacatt  | tgtctacgcc | aactcttacg | acctattctt  | 720 |
| gaaactagtt  | ttgaactatc | aactatttgg  | cttgaagaa  | cgagacaagc | cgtgtgtgtg  | 780 |
| cggtactttt  | ccaccgtt   |             |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1572369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2272:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Ser | Lys | Ala | Asp | Ser | Ser | Pro | Tyr | Gly | Ile | Asp | Phe | Ala | Pro | Ser |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Asn | Gly | Gln | Pro | Thr | Gly | Arg | Phe | Thr | Asn | Gly | Arg | Thr | Ile | Ser | Asp |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ile | Val | Gly | Glu | Ala | Leu | Gly | Ala | Lys | Ser | Pro | Pro | Pro | Pro | Tyr | Leu |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Glu | Pro | Asn | Thr | Glu | Ala | Asn | Thr | Ile | Leu | Asn | Gly | Ile | Asn | Tyr | Ala |  |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |  |
| Ser | Gly | Ala | Ala | Gly | Ile | Leu | Asp | Asp | Thr | Gly | Leu | Leu | Val | His | Arg |  |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |  |
| Gly | Glu | Phe | Arg |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1572370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2273:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Tyr | Lys | Ile | Pro | Trp | Ser | Ser | Ile | Leu | Thr | Thr | His | Leu | Lys |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Arg | Leu | His | Gln | Leu | Gly | Gly | Arg | Lys | Phe | Val | Val | Val | Gly | Val | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro | Leu | Gly | Cys | Ile | Pro | Phe | Ala | Arg | Ala | Leu | Asn | Xaa | Ile | Pro | Ala |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Gly | Lys | Cys | Ser | Glu | Gln | Val | Asn | Gln | Val | Val | Arg | Gly | Tyr | Asn | Met |  |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |  |



Lys Leu Ile His Ser Leu Lys Thr Leu Asn Asn Glu Leu Arg Ser Glu  
65 70 75 80  
Asp Tyr Asn Thr Thr Phe Val Tyr Ala Asn Ser Tyr Asp Leu Phe Leu  
85 90 95  
Lys Leu Val Leu Asn Tyr Gln Leu Phe Gly Leu Lys Asn Ala Asp Lys  
100 105 110  
Pro Cys Cys Gly Gly Tyr Phe Pro Pro  
115 120

(2) INFORMATION FOR SEQ ID NO:2274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1080

(D) OTHER INFORMATION: / Ceres Seq. ID 1572375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2274:

gatcacaaaa aattagaatc atggaggctc agagagacca gcacaagcct ccgttgtctc 60  
tacaagaacaa caaatcccca tcatcacaaa acttccagct cgtcgacctc agcaacacca 120  
atggggagct cgtggcgctg aaagtggcaa agcgagcgca agagtgggga atttttcagg 180  
tagttaacca cgggatccca acogaactaa tccggagggt gcacaagggt gatacacagt 240  
tctttgagct cccagagtc cagaagaag cgtggcccaa accagcgaa ccaaaagaga 300  
tacaaggata tgagatggat gatgtacaag gtagaaggag tcatatcttc cataatctat 360  
atcatcatc gtacgtcaat tatgcatctt gccctaagaa tctctcgtga tacagagagg 420  
tgactgagga gtttgcaaa cgtgcaaaag agctagcgga agagatcttc cgtTtgctat 480  
ccgaagKtt aggtttacaa cgtgagatgt tgaagttagc attcggggac gatagtgtgt 540  
gttatcttat gaagatcaac tattaccggt cgtgtccaga gccagattgg gtcattggaa 600  
taaaagccca cactgatttc aatgaactca cacttctcat tcccaatgaa attttcggac 660  
ttcaagtgtt caaggaagac cgtcgtgttg atgtagatta tatatattccc gcggttatta 720  
tcatcatcgg agatcagatc atgaagatga gcaacggaag gtacaacaat gtgttgcata 780  
gaaccttgat ggataaaaaa aaaaacgagga tgtgtcggt ggttcatatc aagcctcctt 840  
atgatattgt tgtgaagcca ttcccgaac tcaccagcgg cgataaatctt cccaagttag 900  
agcctttaac ttaccaggat tacatagaca ttgaagtcct caagctttct cgactgatca 960  
agaattgact tctttgtcgt tgtatgtatg ttgtttgttg ttgtctctgt tcatttggcc 1020  
gtttgcatc gtgtgaacgg gtttctatta attgaagttc aaacaaaaaa aatttgactc 1080

(2) INFORMATION FOR SEQ ID NO:2275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..321

(D) OTHER INFORMATION: / Ceres Seq. ID 1572376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2275:

Ser Gln Lys Ile Arg Ile Met Glu Val Glu Arg Asp Gln His Lys Pro  
1 5 10 15  
Pro Leu Ser Leu Gln Asn Asn Lys Ile Pro Ser Ser Gln Asn Phe Pro  
20 25 30  
Val Val Asp Leu Ser Asn Thr Asn Gly Glu Leu Val Ala Arg Lys Val  
35 40 45  
Ala Lys Ala Ser Glu Glu Trp Gly Ile Phe Gln Val Val Asn His Gly  
50 55 60  
Ile Pro Thr Glu Leu Ile Arg Arg Leu His Lys Val Asp Thr Gln Phe  
65 70 75 80

```

Phe Glu Leu Pro Glu Ser Lys Lys Glu Ala Val Ala Lys Pro Ala Asn
 85 90 95
Ser Lys Glu Ile Gln Gly Tyr Glu Met Asp Asp Val Gln Gly Arg Arg
 100 105 110
Ser His Ile Phe His Asn Leu Tyr Pro Ser Ser Ser Val Asn Tyr Ala
 115 120 125
Phe Trp Pro Lys Asn Pro Pro Glu Tyr Arg Glu Val Thr Glu Glu Phe
 130 135 140
Ala Lys His Ala Lys Gln Leu Ala Glu Glu Ile Leu Gly Leu Leu Ser
 145 150 155 160
Glu Xaa Leu Gly Leu Gln Arg Glu Met Leu Lys Leu Ala Phe Gly Asp
 165 170 175
Asp Ser Ala Gly Tyr Leu Met Lys Ile Asn Tyr Tyr Arg Pro Cys Pro
 180 185 190
Glu Pro Asp Trp Val Met Gly Ile Lys Ala His Thr Asp Phe Asn Glu
 195 200 205
Leu Thr Leu Leu Ile Pro Asn Glu Ile Phe Gly Leu Gln Val Phe Lys
 210 215 220
Glu Asp Arg Trp Leu Asp Val Asp Tyr Ile Tyr Pro Ala Val Ile Ile
 225 230 235 240
Ile Ile Gly Asp Gln Ile Met Lys Met Ser Asn Gly Arg Tyr Asn Asn
 245 250 255
Val Leu His Arg Thr Leu Met Asp Lys Lys Thr Arg Met Ser Ser
 260 265 270
Val Val His Ile Lys Pro Pro Tyr Asp Met Val Val Lys Pro Phe Pro
 275 280 285
Glu Leu Thr Ser Gly Asp Asn Pro Pro Lys Phe Glu Pro Leu Thr Tyr
 290 295 300
Gln Asp Tyr Ile Asp Ile Glu Val Pro Lys Leu Ser Arg Leu Ile Lys
 305 310 315 320
Asn

```

(2) INFORMATION FOR SEQ ID NO:2276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2276:

```

Met Glu Val Glu Arg Asp Gln His Lys Pro Pro Leu Ser Leu Gln Asn
1 5 10 15
Asn Lys Ile Pro Ser Ser Gln Asn Phe Pro Val Val Asp Leu Ser Asn
 20 25 30
Thr Asn Gly Glu Leu Val Ala Arg Lys Val Ala Lys Ala Ser Glu Glu
 35 40 45
Trp Gly Ile Phe Gln Val Val Asn His Gly Ile Pro Thr Glu Leu Ile
 50 55 60
Arg Arg Leu His Lys Val Asp Thr Gln Phe Phe Glu Leu Pro Glu Ser
 65 70 75 80
Lys Lys Glu Ala Val Ala Lys Pro Ala Asn Ser Lys Glu Ile Gln Gly
 85 90 95
Tyr Glu Met Asp Asp Val Gln Gly Arg Arg Ser His Ile Phe His Asn
 100 105 110
Leu Tyr Pro Ser Ser Ser Val Asn Tyr Ala Phe Trp Pro Lys Asn Pro
 115 120 125
Pro Glu Tyr Arg Glu Val Thr Glu Glu Phe Ala Lys His Ala Lys Gln

```

|                     |                             |                         |
|---------------------|-----------------------------|-------------------------|
| 130                 | 135                         | 140                     |
| Leu Ala Glu Glu Ile | Leu Gly Leu Leu Ser         | Glu Xaa Leu Gly Leu Gln |
| 145                 | 150                         | 155                     |
| Arg Glu Met Leu Lys | Leu Ala Phe Gly Asp         | Asp Ser Ala Gly Tyr Leu |
| 165                 | 170                         | 175                     |
| Met Lys Ile Asn Tyr | Tyr Arg Pro Cys Pro         | Glu Pro Asp Trp Val Met |
| 180                 | 185                         | 190                     |
| Gly Ile Lys Ala His | Thr Asp Phe Asn Glu Leu Thr | Leu Leu Ile Pro         |
| 195                 | 200                         | 205                     |
| Asn Glu Ile Phe Gly | Leu Gln Val Phe Lys Glu Asp | Arg Trp Leu Asp         |
| 210                 | 215                         | 220                     |
| Val Asp Tyr Ile Tyr | Pro Ala Val Ile Ile         | Ile Gly Asp Gln Ile     |
| 225                 | 230                         | 235                     |
| Met Lys Met Ser Asn | Gly Arg Tyr Asn Asn Val     | Leu His Arg Thr Leu     |
| 245                 | 250                         | 255                     |
| Met Asp Lys Lys Lys | Thr Arg Met Ser Ser Val     | Val His Ile Lys Pro     |
| 260                 | 265                         | 270                     |
| Pro Tyr Asp Met Val | Val Lys Pro Phe Pro Glu     | Leu Thr Ser Gly Asp     |
| 275                 | 280                         | 285                     |
| Asn Pro Pro Lys Phe | Glu Pro Leu Thr Tyr Gln     | Asp Tyr Ile Asp Ile     |
| 290                 | 295                         | 300                     |
| Glu Val Pro Lys Leu | Ser Arg Leu Ile Lys Asn     |                         |
| 305                 | 310                         | 315                     |

(2) INFORMATION FOR SEQ ID NO:2277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1572378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2277:

|                                                                 |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| Met Asp Asp Val Gln Gly Arg Arg Ser His Ile Phe His Asn Leu Tyr | 1   | 5   | 10  | 15  |
| Pro Ser Ser Ser Val Asn Tyr Ala Phe Trp Pro Lys Asn Pro Pro Glu | 20  | 25  | 30  |     |
| Tyr Arg Glu Val Thr Glu Glu Phe Ala Lys His Ala Lys Gln Leu Ala | 35  | 40  | 45  |     |
| Glu Glu Ile Leu Gly Leu Leu Ser Glu Xaa Leu Gly Leu Gln Arg Glu | 50  | 55  | 60  |     |
| Met Leu Lys Leu Ala Phe Gly Asp Asp Ser Ala Gly Tyr Leu Met Lys | 65  | 70  | 75  | 80  |
| Ile Asn Tyr Tyr Arg Pro Cys Pro Glu Pro Asp Trp Val Met Gly Ile | 85  | 90  | 95  |     |
| Lys Ala His Thr Asp Phe Asn Glu Leu Thr Leu Leu Ile Pro Asn Glu | 100 | 105 | 110 |     |
| Ile Phe Gly Leu Gln Val Phe Lys Glu Asp Arg Trp Leu Asp Val Asp | 115 | 120 | 125 |     |
| Tyr Ile Tyr Pro Ala Val Ile Ile Ile Gly Asp Gln Ile Met Lys     | 130 | 135 | 140 |     |
| Met Ser Asn Gly Arg Tyr Asn Asn Val Leu His Arg Thr Leu Met Asp | 145 | 150 | 155 | 160 |
| Lys Lys Lys Thr Arg Met Ser Ser Val Val His Ile Lys Pro Pro Tyr | 165 | 170 | 175 |     |
| Asp Met Val Val Lys Pro Phe Pro Glu Leu Thr Ser Gly Asp Asn Pro | 180 | 185 | 190 |     |
| Pro Lys Phe Glu Pro Leu Thr Tyr Gln Asp Tyr Ile Asp Ile Glu Val | 195 | 200 | 205 |     |

Pro Lys Leu Ser Arg Leu Ile Lys Asn  
210 215

(2) INFORMATION FOR SEQ ID NO:2278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..729
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2278:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| acactcatct | octaattccc | ttacataata | ttttcttaag | ataagcaaaa | aatcatggcg | 60  |
| agaagcgctc | agtttgggtg | ggaaacttga | gacagaagtg | gagatcaaa  | cttcggccaa | 120 |
| aaagttccat | cacatgttta | ccgagagacc | acaccatgtc | tccaaagcaa | ctccagataa | 180 |
| aattcatgga | tgtgagctgc | acgaagcgca | ctggggccaa | gtcggctcta | tcgtcatctg | 240 |
| gaaatacgtt | catgatggaa | agttacacgt | ggggaagaat | aagatcgagg | cggtggatcc | 300 |
| ggagaagaac | ctgatcacgt | tcaaggtttt | agaaggtgat | ctgatgaatg | agtacaagag | 360 |
| cttcgcattt | acactccaag | tgacccttaa | gcaaggggag | tcaggaggta | ttgcgcactg | 420 |
| gcacctggag | tatgagaaaa | ttagcgagga | ggtagctcat | cccgaacc   | ttctccaatt | 480 |
| ctgtgtcgag | atctccaaag | agatcgacga | acatctcttg | gccgaggaat | agaaaaatac | 540 |
| tcctcgtctg | tgtgtgggtc | tttgaactt  | aagcaagctc | ttgaaactgc | aataataaat | 600 |
| gaacgggtcc | gtctttatgt | aagagaaaaa | agatatatat | atatgtgttg | gtgtgtgtaa | 660 |
| tgctgttatg | ctactacta  | cggttgagtt | atgttggaa  | agtaaaaRgc | atataatcta | 720 |
| ttttgtcc   |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2279:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Ala | Ser | Ser | Leu | Val | Gly | Lys | Leu | Glu | Thr | Glu | Val | Glu |
| 1   |     | 5   |     |     |     |     |     | 10  |     |     | 15  |     |     |     |     |
| Ile | Lys | Ala | Ser | Ala | Lys | Lys | Phe | His | His | Met | Phe | Thr | Glu | Arg | Pro |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| His | His | Val | Ser | Lys | Ala | Thr | Pro | Asp | Lys | Ile | His | Gly | Cys | Glu | Leu |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| His | Glu | Gly | Asp | Trp | Gly | Lys | Val | Gly | Ser | Ile | Val | Ile | Trp | Lys | Tyr |
|     |     | 50  |     |     |     |     |     | 55  |     |     | 60  |     |     |     |     |
| Val | His | Asp | Gly | Lys | Leu | Thr | Val | Gly | Lys | Asn | Lys | Ile | Glu | Ala | Val |
|     |     | 65  |     |     |     |     |     | 70  |     |     | 75  |     |     | 80  |     |
| Asp | Pro | Glu | Lys | Asn | Leu | Ile | Thr | Phe | Lys | Val | Leu | Glu | Gly | Asp | Leu |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Met | Asn | Glu | Tyr | Lys | Ser | Phe | Ala | Phe | Thr | Leu | Gln | Val | Thr | Pro | Lys |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Gln | Gly | Glu | Ser | Gly | Ser | Ile | Ala | His | Trp | His | Leu | Glu | Tyr | Glu | Lys |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Ile | Ser | Glu | Glu | Val | Ala | His | Pro | Glu | Thr | Leu | Leu | Gln | Phe | Cys | Val |
|     |     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |
| Glu | Ile | Ser | Lys | Glu | Ile | Asp | Glu | His | Leu | Leu | Ala | Glu | Glu |     |     |
|     |     | 145 |     |     |     |     |     | 150 |     |     |     | 155 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2280:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..132  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572399  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2280:  
Met Phe Thr Glu Arg Pro His His Val Ser Lys Ala Thr Pro Asp Lys  
1 5 10 15  
Ile His Gly Cys Glu Leu His Glu Gly Asp Trp Gly Lys Val Gly Ser  
20 25 30  
Ile Val Ile Trp Lys Tyr Val His Asp Gly Lys Leu Thr Val Gly Lys  
35 40 45  
Asn Lys Ile Glu Ala Val Asp Pro Glu Lys Asn Leu Ile Thr Phe Lys  
50 55 60  
Val Leu Glu Gly Asp Leu Met Asn Glu Tyr Lys Ser Phe Ala Phe Thr  
65 70 75 80  
Leu Gln Val Thr Pro Lys Gln Gly Glu Ser Gly Ser Ile Ala His Trp  
85 90 95  
His Leu Glu Tyr Glu Lys Ile Ser Glu Val Ala His Pro Glu Thr  
100 105 110  
Leu Leu Gln Phe Cys Val Glu Ile Ser Lys Glu Ile Asp Glu His Leu  
115 120 125  
Leu Ala Glu Glu  
130

(2) INFORMATION FOR SEQ ID NO:2281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..572

(D) OTHER INFORMATION: / Ceres Seq. ID 1572400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2281:

|             |             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| attcataaat  | ctctcaaaag  | aagaactaag  | agctttacta  | cagtcctact  | ctctacacat  | 60  |
| cttctcttct  | ctctcaagag  | ctagtcgatg  | ccaaactcat  | aacttttttt  | ctcttaactca | 120 |
| caattttatt  | caactttcgt  | tgtctcacta  | tgtcaaaaaga | agctgagtag  | catccagaaa  | 180 |
| gtgtgaagttt | ttattttttg  | gtaaaaataga | aagttatgga  | ccagggaagtc | tgaatcatca  | 240 |
| ccaatgtgga  | ggacaatgca  | caaggagatg  | tagcaataca  | aagtatcata  | agccatgcac  | 300 |
| gttctcttcg  | caaaaagtgt  | gtgctaagt   | cctttgtgtc  | cctccaggca  | cgtacggcaa  | 360 |
| caaaacaagt  | tgtctcttgt  | acaacaactg  | gaagactcaa  | caaggtggac  | caaaatgtcc  | 420 |
| ataaacaaaa  | agagagaaaac | ccaatctgt   | ttctattttt  | atttaattat  | ttccagtagt  | 480 |
| cttttgttgt  | cgtgatggtt  | aaattatagt  | gtttttgcag  | gtatcattta  | tcatcgataa  | 540 |
| acaatatcat  | ataaaaattc  | ctatgtttct  | tg          |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..40  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2282:

Met Ala Lys Leu Ile Thr Ser Phe Leu Leu Thr Ile Leu Phe Thr  
1 5 10 15  
Phe Val Cys Leu Thr Met Ser Lys Glu Ala Glu Tyr His Pro Glu Ser  
20 25 30  
Val Ser Phe Tyr Phe Leu Val Lys  
35 40

(2) INFORMATION FOR SEQ ID NO:2283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..41
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2283:

Met Phe Phe Cys Gln Lys Cys Cys Ala Lys Cys Leu Cys Val Pro Pro  
1 5 10 15  
Gly Thr Tyr Gly Asn Lys Gln Val Cys Pro Cys Tyr Asn Asn Trp Lys  
20 25 30  
Thr Gln Gln Gly Gly Pro Lys Cys Pro  
35 40

(2) INFORMATION FOR SEQ ID NO:2284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..55
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2284:

Met Pro Leu Cys Pro Ser Arg His Val Arg Gln Gln Thr Ser Val Ser  
1 5 10 15  
Leu Leu Gln Gln Leu Glu Asp Ser Thr Arg Trp Thr Lys Met Ser Ile  
20 25 30  
Asn Lys Lys Arg Glu Thr Pro Ile Cys Phe Leu Phe Tyr Leu Ile Ile  
35 40 45  
Ser Ser Met Leu Leu Leu Ser  
50 55

(2) INFORMATION FOR SEQ ID NO:2285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1459
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2285:

cggagggtgat cggttgctctc tgggttaatg aagctgccac gaattggcgt atttagatt 60  
gatacgtcaa agctcctctc cgcgcacgtt agctaaagga atgtcttgta ctcttttgt 120  
tggtgtgtgt gattttttga acaagaaaag aaactaatca aaaagacgaa gaggaagag 180  
aagctcacgc tttctatctc tcattttaac cactgatctt ctcgattgc gtcttgcttc 240

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| tcgtcggttg  | cttcgcatct  | ctctctggat | ttcttcaatt  | tcgtacggat  | taggttaatt  | 300  |
| gtgtataaag  | gagtttagtt  | gatacttggt | ttgtacattt  | gggtagatga  | tgcgtactgt  | 360  |
| tgctttacca  | ttgtcccatg  | atctgaatgt | tcataagatc  | catgaagctt  | ctggatccca  | 420  |
| taatagtgtc  | gctggtaaaa  | atcgtgtgta | tctgactcgg  | actggttctt  | catcatgtgc  | 480  |
| cacgagacaa  | gacgttttga  | gtcttcagct | actagagagc  | ttgagtgggt  | caatagtacc  | 540  |
| tgtatcatct  | agggtgtaag  | catttgtttg | ccggtcagct  | ctctctctcg  | ggaatggaaa  | 600  |
| tgaaggccct  | attcttaaat  | caactgcagt | aattattcaca | agggttatatg | atgcttttag  | 660  |
| tggaaatcct  | catttagtga  | aactaattcc | agcgggtggg  | attcttgcat  | tgtctacatg  | 720  |
| gggtcttaga  | ccccttctgc  | gccttgccag | aactaccctg  | tttgagaagg  | ggaatgatgc  | 780  |
| aaatttcacag | aagagttagca | cgcagtagat | tgttggtgca  | tatcttcaac  | ctttgctgct  | 840  |
| ttggagcgga  | gcaatctctt  | tatgcagaac | attggaccaca | atagattatgc | cttcaagtgc  | 900  |
| cggccaggtc  | attaaacagc  | gtcttctgat | ctttgctcgg  | tcacatcaaa  | cgggtgtggc  | 960  |
| attttctctgc | tgtttatcaa  | gcctacttca | gcagggtcag  | aaatttttta  | tggagacaaa  | 1020 |
| taatcctctg  | gataccagaa  | atatgggttt | cagttttgct  | ggaaaagctg  | tttacaactg  | 1080 |
| tgcgtgggtt  | gctgctgctt  | cattgtttat | ggaaactgta  | ggctctctca  | ccccaaaagt  | 1140 |
| gcataacggt  | gggggtctcg  | ggacagtact | gctaactctt  | gctggccctg  | agataactact | 1200 |
| taactttctt  | tcaagcatta  | tgatttcagc | tacacggccc  | tttgtcttga  | atgagtggtt  | 1260 |
| ccagaccaag  | ataggaggct  | atgaagtctt | tggcacagta  | gagcaagctg  | gttggtggct  | 1320 |
| acctacaatt  | atcagagggt  | atgaccggga | agcagttcat  | attcctaacc  | accagttcag  | 1380 |
| tgtaaatatt  | gtgagaatac  | tcactcagaa | gacgcattgg  | cgcacataaa  | cacatcttgc  | 1440 |
| catcagtcac  | cttgatgtc   |            |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..372

(D) OTHER INFORMATION: / Ceres Seq. ID 1572405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2286:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Met | Arg | Thr | Val | Ala | Leu | Pro | Leu | Ser | His | Asp | Leu | Asn | Val |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| His | Lys | Ile | His | Glu | Ala | Ser | Gly | Phe | His | Asn | Ser | Ala | Ala | Gly | Lys |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asn | Arg | Val | Tyr | Leu | Thr | Arg | Thr | Gly | Leu | Ser | Ser | Cys | Ala | Thr | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Asp | Val | Trp | Ser | Leu | Gln | Leu | Glu | Ser | Leu | Ser | Gly | Ser | Ile |     |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Val | Pro | Val | Ser | Ser | Arg | Cys | Asn | Ala | Phe | Val | Cys | Arg | Ser | Ala | Leu |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     | 80  |     |     |
| Ser | Pro | Gly | Asn | Gly | Asn | Glu | Gly | Pro | Ile | Leu | Lys | Ser | Thr | Ala | Val |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Ile | Phe | Thr | Arg | Val | Tyr | Asp | Ala | Leu | Gly | Gly | Asn | Pro | His | Leu | Val |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Lys | Leu | Ile | Pro | Ala | Val | Gly | Ile | Leu | Ala | Phe | Ala | Thr | Trp | Gly | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Pro | Leu | Leu | Arg | Leu | Ala | Arg | Thr | Thr | Leu | Phe | Glu | Lys | Gly | Asn |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Asp | Ala | Asn | Ser | Gln | Lys | Ser | Ser | Thr | Gln | Tyr | Ile | Val | Val | Ser | Tyr |
|     |     |     | 145 |     |     |     | 150 |     |     | 155 |     |     |     | 160 |     |
| Leu | Gln | Pro | Leu | Leu | Trp | Ser | Gly | Ala | Ile | Leu | Leu | Cys | Arg | Thr |     |
|     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |     |
| Leu | Asp | Pro | Ile | Val | Leu | Pro | Ser | Ser | Ala | Gly | Gln | Ala | Ile | Lys | Gln |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Arg | Leu | Leu | Ile | Phe | Ala | Arg | Ser | Ile | Ser | Thr | Val | Leu | Ala | Phe | Ser |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| Cys | Cys | Leu | Ser | Ser | Leu | Gln | Gln | Val | Gln | Lys | Phe | Phe | Met | Glu |     |
|     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |

Thr Asn Asn Pro Ala Asp Thr Arg Asn Met Gly Phe Ser Phe Ala Gly  
225 230 235 240  
Lys Ala Val Tyr Thr Thr Ala Ala Trp Val Ala Ala Ser Leu Phe Met  
245 250 255  
Glu Leu Leu Gly Phe Ser Thr Gln Lys Trp Leu Thr Ala Gly Gly Leu  
260 265 270  
Gly Thr Val Leu Leu Thr Leu Ala Gly Arg Glu Ile Leu Thr Asn Phe  
275 280 285  
Leu Ser Ser Ile Met Ile His Ala Thr Arg Pro Phe Val Leu Asn Glu  
290 295 300  
Trp Ile Gln Thr Lys Ile Gly Gly Tyr Glu Val Ser Gly Thr Val Glu  
305 310 315 320  
Gln Val Gly Trp Trp Ser Pro Thr Ile Ile Arg Gly Asp Asp Arg Glu  
325 330 335  
Ala Val His Ile Pro Asn His Gln Phe Ser Val Asn Ile Val Arg Asn  
340 345 350  
Leu Thr Gln Lys Thr His Trp Arg Ile Lys Thr His Leu Ala Ile Ser  
355 360 365  
His Leu Asp Val  
370

(2) INFORMATION FOR SEQ ID NO:2287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 371 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..371

(D) OTHER INFORMATION: / Ceres Seq. ID 1572406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2287:

Met Met Arg Thr Val Ala Leu Pro Leu Ser His Asp Leu Asn Val His  
1 5 10 15  
Lys Ile His Glu Ala Ser Gly Phe His Asn Ser Ala Ala Gly Lys Asn  
20 25 30  
Arg Val Tyr Leu Thr Arg Thr Gly Leu Ser Ser Cys Ala Thr Arg Gln  
35 40 45  
Asp Val Trp Ser Leu Gln Leu Leu Glu Ser Leu Ser Gly Ser Ile Val  
50 55 60  
Pro Val Ser Ser Arg Cys Asn Ala Phe Val Cys Arg Ser Ala Leu Ser  
65 70 75 80  
Pro Gly Asn Gly Asn Glu Gly Pro Ile Leu Lys Ser Thr Ala Val Ile  
85 90 95  
Phe Thr Arg Val Tyr Asp Ala Leu Gly Gly Asn Pro His Leu Val Lys  
100 105 110  
Leu Ile Pro Ala Val Gly Ile Leu Ala Phe Ala Thr Trp Gly Leu Arg  
115 120 125  
Pro Leu Leu Arg Leu Ala Arg Thr Thr Leu Phe Glu Lys Gly Asn Asp  
130 135 140  
Ala Asn Ser Gln Lys Ser Ser Thr Gln Tyr Ile Val Val Ser Tyr Leu  
145 150 155 160  
Gln Pro Leu Leu Leu Trp Ser Gly Ala Ile Leu Leu Cys Arg Thr Leu  
165 170 175  
Asp Pro Ile Val Leu Pro Ser Ser Ala Gly Gln Ala Ile Lys Gln Arg  
180 185 190  
Leu Leu Ile Phe Ala Arg Ser Ile Ser Thr Val Leu Ala Phe Ser Cys  
195 200 205  
Cys Leu Ser Ser Leu Leu Gln Gln Val Gln Lys Phe Phe Met Glu Thr  
210 215 220  
Asn Asn Pro Ala Asp Thr Arg Asn Met Gly Phe Ser Phe Ala Gly Lys



|                                                                 |                                             |     |  |     |  |     |
|-----------------------------------------------------------------|---------------------------------------------|-----|--|-----|--|-----|
| 225                                                             |                                             | 230 |  | 235 |  | 240 |
| Ala Val Tyr Thr                                                 | Ala Ala Trp Val Ala Ala Ser Leu Phe Met Glu |     |  |     |  |     |
|                                                                 | 245                                         | 250 |  | 255 |  |     |
| Leu Leu Gly Phe Ser Thr Gln Lys Trp Leu Thr Ala Gly Gly Leu Gly |                                             |     |  |     |  |     |
|                                                                 | 260                                         | 265 |  | 270 |  |     |
| Thr Val Leu Leu Thr Leu Ala Gly Arg Glu Ile Leu Thr Asn Phe Leu |                                             |     |  |     |  |     |
|                                                                 | 275                                         | 280 |  | 285 |  |     |
| Ser Ser Ile Met Ile His Ala Thr Arg Pro Phe Val Leu Asn Glu Trp |                                             |     |  |     |  |     |
|                                                                 | 290                                         | 295 |  | 300 |  |     |
| Ile Gln Thr Lys Ile Gly Gly Tyr Glu Val Ser Gly Thr Val Glu Gln |                                             |     |  |     |  |     |
|                                                                 | 305                                         | 310 |  | 315 |  | 320 |
| Val Gly Trp Trp Ser Pro Thr Ile Ile Arg Gly Asp Asp Arg Glu Ala |                                             |     |  |     |  |     |
|                                                                 | 325                                         | 330 |  | 335 |  |     |
| Val His Ile Pro Asn His Gln Phe Ser Val Asn Ile Val Arg Asn Leu |                                             |     |  |     |  |     |
|                                                                 | 340                                         | 345 |  | 350 |  |     |
| Thr Gln Lys Thr His Trp Arg Ile Lys Thr His Leu Ala Ile Ser His |                                             |     |  |     |  |     |
|                                                                 | 355                                         | 360 |  | 365 |  |     |
| Leu Asp Val                                                     |                                             |     |  |     |  |     |
| 370                                                             |                                             |     |  |     |  |     |

(2) INFORMATION FOR SEQ ID NO:2288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..370

(D) OTHER INFORMATION: / Ceres Seq. ID 1572407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2288:

|                                                                 |             |
|-----------------------------------------------------------------|-------------|
| Met Arg Thr Val Ala Leu Pro Leu Ser His Asp Leu Asn Val His Lys |             |
| 1                                                               | 5 10 15     |
| Ile His Glu Ala Ser Gly Phe His Asn Ser Ala Ala Gly Lys Asn Arg |             |
|                                                                 | 20 25 30    |
| Val Tyr Leu Thr Arg Thr Gly Leu Ser Ser Cys Ala Thr Arg Gln Asp |             |
|                                                                 | 35 40 45    |
| Val Trp Ser Leu Gln Leu Leu Glu Ser Leu Ser Gly Ser Ile Val Pro |             |
|                                                                 | 50 55 60    |
| Val Ser Ser Arg Cys Asn Ala Phe Val Cys Arg Ser Ala Leu Ser Pro |             |
| 65                                                              | 70 75 80    |
| Gly Asn Gly Asn Glu Gly Pro Ile Leu Lys Ser Thr Ala Val Ile Phe |             |
|                                                                 | 85 90 95    |
| Thr Arg Val Tyr Asp Ala Leu Gly Gly Asn Pro His Leu Val Lys Leu |             |
|                                                                 | 100 105 110 |
| Ile Pro Ala Val Gly Ile Leu Ala Phe Ala Thr Trp Gly Leu Arg Pro |             |
|                                                                 | 115 120 125 |
| Leu Leu Arg Leu Ala Arg Thr Thr Leu Phe Glu Lys Gly Asn Asp Ala |             |
|                                                                 | 130 135 140 |
| Asn Ser Gln Lys Ser Ser Thr Gln Tyr Ile Val Val Ser Tyr Leu Gln |             |
| 145                                                             | 150 155 160 |
| Pro Leu Leu Leu Trp Ser Gly Ala Ile Leu Leu Cys Arg Thr Leu Asp |             |
|                                                                 | 165 170 175 |
| Pro Ile Val Leu Pro Ser Ser Ala Gly Gln Ala Ile Lys Gln Arg Leu |             |
|                                                                 | 180 185 190 |
| Leu Ile Phe Ala Arg Ser Ile Ser Thr Val Leu Ala Phe Ser Cys Cys |             |
|                                                                 | 195 200 205 |
| Leu Ser Ser Leu Leu Gln Gln Val Gln Lys Phe Phe Met Glu Thr Asn |             |
|                                                                 | 210 215 220 |
| Asn Pro Ala Asp Thr Arg Asn Met Gly Phe Ser Phe Ala Gly Lys Ala |             |
| 225                                                             | 230 235 240 |

Val Tyr Thr Ala Ala Trp Val Ala Ala Ala Ser Leu Phe Met Glu Leu  
245 250 255  
Leu Gly Phe Ser Thr Gln Lys Trp Leu Thr Ala Gly Gly Leu Gly Thr  
260 265 270  
Val Leu Leu Thr Leu Ala Gly Arg Glu Ile Leu Thr Asn Phe Leu Ser  
275 280 285  
Ser Ile Met Ile His Ala Thr Arg Pro Phe Val Leu Asn Glu Trp Ile  
290 295 300  
Gln Thr Lys Ile Gly Gly Tyr Glu Val Ser Gly Thr Val Glu Gln Val  
305 310 315 320  
Gly Trp Trp Ser Pro Thr Ile Ile Arg Gly Asp Asp Arg Glu Ala Val  
325 330 335  
His Ile Pro Asn His Gln Phe Ser Val Asn Ile Val Arg Asn Leu Thr  
340 345 350  
Gln Lys Thr His Trp Arg Ile Lys Thr His Leu Ala Ile Ser His Leu  
355 360 365  
Asp Val  
370

(2) INFORMATION FOR SEQ ID NO:2289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..605
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2289:

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| gcaccoccttt | tattgtagcg | acgcaagaag  | aagcagctat | agcgtacgat | atcgcagcta | 60  |
| tcgagtaccg  | tggaactaac | gccgttaacta | acttcgacat | cagccgttat | ctgaaactcc | 120 |
| cgggtgccga  | gaaccctatc | gataccgcga  | ataatctcct | cgagagtcgc | cattctgac  | 180 |
| ttagcccat   | tataaaacct | aaccacgagt  | ctgaactatc | acagagtcac | tcttcgtcag | 240 |
| aggacaacga  | tgatcggaaa | acaaagctct  | tgaagtcgtc | acctttagtg | gcagaggagg | 300 |
| taatcggaac  | atcgacgcca | cctgagattg  | ctccgcctcg | tcggagcttc | ccggaagata | 360 |
| tccagacgta  | tttcgggtgt | caaaaactccg | gcaagttaac | ggcggaggaa | gatgatgta  | 420 |
| ctcttcggtga | tttagattct | ttccttaacg  | ctgatttcta | cagcagtgta | aatgatgtg  | 480 |
| aaagtgtgt   | tctctcgata | agttttgttt  | tttagttgtt | cagaatctcg | gtttcgaaat | 540 |
| tcaacattga  | cacatcgatt | attctttctt  | gtgacaatct | tataataata | agtttgaat  | 600 |
| ttttt       |            |             |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2290:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Pro | Phe | Ile | Val | Ala | Thr | Gln | Glu | Glu | Ala | Ala | Ile | Ala | Tyr | Asp |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |
| Ile | Ala | Ala | Ile | Glu | Tyr | Arg | Gly | Leu | Asn | Ala | Val | Thr | Asn | Phe | Asp |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Ile | Ser | Arg | Tyr | Leu | Lys | Leu | Pro | Val | Pro | Glu | Asn | Pro | Ile | Asp | Thr |
|     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |     |
| Ala | Asn | Asn | Leu | Leu | Glu | Ser | Pro | His | Ser | Asp | Leu | Ser | Pro | Phe | Ile |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |

Lys Pro Asn His Glu Ser Asp Leu Ser Gln Ser Gln Ser Ser Ser Glu  
65 70 75 80  
Asp Asn Asp Asp Arg Lys Thr Lys Leu Leu Lys Ser Ser Pro Leu Val  
85 90 95  
Ala Glu Glu Val Ile Gly Pro Ser Thr Pro Pro Glu Ile Ala Pro Pro  
100 105 110  
Arg Arg Ser Phe Pro Glu Asp Ile Gln Thr Tyr Phe Gly Cys Gln Asn  
115 120 125  
Ser Gly Lys Leu Thr Ala Glu Glu Asp Asp Val Ile Phe Gly Asp Leu  
130 135 140  
Asp Ser Phe Leu Thr Pro Asp Phe Tyr Ser Glu Leu Asn Asp Cys  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1393
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2291:

|             |             |             |             |             |            |      |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| aagccataga  | tattgaagaa  | atacactttt  | tgtctttttg  | ttgctgtgcA  | acgtcataga | 60   |
| tctaactccg  | gaagaagaag  | acgaacacac  | gtcatctccg  | tccccagctc  |            | 120  |
| cgggcaagaa  | gaagcagaat  | ctgggatgga  | tggagtgatg  | gaggggatgg  | agcagtggtt | 180  |
| tcggggagat  | tctctccag   | aggatcacag  | cttctcattt  | ggagaatcct  | cttctctctc | 240  |
| cttcgcgtcaa | cgacctcaat  | tgcgttgtca  | ctggtctcac  | cagcggtcatt | ggcgtgtaaa | 300  |
| ccgcgaggca  | gcttgacaga  | gctgggtgctc | atgtttgtgat | ggcgttaagg  | aaacaaaagg | 360  |
| cggtctcagga | gctgatactg  | caatggcaga  | acgaatggctc | tggtaaaagt  | ctccactca  | 420  |
| ataattgagc  | aattggagatt | gattctactc  | cactggattc  | tgtcgcgaga  | tttctgtagg | 480  |
| ctttcaacgc  | tcggttagga  | ctttgcatg   | ttctgattaa  | caatgctggg  | atgtttgcta | 540  |
| tgggagaggg  | gcacaaaattc | tcagaggaag  | gatatgagca  | gcacatgcga  | gtgaatcatt | 600  |
| tagctccagc  | gctgctttca  | gtactctctt  | tgcgtctctc  | gattccgaggc | tctctagacc | 660  |
| gaatcattaa  | tgtgaattcc  | gttatgcata  | gtgtcggttt  | tgttgaccgc  | gatgacatga | 720  |
| atgtgtgttc  | tgttagacgt  | aagtactcaa  | gccttatagg  | atactcaagc  | agcaagcttg | 780  |
| cccgatattt  | gtttagttag  | attcttttca  | aaaagcttcc  | tctggaaaca  | ggagtcagcg | 840  |
| tcgtatgtct  | atccccctggt | gttgtctctaa | caaatgtttgc | cagggatctc  | tccaggattc | 900  |
| ttcaagctct  | ttacgcagtg  | ataccttatt  | tcatattttc  | accccaagaa  | ggttgtagaa | 960  |
| gttctctatt  | ctcggccaca  | gactctcaga  | ttccagagta  | ctgggaaaca  | ctaaaaaacg | 1020 |
| atgattggcc  | gttttgccca  | tcatctctc   | aagattggcc  | ccctgcacaa  | cttctccga  | 1080 |
| aagcacacaa  | cacagaaact  | gcacagagag  | tgtggaaaaa  | gacgttagag  | ctgtgtggct | 1140 |
| ttcctctcga  | tgcagttgag  | aagctcatag  | aaggggaaaa  | tatccaatgc  | cggtagggag | 1200 |
| cacacacaga  | atagtctttc  | aaaattacca  | caggttaagt  | gacccattac  | agatcaaa   | 1260 |
| gtaggtaatt  | gagaaaaata  | ctttttttt   | tgtttctgt   | tattcaatca  | cacgatacac | 1320 |
| tggggaatgg  | atccccccag  | catgtagttt  | gcttgagaat  | gtttgattgt  | tggataaaaa | 1380 |
| tcgaagcttta | gct         |             |             |             |            |      |

(2) INFORMATION FOR SEQ ID NO:2292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..376
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2292:

Met Ser Asp Glu Thr Thr Ser Ser Pro Ser Pro Ala Pro Ala Lys Lys

(2) INFORMATION FOR SEQ ID NO:2293:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
{ix} FEATURE:
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(A) NAME/KEY: peptide

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(A) NAME/REF: peptid
(B) LOCATION: 1..354
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1572452

(81) SEQUENCE DESCRIPTION: SEQ ID NO:2293:

Met Glu Trp Met Arg Gly Trp Ser Ser Val Phe Gly Glu Ile Leu Phe  
1 5 10 15

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Gly | Trp | Ser | Ser | Val | Phe | Gly | Glu | Ile | Leu | Phe | Gln | Arg | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Ala | Ser | His | Leu | Glu | Asn | Pro | Leu | Pro | Leu | Pro | Ser | Val | Asn | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Thr | Cys | Val | Val | Thr | Gly | Ser | Thr | Ser | Gly | Ile | Gly | Arg | Glu | Thr |

|                 |                     |                                 |
|-----------------|---------------------|---------------------------------|
| 35              | 40                  | 45                              |
| Ala Arg Gln Leu | Ala Glu Ala Gly     | Ala His Val Val Met Ala Val Arg |
| 50              | 55                  | 60                              |
| Asn Thr Lys Ala | Ala Gln Glu Leu Ile | Leu Gln Trp Gln Asn Glu Trp     |
| 65              | 70                  | 75                              |
| Ser Gly Lys Gly | Leu Pro Leu Asn Ile | Glu Ala Met Glu Ile Asp Leu     |
| 85              | 90                  | 95                              |
| Leu Ser Leu Asp | Ser Val Ala Arg Phe | Ala Glu Ala Phe Asn Ala Arg     |
| 100             | 105                 | 110                             |
| Leu Gly Pro Leu | His Val Leu Ile     | Asn Asn Ala Gly Met Phe Ala Met |
| 115             | 120                 | 125                             |
| Gly Glu Ala Gln | Lys Phe Ser Glu     | Glu Gly Tyr Glu Gln His Met Gln |
| 130             | 135                 | 140                             |
| Val Asn His Leu | Ala Pro Ala Leu     | Leu Ser Val Leu Leu Pro Ser     |
| 145             | 150                 | 155                             |
| Leu Ile Arg Gly | Ser Pro Ser Arg Ile | Ile Asn Val Asn Ser Val Met     |
| 165             | 170                 | 175                             |
| His Ser Val Gly | Phe Val Asp Pro     | Asp Asp Met Asn Val Val Ser Gly |
| 180             | 185                 | 190                             |
| Arg Arg Lys Tyr | Ser Ser Leu Ile     | Gly Tyr Ser Ser Ser Lys Leu Ala |
| 195             | 200                 | 205                             |
| Gln Ile Met Phe | Ser Ser Ile Leu     | Phe Lys Lys Leu Pro Leu Glu Thr |
| 210             | 215                 | 220                             |
| Gly Val Ser Val | Val Cys Leu Ser     | Pro Gly Val Val Leu Thr Asn Val |
| 225             | 230                 | 235                             |
| Ala Arg Asp Leu | Ser Arg Ile Leu     | Gln Ala Leu Tyr Ala Val Ile Pro |
| 245             | 250                 | 255                             |
| Tyr Phe Ile Phe | Ser Pro Gln Glu     | Gly Cys Arg Ser Ser Leu Phe Ser |
| 260             | 265                 | 270                             |
| Ala Thr Asp Pro | Gln Ile Pro Glu     | Tyr Trp Glu Thr Leu Lys Asn Asp |
| 275             | 280                 | 285                             |
| Asp Trp Pro Val | Cys Pro Phe Ile     | Ser Gln Asp Cys Arg Pro Ala Asn |
| 290             | 295                 | 300                             |
| Pro Ser Glu Glu | Ala His Asn Thr     | Glu Thr Ala Gln Arg Val Trp Lys |
| 305             | 310                 | 315                             |
| Lys Thr Leu Glu | Leu Val Gly Leu     | Pro Leu Asp Ala Val Glu Lys Leu |
| 325             | 330                 | 335                             |
| Ile Glu Gly Glu | Asn Ile Gln Cys     | Arg Tyr Gly Ala Gln His Glu     |
| 340             | 345                 | 350                             |

(2) INFORMATION FOR SEQ ID NO:2295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1506
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2295:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| accgagaaat  | gggtagctga | gcgaatacac | aaaccaacgg | caacgcacgg | ccaccgctgt | 60  |
| cgaatcaaaa  | gctccggctt | acgaacggcg | ttgatgggtc | tcattctctt | cctctctctt | 120 |
| taactctcga  | tcaagctatt | atagagtctg | atccgtcgaa | gaagaggaaa | atggggatgc | 180 |
| ttctctcaga  | agtgggttat | cgtgtgatgt | gtcgggtggg | agacggggaa | caccatccgg | 240 |
| tgaagaataat | tgaagcgcgg | cggataYcat | aacggcggtc | aaaatgatta | cgagtattac | 300 |
| gttcattaca  | ctgagtttaa | taggaggtcg | gatgaatgga | ctcagctgga | ccaactggac | 360 |
| cttgattcag  | tagagtgcgc | tgtagatgaa | aaattggaag | acaagtgaa  | acagcttgaa | 420 |
| gatgacacgt  | caccagaaga | ggaagatcga | tgaGgacaca | tatagagggg | catgaagagc | 480 |
| tggtatcagc  | aagtttgcgt | gaacatgaag | agtttcacga | agtgaagaac | atatacaaaa | 540 |
| ttgagcttgg  | aaaatatgat | attgagactt | ggtactcttc | cccttttcgc | ccagaatata | 600 |

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| atgactgtgtg | gaagctcttt  | ttttgtgagt | tttgccgtgaa | cttcatgaaa  | cgcaaaagagc | 660  |
| agcttcaaaag | gcataatgag  | aagtgtgacc | tgaagcaccc  | acctgtgtgat | gaaatttacc  | 720  |
| atctctgteta | cttgcacaatg | tttgaggtag | atggcaaaaa  | gaacaaggtt  | tatgcacaga  | 780  |
| gaagtggtat  | ccctggcaaa  | ttatttcttg | accacaaaaac | tctttactac  | gatgtgtatt  | 840  |
| atctctgteta | cttgcacaatg | tttgaggtag | atggcaaaaa  | gaacaaggtt  | tatgcacaga  | 900  |
| tttcaaaaga  | gaagcattcg  | gaagaagcat | acaacttagc  | ttgcattcta  | acctgccttt  | 960  |
| catatacaaa  | aaaagcgtat  | ggaaggttct | taatagcctt  | ttcctatgaa  | ctgtcaaaaga | 1020 |
| aagagggaaga | agttgggaca  | ccggRaaaga | cccttgcggg  | atctaggctt  | actaagctac  | 1080 |
| agaggttatt  | ggactcgtgt  | tcattatgaa | atcttgaaaa  | aacataaggg  | aaacattttct | 1140 |
| atcaaggagc  | tgagcgacgt  | gacagcaatc | aaagcggaag  | atatattaag  | cacacttcag  | 1200 |
| agcctagaag  | tgatacagta  | caggaaagga | cagcatgtga  | ctgtgctgga  | tccaaaggtt  | 1260 |
| ctggaccgac  | atctgaaagc  | tgacggccga | ggtgtgtctt  | atgtagatgc  | tagcaaatcg  | 1320 |
| atttgacac   | cttacaagga  | ccagagttaa | gagtaagtac  | actcctcttg  | tgccatttga  | 1380 |
| tttgatttga  | gtgtgtaagt  | aaggggctgt | cttattctcc  | tgaaatgtaa  | gtgtacttta  | 1440 |
| cttgtaaatg  | ttgaaatcgt  | acttggaatg | gtgtttgttt  | acaactNctt  | ataatgagga  | 1500 |
| aatttg      |             |            |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..225
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2296:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Thr | His | Ile | Glu | Gly | His | Glu | Glu | Leu | Asp | Ala | Ala | Ser | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Glu | His | Glu | Glu | Phe | Thr | Lys | Val | Lys | Asn | Ile | Ser | Thr | Ile | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Gly | Lys | Tyr | Glu | Ile | Glu | Thr | Trp | Tyr | Phe | Ser | Pro | Phe | Pro | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Tyr | Asn | Asp | Cys | Val | Lys | Leu | Phe | Phe | Cys | Glu | Phe | Cys | Leu | Asn |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Met | Lys | Arg | Lys | Glu | Gln | Leu | Gln | Arg | His | Met | Xaa | Lys | Cys | Asp |
|     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Lys | His | Pro | Pro | Gly | Asp | Glu | Ile | Tyr | Arg | Ser | Gly | Thr | Leu | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Met | Phe | Glu | Val | Asp | Gly | Lys | Lys | Asn | Lys | Val | Tyr | Ala | Gln | Asn | Leu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Tyr | Leu | Ala | Lys | Leu | Phe | Leu | Asp | His | Lys | Thr | Leu | Tyr | Tyr | Asp |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Val | Asp | Leu | Phe | Leu | Phe | Tyr | Val | Leu | Cys | Glu | Cys | Asp | Asp | Arg | Gly |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Cys | His | Met | Val | Gly | Tyr | Phe | Ser | Lys | Glu | Lys | His | Ser | Glu | Glu | Ala |
|     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Tyr | Asn | Leu | Ala | Cys | Ile | Leu | Thr | Leu | Pro | Ser | Tyr | Gln | Arg | Lys | Gly |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Tyr | Gly | Lys | Phe | Leu | Ile | Ala | Phe | Ser | Tyr | Glu | Leu | Ser | Lys | Lys | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Lys | Val | Gly | Thr | Pro | Xaa | Lys | Thr | Leu | Val | Gly | Ser | Arg | Leu | Thr |
|     |     | 195 |     |     |     |     |     | 200 |     |     |     | 205 |     |     |     |
| Lys | Leu | Gln | Arg | Leu | Leu | Asp | Ser | Cys | Ser | Ile | Arg | Asn | Leu | Glu | Lys |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

Thr  
225

(2) INFORMATION FOR SEQ ID NO:2297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2297:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Lys | Arg | Lys | Glu | Gln | Leu | Gln | Arg | His | Met | Xaa | Lys | Cys | Asp | Leu |  |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |  |
| Lys | His | Pro | Pro | Gly | Asp | Glu | Ile | Tyr | Arg | Ser | Gly | Thr | Leu | Ser | Met |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Phe | Glu | Val | Asp | Gly | Lys | Lys | Asn | Lys | Val | Tyr | Ala | Gln | Asn | Leu | Cys |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Tyr | Leu | Ala | Lys | Leu | Phe | Leu | Asp | His | Lys | Thr | Leu | Tyr | Tyr | Asp | Val |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |  |
| Asp | Leu | Phe | Leu | Phe | Tyr | Val | Leu | Cys | Glu | Cys | Asp | Asp | Arg | Gly | Cys |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| His | Met | Val | Gly | Tyr | Phe | Ser | Lys | Glu | Lys | His | Ser | Glu | Glu | Ala | Tyr |  |
|     |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |  |
| Asn | Leu | Ala | Cys | Ile | Leu | Thr | Leu | Pro | Ser | Tyr | Gln | Arg | Lys | Gly | Tyr |  |
|     |     |     | 100 |     |     |     |     |     |     | 105 |     |     |     | 110 |     |  |
| Gly | Lys | Phe | Leu | Ile | Ala | Phe | Ser | Tyr | Glu | Leu | Ser | Lys | Lys | Glu | Gly |  |
|     |     |     | 115 |     |     |     |     |     |     | 120 |     |     |     | 125 |     |  |
| Lys | Val | Gly | Thr | Pro | Xaa | Lys | Thr | Leu | Val | Gly | Ser | Arg | Leu | Thr | Lys |  |
|     |     |     | 130 |     |     |     |     |     |     | 135 |     |     |     | 140 |     |  |
| Leu | Gln | Arg | Leu | Leu | Asp | Ser | Cys | Ser | Ile | Arg | Asn | Leu | Glu | Lys | Thr |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |

(2) INFORMATION FOR SEQ ID NO:2298:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 150 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2298:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Xaa | Lys | Cys | Asp | Leu | Lys | His | Pro | Pro | Gly | Asp | Glu | Ile | Tyr | Arg |  |
| 1   |     |     | 5   |     |     |     |     |     |     | 10  |     |     |     | 15  |     |  |
| Ser | Gly | Thr | Leu | Ser | Met | Phe | Glu | Val | Asp | Gly | Lys | Lys | Asn | Lys | Val |  |
|     |     |     | 20  |     |     |     |     |     |     | 25  |     |     |     | 30  |     |  |
| Tyr | Ala | Gln | Asn | Leu | Cys | Tyr | Leu | Ala | Lys | Leu | Phe | Leu | Asp | His | Lys |  |
|     |     |     | 35  |     |     |     |     |     |     | 40  |     |     |     | 45  |     |  |
| Thr | Leu | Tyr | Tyr | Asp | Val | Asp | Leu | Phe | Leu | Phe | Tyr | Val | Leu | Cys | Glu |  |
|     |     |     | 50  |     |     |     |     |     |     | 55  |     |     |     | 60  |     |  |
| Cys | Asp | Asp | Arg | Gly | Cys | His | Met | Val | Gly | Tyr | Phe | Ser | Lys | Glu | Lys |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| His | Ser | Glu | Glu | Ala | Tyr | Asn | Leu | Ala | Cys | Ile | Leu | Thr | Leu | Pro | Ser |  |
|     |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |  |
| Tyr | Gln | Arg | Lys | Gly | Tyr | Gly | Lys | Phe | Leu | Ile | Ala | Phe | Ser | Tyr | Glu |  |
|     |     |     | 100 |     |     |     |     |     |     | 105 |     |     |     | 110 |     |  |
| Leu | Ser | Lys | Lys | Glu | Gly | Lys | Val | Gly | Thr | Pro | Xaa | Lys | Thr | Leu | Val |  |
|     |     |     | 115 |     |     |     |     |     |     | 120 |     |     |     | 125 |     |  |
| Gly | Ser | Arg | Leu | Thr | Lys | Leu | Gln | Arg | Leu | Leu | Asp | Ser | Cys | Ser | Ile |  |
| 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |  |



Arg Asn Leu Glu Lys Thr  
145 150

(2) INFORMATION FOR SEQ ID NO:2299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 889 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..889

(D) OTHER INFORMATION: / Ceres Seq. ID 1572462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2299:

|                                           |     |
|-------------------------------------------|-----|
| aaaacgaact agagacagtt tgattcgaaa atcttgcg | 60  |
| ccagaatta agcaattact gggaaacctag ctcttgc  | 120 |
| cgacagctcg cctttggaag aagccatttc tgggtcg  | 180 |
| agctgcttcg tcgcccgtct ctaagaatat tgttcg   | 240 |
| taaccagaga ctcttgcctc ttcgatcagt tgttccca | 300 |
| ctcaataatc aaagatgcta ttgattacat agaaggat | 360 |
| cgaagctgag atcagagaa                      | 420 |
| atcttgcagc tgatttact gttcctgtca catccaag  | 480 |
| gttcttcac                                 | 540 |
| caatgttggt gagtgttaaca tgtaataaga gga     | 600 |
| ctcttgcagc attgaatctc aaaatcctca ctcca    | 660 |
| ttctccacac tgtctttatt gaggcggatg aaga     | 720 |
| tagaaacagg aatagagagt tataatgaaa ctcaa    | 780 |
| tttctaata atactttttt tcttctttt ttggttc    | 840 |
| aatgatgtgc tctcttttca ttttatgat ctctac    |     |

(2) INFORMATION FOR SEQ ID NO:2300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..141

(D) OTHER INFORMATION: / Ceres Seq. ID 1572463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2300:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Lys Arg Thr Arg Asp Ser Leu Ile Arg Lys Ser Cys Arg Lys Met Glu |  |
| 1 5 10 15                                                       |  |
| Asp Ile Val Asp Gln Glu Leu Ser Asn Tyr Trp Glu Pro Ser Ser Leu |  |
| 20 25 30                                                        |  |
| Leu Gln Asn Glu Tyr Phe Glu Tyr Asp Ser Trp Pro Leu Glu Glu Ala |  |
| 35 40 45                                                        |  |
| Ile Ser Gly Ser Tyr Asp Ser Ser Pro Asp Gly Ala Ala Ser Ser     |  |
| 50 55 60                                                        |  |
| Pro Ala Ser Lys Asn Ile Val Ser Glu Arg Asn Arg Arg Gln Lys Leu |  |
| 65 70 75 80                                                     |  |
| Asn Gln Arg Leu Phe Ala Leu Arg Ser Val Val Pro Asn Ile Thr Lys |  |
| 85 90 95                                                        |  |
| Met Asp Lys Ala Ser Ile Ile Lys Asp Ala Ile Ser Tyr Ile Glu Gly |  |
| 100 105 110                                                     |  |
| Leu Gln Tyr Glu Glu Lys Lys Leu Glu Ala Glu Ile Arg Glu Leu Glu |  |
| 115 120 125                                                     |  |
| Ser Thr Pro Lys Ser Ser Leu Ser Phe Ser Lys Gly Phe             |  |
| 130 135 140                                                     |  |

(2) INFORMATION FOR SEQ ID NO:2301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..127
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1572464
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2301:

```

Met Glu Asp Ile Val Asp Gln Glu Leu Ser Asn Tyr Trp Glu Pro Ser
1 5 10 15
Ser Leu Leu Gln Asn Glu Tyr Phe Glu Tyr Asp Ser Trp Pro Leu Glu
 20 25 30
Glu Ala Ile Ser Gly Ser Tyr Asp Ser Ser Ser Pro Asp Gly Ala Ala
 35 40 45
Ser Ser Pro Ala Ser Lys Asn Ile Val Ser Glu Arg Asn Arg Arg Gln
 50 55 60
Lys Leu Asn Gln Arg Leu Phe Ala Leu Arg Ser Val Val Pro Asn Ile
65 70 75 80
Thr Lys Met Asp Lys Ala Ser Ile Ile Lys Asp Ala Ile Ser Tyr Ile
 85 90 95
Glu Gly Leu Gln Tyr Glu Glu Lys Lys Leu Glu Ala Glu Ile Arg Glu
 100 105 110
Leu Glu Ser Thr Pro Lys Ser Ser Leu Ser Phe Ser Lys Gly Phe
 115 120 125

```

- (2) INFORMATION FOR SEQ ID NO:2302:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 147 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..147
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1572465
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2302:

```

Met Lys Lys Arg Ser Ser Lys Leu Arg Ser Glu Asn Leu Asn Leu His
1 5 10 15
Gln Arg Val Ala Leu Val Ser Ala Lys Asp Phe Asp Arg Asp Leu Leu
 20 25 30
Val Pro Val Thr Ser Lys Lys Met Lys Gln Leu Asp Ser Gly Ser Ser
 35 40 45
Thr Ser Leu Ile Glu Val Leu Glu Leu Lys Val Thr Phe Met Gly Glu
 50 55 60
Arg Thr Met Val Val Ser Val Thr Cys Asn Lys Arg Thr Asp Thr Met
65 70 75 80
Val Lys Leu Cys Glu Val Phe Glu Ser Leu Asn Leu Lys Ile Leu Thr
 85 90 95
Ser Asn Leu Thr Ser Phe Ser Gly Met Ile Phe His Thr Val Phe Ile
 100 105 110
Glu Ala Asp Glu Glu Glu Gln Glu Val Leu Arg Leu Lys Ile Glu Thr
 115 120 125
Gly Ile Gly Ala Tyr Asn Glu Thr Gln Ser Pro Thr Leu Ser Ile Asp
 130 135 140
Ser Leu Tyr
145

```

- (2) INFORMATION FOR SEQ ID NO:2303:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1010 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1010  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2303:

|            |            |             |             |             |            |     |
|------------|------------|-------------|-------------|-------------|------------|-----|
| atccattaga | ggaggagcgc | atgtttctgc  | ttccatggta  | acgcctctcgt | ctccatctcc | 60  |
| ctcgctctct | tgcgtagaga | acgtgacatg  | taaattctct  | cacgtttctc  | gggttctaat | 120 |
| ctccggtacc | gataatatta | atcacgggtga | atcgctggaa  | gccaaaaaac  | tgagagatgt | 180 |
| tcattctctc | gaaagggtat | tggaggattt  | cactgagcgt  | gcaagagaga  | acactgagaa | 240 |
| ggacctcgag | actctgtgga | ctctcgctgc  | ctttcttgaa  | agaggaattt  | tttatgtaac | 300 |
| cactctgata | atacctaagc | aagaatcaac  | ttctaattct  | tgctcaggta  | tgaatgaagt | 360 |
| ggaagtgttt | tcattcaaaa | acgaagagaga | actctatccc  | gtagGatgga  | ttcatactca | 420 |
| tcctctctcg | ggttggttca | tgctatctgt  | agatctgcat  | acacattatt  | cttatcaggt | 480 |
| aatggtgcca | gaggcttttg | caatcgctgt  | agctccaact  | gatagctcta  | attacgggat | 540 |
| atttaagcta | acggaccctg | gaggaaatgga | ggtagctgaga | ggctgctcag  | agactggatt | 600 |
| ccaccgcgac | aaagaaccag | aagatgggaa  | cccagtttat  | gagcattgct  | caaacgtcta | 660 |
| caagaactcg | aaccttaggt | tcgagatttt  | tgatctacgt  | taaggtaacg  | actctgtggt | 720 |
| acttatcagt | aaaaagggtc | aaactttatc  | cactgtgggc  | taaggatgtc  | aataataaac | 780 |
| gtcatcataa | ccaccaccct | ccttctatta  | agcttagcaa  | tgtttaataa  | ttgtcatgtc | 840 |
| cgggttatga | acacaaggta | ccttctatta  | agcttagcaa  | tgtttaataa  | ttgtcatgtc | 900 |
| cttagatttg | gatcaattgg | ttccattatg  | gaagaacaac  | aatgaccata  | gacataagac | 960 |
| attgtattgg | cgtatgcaat | tggttatatc  | ctgtacacaa  | gtatacattg  |            |     |

(2) INFORMATION FOR SEQ ID NO:2304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..233  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2304:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ile | Arg | Gly | Gly | Ala | Asp | Val | Ser | Ala | Ser | Met | Val | Thr | Leu | Ser |
| 1   |     |     |     | 5   |     |     |     |     |     |     |     | 10  |     |     | 15  |
| Ser | Pro | Ser | Pro | Ser | Leu | Ser | Cys | Val | Glu | Asn | Val | Thr | Cys | Lys | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | His | Val | Ser | Arg | Val | Leu | Ile | Ser | Gly | Thr | Asp | Asn | Ile | Asn | His |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Glu | Ser | Ser | Glu | Ala | Lys | Ile | Leu | Arg | Asp | Val | His | Ile | Ser | Glu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Arg | Leu | Leu | Glu | Asp | Phe | Thr | Glu | Leu | Ala | Arg | Glu | Asn | Thr | Glu | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Leu | Glu | Thr | Cys | Gly | Thr | Leu | Ala | Ala | Phe | Leu | Glu | Arg | Gly | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Tyr | Val | Thr | Thr | Leu | Ile | Ile | Pro | Lys | Gln | Glu | Ser | Thr | Ser | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Cys | Gln | Ala | Met | Asn | Glu | Val | Glu | Val | Phe | Ser | Ile | Gln | Asn | Glu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Glu | Leu | Tyr | Pro | Val | Gly | Trp | Ile | His | Thr | His | Pro | Ser | Gln | Gly |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Cys | Phe | Met | Ser | Ser | Val | Asp | Leu | His | Thr | His | Tyr | Ser | Tyr | Gln | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Met | Val | Pro | Glu | Ala | Phe | Ala | Ile | Val | Val | Ala | Pro | Thr | Asp | Ser | Ser |
|     |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |     |
| Asn | Tyr | Gly | Ile | Phe | Lys | Leu | Thr | Asp | Pro | Gly | Gly | Met | Glu | Val | Leu |

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Met Asn Glu Val Glu Val Phe Ser Ile Gln Asn Glu Arg Glu Leu Tyr  
1 5 10 15

Pro Val Gly Trp Ile His Thr His Pro Ser Gln Gly Cys Phe Met Ser  
20 25 30  
Ser Val Asp Leu His Thr His Tyr Ser Tyr Gln Val Met Val Pro Glu  
35 40 45  
Ala Phe Ala Ile Val Val Ala Pro Thr Asp Ser Ser Asn Tyr Gly Ile  
50 55 60  
Phe Lys Leu Thr Asp Pro Gly Gly Met Glu Val Leu Arg Gly Cys Ser  
65 70 75 80  
Glu Thr Gly Phe His Pro His Lys Glu Pro Glu Asp Gly Asn Pro Val  
85 90 95  
Tyr Glu His Cys Ser Asn Val Tyr Lys Asn Ser Asn Leu Arg Phe Glu  
100 105 110  
Ile Phe Asp Leu Arg  
115

(2) INFORMATION FOR SEQ ID NO:2307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 868 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..868
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2307:

|             |             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| aatacacttg  | taattctaa   | cttctctct   | ttccaaaaat  | ggcgctcatca | tcggcctttag | 60  |
| ctctcaaggag | actctctct   | tcttccaccg  | tcgcccgtccc | tcgcccctta  | agagccggttc | 120 |
| gtccgggtgtc | tgcttcttct  | cgctcttcca  | ataccaacgc  | cgccagaaaac | atgaagacgc  | 180 |
| gtgtcgatag  | gaaccatcac  | tcaaacccgac | atgtttctcg  | ccacggcgccg | gatttcttct  | 240 |
| cagatataact | cgatccgttt  | actccaacga  | gaagcttgag  | ccagatgctg  | aatttcatgg  | 300 |
| accaggttaag | cgaaatccct  | ttggtatcac  | ctactctggg  | aatgggagct  | tctggagtta  | 360 |
| gacgtggttg  | gaacgtgaaa  | gagaaagacg  | acgcgttgca  | tctaaggata  | gatagccgg   | 420 |
| gactaagcag  | agaggatgtg  | aaattgacct  | tggaacagaa  | cacatttggtg | attagaggag  | 480 |
| aaggggaaac  | agaggagggga | gaagatgttt  | ctggagatgg  | acggagggttt | accagtagga  | 540 |
| ttgagttacc  | ggagaaaagta | tacaagactg  | atgagatTAA  | ggcggaaAtg  | aagaatgggt  | 600 |
| tgtTgaaAgt  | ggtgatTCca  | aagattaaAg  | agGatgagcg  | taAcaAtatT  | cgtcacataa  | 660 |
| acgttgacta  | gagtggttta  | ttttggattg  | tttgagatgg  | aatggaagta  | agtgaagtga  | 720 |
| ttttgaaact  | ttaaggtgtc  | ctttggtgaa  | tcaaggagaa  | tgacatttcc  | cacggtccta  | 780 |
| tgtgttcggg  | attttgactt  | ttttcgttac  | atcaatgata  | tatgtacggt  | tgactacttt  | 840 |
| catatcatag  | gttcggattt  | gtttctcc    |             |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..222
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2308:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Val | Asn | Ser | Lys | Leu | Leu | Leu | Phe | Pro | Lys | Met | Ala | Ser | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Ala | Leu | Ala | Leu | Arg | Arg | Leu | Leu | Ser | Ser | Ser | Thr | Val | Ala | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Arg | Ala | Leu | Arg | Ala | Val | Arg | Pro | Val | Ser | Ala | Ser | Ser | Arg | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Asn | Thr | Asn | Ala | Ala | Arg | Asn | Tyr | Glu | Asp | Gly | Val | Asp | Arg | Asn |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |

His His Ser Asn Arg His Val Ser Arg His Gly Gly Asp Phe Phe Ser  
65 70 75 80  
Asp Ile Leu Asp Pro Phe Thr Pro Thr Arg Ser Leu Ser Gln Met Leu  
85 90 95  
Asn Phe Met Asp Gln Val Ser Glu Ile Pro Leu Val Ser Ala Thr Arg  
100 105 110  
Gly Met Gly Ala Ser Gly Val Arg Arg Gly Trp Asn Val Lys Glu Lys  
115 120 125  
Asp Asp Ala Leu His Leu Arg Ile Asp Met Pro Gly Leu Ser Arg Glu  
130 135 140  
Asp Val Lys Leu Ala Leu Glu Gln Asn Thr Leu Val Ile Arg Gly Glu  
145 150 155 160  
Gly Glu Thr Glu Glu Gly Glu Asp Val Ser Gly Asp Gly Arg Arg Phe  
165 170 175  
Thr Ser Arg Ile Glu Leu Pro Glu Lys Val Tyr Lys Thr Asp Glu Ile  
180 185 190  
Lys Ala Glu Met Lys Asn Gly Val Leu Lys Val Val Ile Pro Lys Ile  
195 200 205  
Lys Glu Asp Glu Arg Asn Asn Ile Arg His Ile Asn Val Asp  
210 215 220

(2) INFORMATION FOR SEQ ID NO:2309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..210
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2309:

Met Ala Ser Ser Ser Ala Leu Ala Leu Arg Arg Leu Leu Ser Ser Ser  
1 5 10 15  
Thr Val Ala Val Pro Arg Ala Leu Arg Ala Val Arg Pro Val Ser Ala  
20 25 30  
Ser Ser Arg Leu Phe Asn Thr Asn Ala Ala Arg Asn Tyr Glu Asp Gly  
35 40 45  
Val Asp Arg Asn His His Ser Asn Arg His Val Ser Arg His Gly Gly  
50 55 60  
Asp Phe Phe Ser Asp Ile Leu Asp Pro Phe Thr Pro Thr Arg Ser Leu  
65 70 75 80  
Ser Gln Met Leu Asn Phe Met Asp Gln Val Ser Glu Ile Pro Leu Val  
85 90 95  
Ser Ala Thr Arg Gly Met Gly Ala Ser Gly Val Arg Arg Gly Trp Asn  
100 105 110  
Val Lys Glu Lys Asp Asp Ala Leu His Leu Arg Ile Asp Met Pro Gly  
115 120 125  
Leu Ser Arg Glu Asp Val Lys Leu Ala Leu Glu Gln Asn Thr Leu Val  
130 135 140  
Ile Arg Gly Glu Gly Glu Thr Glu Glu Gly Glu Asp Val Ser Gly Asp  
145 150 155 160  
Gly Arg Arg Phe Thr Ser Arg Ile Glu Leu Pro Glu Lys Val Tyr Lys  
165 170 175  
Thr Asp Glu Ile Lys Ala Glu Met Lys Asn Gly Val Leu Lys Val Val  
180 185 190  
Ile Pro Lys Ile Lys Glu Asp Glu Arg Asn Asn Ile Arg His Ile Asn  
195 200 205  
Val Asp  
210

(2) INFORMATION FOR SEQ ID NO:2310:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 128 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..128  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572498  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2310:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Asn | Phe | Met | Asp | Gln | Val | Ser | Glu | Ile | Pro | Leu | Val | Ser | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Arg | Gly | Met | Gly | Ala | Ser | Gly | Val | Arg | Arg | Gly | Trp | Asn | Val | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Lys | Asp | Asp | Ala | Leu | His | Leu | Arg | Ile | Asp | Met | Pro | Gly | Leu | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Glu | Asp | Val | Lys | Leu | Ala | Leu | Glu | Gln | Asn | Thr | Leu | Val | Ile | Arg |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly | Glu | Gly | Glu | Thr | Glu | Glu | Gly | Glu | Asp | Val | Ser | Gly | Asp | Gly | Arg |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |     |
| Arg | Phe | Thr | Ser | Arg | Ile | Glu | Leu | Pro | Glu | Lys | Val | Tyr | Lys | Thr | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Ile | Lys | Ala | Glu | Met | Lys | Asn | Gly | Val | Leu | Lys | Val | Val | Ile | Pro |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Lys | Ile | Lys | Glu | Asp | Glu | Arg | Asn | Asn | Ile | Arg | His | Ile | Asn | Val | Asp |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:2311:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 911 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..911  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572503  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2311:

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| agtgaacccg  | aggagacag  | cgagatgag  | ccggagatag | ttctgttcgg  | ogaactcgatc | 60  |
| acggcgccagt | cttttaggtc | cgcggtttgg | ggatctgctc | ttgccgacgc  | ttactctcgc  | 120 |
| aaggctgatg  | ttgtgtgttc | aggctacggc | ggctacaaca | cccgatgggc  | ttctctcttg  | 180 |
| cttcatcaca  | ttctccctct | gggtctcttg | ttctctcttg | ttgtacgac   | gatattcttc  | 240 |
| ggtgcacacg  | atgcagctct | caaaggaaga | accagtgata | gacaacatgt  | gccggtggaa  | 300 |
| gagtaacacg  | ataatgtcag | aaagattgtt | cagcatttga | agaaaatgtc  | acctacaagt  | 360 |
| ctaattgtgc  | ttataactcc | accaccaatt | gatgaagctg | gacgGtcaaa  | gttatgcaga  | 420 |
| atcaaatctac | ggtgagaag  | ctatgaaaga | gcctgagaga | acaaacgaaa  | caacaggggt  | 480 |
| atatgcacaa  | cattgtgttg | cattggccga | ggaaactcgt | ctgcgatgtg  | tcaacttatg  | 540 |
| gtctcaagat  | caggaaacca | attattggca | gaaaaagtac | ctaagtgtatg | ggctccatct  | 600 |
| caagcctgaa  | ggcaatgggg | tagtttttga | tgaagtctcg | agagttttta  | gagaagcttg  | 660 |
| gctctctccc  | gaagaaatgc | cgtttgattt | cccccatcat | tcccatatcg  | atggtaaaaa  | 720 |
| cccatgaaaa  | gotttttgag | agcgttgctt | ataacgatca | taaatgtgtg  | gatttgaaga  | 780 |
| ttgtttttga  | tttaaaattg | tgaacacgtt | tcaatgtgtg | gatttgaaga  | actctcgcat  | 840 |
| gtgaataaat  | acctaaaaag | tgcacatcca | ctagagatcg | ttttcaagag  | aaatgaactt  | 900 |
| atgatgtact  | t          |            |            |             |             |     |

- (2) INFORMATION FOR SEQ ID NO:2312:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 144 amino acids  
(B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..144  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572504  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2312:

```
Ser Glu Pro Glu Gly Asp Ser Glu Met Arg Pro Glu Ile Val Leu Phe
1 5 10 15
Gly Asp Ser Ile Thr Ala Gln Ser Phe Arg Ser Gly Gly Trp Gly Ser
20 25 30
Ala Leu Ala Asp Ala Tyr Ser Arg Lys Ala Asp Val Val Val Arg Gly
35 40 45
Tyr Gly Gly Tyr Asn Thr Arg Trp Ala Leu Phe Leu Leu His His Ile
50 55 60
Phe Pro Leu Gly Ser Ser Pro Pro Val Ala Thr Thr Ile Phe Phe
65 70 75 80
Gly Ala Asn Asp Ala Ala Leu Lys Gly Arg Thr Ser Asp Arg Gln His
85 90 95
Val Pro Val Glu Tyr Thr Asp Asn Val Arg Lys Ile Val Gln His
100 105 110
Leu Lys Lys Cys Ser Pro Thr Met Leu Ile Val Leu Ile Thr Pro Pro
115 120 125
Pro Ile Asp Glu Ala Gly Arg Ser Lys Leu Cys Arg Ile Asn Leu Arg
130 135 140
```

- (2) INFORMATION FOR SEQ ID NO:2313:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 136 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..136  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572505  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2313:

```
Met Arg Pro Glu Ile Val Leu Phe Gly Asp Ser Ile Thr Ala Gln Ser
1 5 10 15
Phe Arg Ser Gly Gly Trp Gly Ser Ala Leu Ala Asp Ala Tyr Ser Arg
20 25 30
Lys Ala Asp Val Val Val Arg Gly Tyr Gly Gly Tyr Asn Thr Arg Trp
35 40 45
Ala Leu Phe Leu Leu His His Ile Phe Pro Leu Gly Ser Ser Ser Pro
50 55 60
Pro Val Ala Thr Thr Ile Phe Phe Gly Ala Asn Asp Ala Ala Leu Lys
65 70 75 80
Gly Arg Thr Ser Asp Arg Gln His Val Pro Val Glu Glu Tyr Thr Asp
85 90 95
Asn Val Arg Lys Ile Val Gln His Leu Lys Lys Cys Ser Pro Thr Met
100 105 110
Leu Ile Val Leu Ile Thr Pro Pro Pro Ile Asp Glu Ala Gly Arg Ser
115 120 125
Lys Leu Cys Arg Ile Asn Leu Arg
130 135
```

- (2) INFORMATION FOR SEQ ID NO:2314:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 120 amino acids



(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..120  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572506  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2314:  
Met Lys Leu Asp Gly Gln Ser Tyr Ala Glu Ser Ile Tyr Gly Glu Lys  
1 5 10 15  
Ala Met Lys Glu Pro Glu Arg Thr Asn Glu Thr Thr Gly Val Tyr Ala  
20 25 30  
Gln His Cys Val Ala Leu Ala Glu Leu Gly Leu Arg Cys Val Asn  
35 40 45  
Leu Trp Ser Lys Met Gln Glu Thr Asn Tyr Trp Gln Lys Lys Tyr Leu  
50 55 60  
Ser Asp Gly Leu His Leu Thr Pro Glu Gly Asn Gly Val Val Phe Asp  
65 70 75 80  
Glu Val Ser Arg Val Phe Arg Glu Ala Trp Leu Ser Pro Glu Glu Met  
85 90 95  
Pro Phe Asp Phe Pro His His Ser His Ile Asp Gly Lys Asn Pro Trp  
100 105 110  
Lys Ala Phe Glu Glu Arg Cys Leu  
115 120

(2) INFORMATION FOR SEQ ID NO:2315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..538  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2315:

atcaaaacRa tcacatacac tatttttctc ctctccttat tgtctatata ttttctctct 60  
ttagcttttt catttcgaaa tggccaccgt tgagggttgaa caagtcactc cagtagcagt 120  
agagaacggt gaggtaccaa caaagacagt ggaggagaca gtggtggaga cagagaagaa 180  
agatgaagaa accgagaaga aaacagagga gaaagacgag aagacagaag tgatcacgga 240  
aactccggtg gttgaggagg aggagaagaa agctgaggaa gtgaccgaaa ctccggcggt 300  
tgtggaggag gagaagaaga cagaggtggt tgaggagaaa cagactgagg ttgcggctgc 360  
tgaggaagtc gcggttgaga aggccgagga gtaaaagagga aggaagaagc tatatatgac 420  
cttttttggt ctcatactgt tttctgttta ttttatttta tcaacatttc ataagtattt 480  
tctatgtttg ttgggtttgt tatgatgaaa tcagatggtt ggatctttta atggttgc

(2) INFORMATION FOR SEQ ID NO:2316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..104  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2316:

Met Ala Thr Val Glu Val Glu Gln Val Thr Pro Val Ala Val Glu Asn  
1 5 10 15  
Val Glu Val Pro Thr Lys Thr Val Glu Glu Thr Val Val Glu Thr Glu

20 25 30  
Lys Lys Asp Glu Glu Thr Glu Lys Lys Thr Glu Glu Lys Asp Glu Lys  
35 40 45  
Thr Glu Val Ile Thr Glu Thr Pro Val Val Glu Glu Glu Lys Lys  
50 55 60  
Ala Glu Glu Val Thr Glu Thr Pro Ala Val Val Glu Glu Glu Lys Lys  
65 70 75 80  
Thr Glu Val Val Glu Glu Lys Gln Thr Glu Val Ala Ala Ala Glu Glu  
85 90 95  
Val Ala Val Glu Lys Ala Glu Glu  
100

(2) INFORMATION FOR SEQ ID NO:2317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1465
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2317:

```
gcagtgaggaga gagagcatgt gaataaaaag cgtgaagcctt ttgatattct cttctctctc 60
ctctctctctt ctctctccgat agattttcgcc ggcgatggcg gtggactcct tagaaacgga 120
gattgacaacg gcggtgcggt ttgtccacct cgcttctctt ctctgtgtta aagttcaaga 180
gaagcttctat ctctctaacg gtggtcacgt taagtctaaa gacgatgatt cccctgtcac 240
cgctcgctgat tttggtgtac aagcaattgt gagctggggt tttagctgaag tgtttgggtga 300
tcaaaacctct tcaattgttg ctgaagaaga cactgagaca ctctctgagg ctgattcttt 360
agggtctttta ggagctgtgt cgaatgcggt taatgaagca ttgtccgaag ctccagaacta 420
cgggctctccg aagccagtta agccattggg gtctagttaa attcttaagg ctattagtag 480
atgtaaactct gttggaggac ctaaaaggaa gcattggggt ctgatccgt ttgatggaaac 540
gttaggggttt gttcgtgggg atcagtatgc tgttgcctta gctttgatag agaattgtaa 600
agttcttttg ggtgtactag gatgtcctaa ttatccggtt aagaaagaat gtttaagtaa 660
tggttgaac caagctatga agacgaaagc ttgttctggt tcagtatcga aaggatgtgt 720
tatgtatgca aagagaggta gtggtcaagc ttggatgcaa cctttgatag ttggaggaaat 780
accagaatct gcaacacttc ttaaggtttc ttacgttgat gatccgggtt tagctacagt 840
ttgtgagcca gttagagagag caaactcaaa ccacttgctc actgcaggac ttgccaatag 900
catgggagtt agaaaagcagc ctatgcgagt gtatagcatg gtgaaatatg cagcgatTgc 960
acgtggagac gctgaagtgt ttatgaagtt tgcacagtca agttacaaa agaatgatag 1020
ggaatcacgca gctggagttg ttatttgga agaagctggt ggtgtggtga ctgatgcggg 1080
agggagaaac tttagactct cgaagagtggt ttacttgaa ggtcttgacc gtggaatcat 1140
cgcatcttgtt ggtcagattt tacatgagaa gattataggt ttggtgcagc atcatcgagc 1200
atctctgagt cctctgaaaaa gcttatccac aatccgtagt ttggtgcagc atcatcgagc 1260
caaaagcaag gaggaacaa ggcattacg gtttaggatg agcaagggcc agtttaaatg 1320
aatgtgaatg gcggagaagt aaataatgc gaggaagcag cggtaaaagt aagaatctag 1380
tttatttacc tatctaaag taataaagct gctgcatttc acgaaccttc atgttctatg 1440
atctttaatg gatgatatca tttt
```

(2) INFORMATION FOR SEQ ID NO:2318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..373
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2318:

Met Ala Val Asp Ser Leu Glu Thr Glu Ile Asp Thr Ala Val Arg Val

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Val His Leu Ala Ser Ser Leu Cys Val Lys Val Gln Glu Lys Leu His |     |     |     |
|                                                                 | 20  | 25  | 30  |
| Leu Pro Asn Gly Gly His Val Lys Ser Lys Asp Asp Asp Ser Pro Val |     |     |     |
|                                                                 | 35  | 40  | 45  |
| Thr Val Ala Asp Phe Gly Val Gln Ala Ile Val Ser Trp Val Leu Ala |     |     |     |
|                                                                 | 50  | 55  | 60  |
| Glu Val Phe Gly Asp Gln Asn Leu Ser Ile Val Ala Glu Glu Asp Thr |     |     |     |
| 65                                                              | 70  | 75  | 80  |
| Glu Thr Leu Ser Glu Ala Asp Ser Leu Gly Leu Gly Ala Val Ser     |     |     |     |
|                                                                 | 85  | 90  | 95  |
| Asn Ala Val Asn Glu Ala Leu Ser Glu Ala Gln Asn Tyr Gly Leu Pro |     |     |     |
|                                                                 | 100 | 105 | 110 |
| Lys Pro Val Lys Pro Leu Gly Ser Ser Glu Ile Leu Lys Ala Ile Ser |     |     |     |
|                                                                 | 115 | 120 | 125 |
| Arg Cys Asn Ser Val Gly Gly Pro Lys Gly Arg His Trp Val Leu Asp |     |     |     |
|                                                                 | 130 | 135 | 140 |
| Pro Val Asp Gly Thr Leu Gly Phe Val Arg Gly Asp Gln Tyr Ala Val |     |     |     |
| 145                                                             | 150 | 155 | 160 |
| Ala Leu Ala Leu Ile Glu Asn Gly Lys Val Leu Leu Gly Val Leu Gly |     |     |     |
|                                                                 | 165 | 170 | 175 |
| Cys Pro Asn Tyr Pro Val Lys Lys Glu Cys Leu Ser Asn Gly Cys Asn |     |     |     |
|                                                                 | 180 | 185 | 190 |
| Gln Ala Met Lys Thr Lys Ala Val Ala Gly Ser Val Ser Lys Gly Cys |     |     |     |
|                                                                 | 195 | 200 | 205 |
| Val Met Tyr Ala Lys Arg Gly Ser Gly Gln Ala Trp Met Gln Pro Leu |     |     |     |
|                                                                 | 210 | 215 | 220 |
| Ile Val Gly Gly Ile Pro Glu Ser Ala Thr Leu Leu Lys Val Ser Ser |     |     |     |
| 225                                                             | 230 | 235 | 240 |
| Val Asp Asp Pro Val Leu Ala Thr Val Cys Glu Pro Val Glu Arg Ala |     |     |     |
|                                                                 | 245 | 250 | 255 |
| Asn Ser Asn His Leu Phe Thr Ala Gly Leu Ala Asn Ser Met Gly Val |     |     |     |
|                                                                 | 260 | 265 | 270 |
| Arg Lys Gln Pro Met Arg Val Tyr Ser Met Val Lys Tyr Ala Ala Ile |     |     |     |
|                                                                 | 275 | 280 | 285 |
| Ala Arg Gly Asp Ala Glu Val Phe Met Lys Phe Ala Gln Ser Ser Tyr |     |     |     |
|                                                                 | 290 | 295 | 300 |
| Lys Glu Lys Ile Trp Asp His Ala Ala Gly Val Val Ile Val Glu Glu |     |     |     |
| 305                                                             | 310 | 315 | 320 |
| Ala Gly Gly Val Val Thr Asp Ala Gly Gly Arg Asn Leu Asp Phe Ser |     |     |     |
|                                                                 | 325 | 330 | 335 |
| Lys Gly Val Tyr Leu Glu Gly Leu Asp Arg Gly Ile Ile Ala Cys Ser |     |     |     |
|                                                                 | 340 | 345 | 350 |
| Gly Gln Val Leu His Glu Lys Ile Gly Ala Val Tyr Ala Ser Trp     |     |     |     |
|                                                                 | 355 | 360 | 365 |
| Glu Ser Ser Ser Leu                                             |     |     |     |
| 370                                                             |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1270
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2319:

atctacaact ttcattcttc cactacattt ctctccttga gtatcttctt atctattttt  
ccaaattcca aaacaattca caaaatggct acatgctggc ctgagccgat tgttttcgctg

60  
120

|            |             |            |            |             |            |      |
|------------|-------------|------------|------------|-------------|------------|------|
| caatccttgt | cccaaacccg  | tgtaccaact | gtaccaaacc | gctatgtgaa  | gccggctcat | 180  |
| cagagaccgg | tctttaaacc  | caccacaatc | gatgctggga | tagaaatccc  | tggtctagac | 240  |
| atgaacgacg | tgtgggggaa  | accagagggg | ctaaggctcg | tgaggagcgc  | gtgtgaggag | 300  |
| tggggtttct | tccaaatggt  | gaaccatggt | gtgacccact | cgttgatgga  | gagagtgaga | 360  |
| ggagcgtgac | gagagttctt  | cgagctaccg | ctagaggaga | aacggaaagta | tgcaaatcca | 420  |
| ccggacacgt | accaggggata | tggaaagcgc | cctgggggtg | tgagagatgc  | taaattagat | 480  |
| tggaagtatt | atttcttctt  | caattacttg | ccttcttcca | taagaaaccc  | ttccagagtg | 540  |
| ccatActcag | ctccttaaga  | tcagagaatt | gatcgaaaag | tacggagaag  | aagtggagaa | 600  |
| actgtgcgaa | aggctaacag  | agacgtgttc | agagagttaa | ggtttaaacc  | caaacaagct | 660  |
| catgcaggct | ttaggaggag  | gcgacaaagt | cggagcttct | ctgaggacaa  | actcttacc  | 720  |
| aaaatgccct | cagccgcagc  | tcaactttag | tctctcttct | cattctgacc  | ctggagacat | 780  |
| caccattctt | ctcccgagc   | agaaggtcgc | tgcccttcag | gtccgtcggt  | gtgatggctg | 840  |
| ggtcaccatt | aaatcagtc   | ctaactgctt | gatcgtaaac | attggagatc  | aaactcagat | 900  |
| acttagcaat | ggaattttaca | aaagcgtgga | acatcaagtg | atcgtaatt   | ccggtatgga | 960  |
| acgagctctt | ttggcattct  | tcataaaccc | gagaagtgat | atcccggttg  | gaccaatcga | 1020 |
| agaactagta | actgcaaac   | gacctgtctt | ttataaacca | atcaggttgc  | acgagtaccg | 1080 |
| ttctctgata | aggcaaaagg  | gtccttggtg | aaaaaaccaa | gtcgactcac  | tggtattaac | 1140 |
| tagataataa | ttgataaaca  | ttccaagtat | tatctgttat | tcctatgtcc  | ttgatattgt | 1200 |
| cggtactaaa | taatatgtga  | accgtatctt | cactttttct | tattatattg  | ctgctctctc | 1260 |
| ttgaggtttg |             |            |            |             |            |      |

(2) INFORMATION FOR SEQ ID NO:2320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..185
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1572529
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2320:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Tyr | Asn | Phe | His | Ser | Ser | Thr | Thr | Phe | Leu | Ser | Leu | Ser | Ile | Phe |
| 1   |     | 5   |     |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Ser | Tyr | Phe | Pro | Asn | Ser | Lys | Thr | Ile | His | Lys | Met | Ala | Thr | Cys |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Trp | Pro | Glu | Pro | Ile | Val | Ser | Val | Gln | Ser | Leu | Ser | Gln | Thr | Gly | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Thr | Val | Pro | Asn | Arg | Tyr | Val | Lys | Pro | Ala | His | Gln | Arg | Pro | Val |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Asn | Thr | Thr | Gln | Ser | Asp | Ala | Gly | Ile | Glu | Ile | Pro | Val | Leu | Asp |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Met | Asn | Asp | Val | Trp | Gly | Lys | Pro | Glu | Gly | Leu | Arg | Leu | Val | Arg | Ser |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ala | Cys | Glu | Glu | Trp | Gly | Phe | Phe | Gln | Met | Val | Asn | His | Gly | Val | Thr |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |
| His | Ser | Leu | Met | Glu | Arg | Val | Arg | Gly | Ala | Trp | Arg | Glu | Phe | Phe | Glu |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Leu | Pro | Leu | Glu | Glu | Lys | Arg | Lys | Tyr | Ala | Asn | Ser | Pro | Asp | Thr | Tyr |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |
| Glu | Gly | Tyr | Gly | Ser | Arg | Leu | Gly | Val | Val | Arg | Asp | Ala | Lys | Leu | Asp |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |     |
| Trp | Ser | Asp | Tyr | Phe | Phe | Leu | Asn | Tyr | Leu | Pro | Ser | Ser | Ile | Arg | Asn |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Pro | Ser | Lys | Trp | Pro | Tyr | Ser | Ala | Ser |     |     |     |     |     |     |     |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

| (X1) SEQUENCE DESCRIPTION: SEQ ID: 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|--------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met                                  | Ala | Thr | Cys | Trp | Pro | Glu | Pro | Ile | Val | Ser | Val | Gln | Ser | Leu | Ser |  |  |
| 1                                    |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Gln                                  | Thr | Gly | Val | Pro | Thr | Val | Pro | Asn | Arg | Tyr | Val | Lys | Pro | Ala | His |  |  |
|                                      |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Gln                                  | Arg | Pro | Val | Phe | Asn | Thr | Thr | Gln | Ser | Asp | Ala | Gly | Ile | Glu | Ile |  |  |
|                                      |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Pro                                  | Val | Leu | Asp | Met | Asn | Asp | Val | Trp | Gly | Lys | Pro | Glu | Gly | Leu | Arg |  |  |
|                                      | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Leu                                  | Val | Arg | Ser | Ala | Cys | Glu | Glu | Trp | Gly | Phe |     | Gln | Met | Val | Asn |  |  |
| 65                                   |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |
| His                                  | Gly | Val | Thr | His | Ser | Leu | Met | Glu | Arg | Val | Arg | Gly | Ala | Trp | Arg |  |  |
|                                      |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Glu                                  | Phe | Phe | Glu | Leu | Pro | Leu | Glu | Glu | Lys | Arg | Lys | Tyr | Ala | Asn | Ser |  |  |
|                                      |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Pro                                  | Asp | Thr | Tyr | Glu | Gly | Tyr | Gly | Ser | Arg | Leu | Gly | Val | Val | Arg | Asp |  |  |
|                                      |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Ala                                  | Lys | Leu | Asp | Trp | Ser | Asp | Tyr | Phe | Phe | Leu | Asn | Tyr | Leu | Pro | Ser |  |  |
|                                      | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Ser                                  | Ile | Arg | Asn | Pro | Ser | Lys | Trp | Pro | Tyr | Ser | Ala | Ser |     |     |     |  |  |
| 145                                  |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |  |  |

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2322:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..161
 (D) OTHER INFORMATION: / Ceres Seq. ID 1572531
```

[illegible]

(2) INFORMATION FOR SEQ ID NO:2323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572538
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2323:

|            |     |           |      |          |     |           |     |          |         |           |         |      |
|------------|-----|-----------|------|----------|-----|-----------|-----|----------|---------|-----------|---------|------|
| acaagtca   | ca  | ccccaccat | gc   | atgtcata | tct | ttttt     | cg  | tat      | cctcaat | att       | tttttt  | 60   |
| ctcttctca  | cat | caaccat   | ttg  | tatttct  | cgg | tacaac    | cc  | aaacctc  | ta      | agccctcg  |         | 120  |
| gcaccagcg  | cc  | acagaga   | gct  | ctccgcc  | gat | tactact   | cca | agaaatg  | tc      | ctcagctt  |         | 180  |
| gaaactctg  | tc  | ggttccgt  | ca   | cttctcag | cgt | tcaaa     | aa  | agtc     | cccat   | ctc       | agctcca | 240  |
| gccaccattc | gc  | ctcttctt  | tc   | acgactgc | ttc | gttgagg   | gt  | tgtgatg  | gtc     | gatattg   |         | 300  |
| atagaaacaa | aga | aaaggaag  | ca   | gaaatga  | gc  | agagagag  | aa  | gcatatga | ga      | ataaggaa  |         | 360  |
| ttgagagagg | aa  | gattttga  | tag  | tatcatc  | aa  | ggcggaag  | cc  | ttggttg  | gt      | ctcattgc  |         | 420  |
| ccttctctcg | tct | tTstct    | tg   | atattctc | gct | attgccc   | ct  | cagagatt | cat     | tcatctg   |         | 480  |
| gcaggtgggc | ct  | tactatca  | agt  | gaaaaaa  | gga | aggtggg   | ac  | gaaaaag  | at      | caacggca  |         | 540  |
| aagaacgtcc | ct  | caaacat   | ac   | ctcgatca | aa  | ctccaccg  | tt  | gatcaact | cat     | caagctc   |         | 600  |
| ttcgcgtcca | aa  | ggactaac  | ct   | gtagagg  | ct  | gtgtgtcc  | tt  | tctgtgtc | cca     | caccatc   |         | 660  |
| ggttgcgcca | tt  | gtaaaaat  | tt   | cttgggtc | gt  | ctctacga  | ct  | acaaaggc | aca     | aaacgac   |         | 720  |
| ccgaccgcag | tct | tggacc    | aa   | agattact | aa  | agagctccg | gat | gtcttgt  | cct     | ttttccg   |         | 780  |
| gcggaagctc | tg  | gaagtcgc  | ct   | ctccgctc | ac  | gctacac   | tc  | ctgtttgt | tt      | tataatg   |         | 840  |
| gatatttcac | agg | cttagga   | acca | acatgg   | gc  | cttctcgg  | gt  | cggacc   | caa     | gctttgttc |         | 900  |
| ttgaccgcag | gc  | gaagccc   | att  | gcactg   | aga | tggcga    | aga | taagcag  | aat     | ttttctca  |         | 960  |
| agggcgtttg | aga | cgctatg   | gata | aaaatgg  | gt  | tccattg   | tg  | taaaagag | gg      | gaagagac  |         | 1020 |
| atggggaaat | ac  | gtacggat  | tg   | tcgagtct | tt  | ttatagat  | tt  | cttttat  | gct     | ctgtgtctg |         | 1080 |
| atgggttttt | tct | gtatctt   | gat  | gtgttct  | gt  | gcatgtg   | tc  | ctttaatt | tatt    | agcatt    |         | 1140 |
| ctcgtgattg | tt  | ttgtgat   | agt  | ataaggt  | att | ttttt     |     |          |         |           |         |      |

(2) INFORMATION FOR SEQ ID NO:2324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..249
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572539
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2324:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | His | Asn | Pro | Thr | Met | His | Val | Ile | Ser | Leu | Ser | Leu | Ser | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Phe | Phe | Phe | Leu | Phe | Leu | Thr | Ser | Thr | Ile | Leu | Ile | Ser | Pro | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Pro | Thr | Thr | Ser | Lys | Pro | Pro | Ala | Pro | Arg | Pro | His | Arg | Glu | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ala | Asp | Tyr | Tyr | Ser | Lys | Lys | Cys | Pro | Gln | Leu | Glu | Thr | Leu | Val |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Gly | Ser | Val | Thr | Ser | Gln | Arg | Phe | Lys | Glu | Val | Pro | Ile | Ser | Ala | Pro |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     |     | 80  |     |
| Ala | Thr | Ile | Arg | Leu | Phe | Phe | His | Asp | Cys | Phe | Val | Glu | Gly | Cys | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Ser | Ile | Leu | Ile | Glu | Thr | Lys | Lys | Gly | Ser | Lys | Lys | Leu | Ala | Glu |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Arg | Glu | Ala | Tyr | Glu | Asn | Lys | Glu | Leu | Arg | Glu | Glu | Gly | Phe | Asp | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Ile | Lys | Ala | Lys | Ala | Leu | Val | Glu | Ser | His | Cys | Pro | Ser | Leu | Val |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 130                                                             | 135 | 140 |
| Ser Xaa Ser Asp Ile Leu Ala Ile Ala Ala Arg Asp Phe Ile His Leu |     |     |
| 145                                                             | 150 | 155 |
| Ala Gly Gly Pro Tyr Tyr Gln Val Lys Lys Gly Arg Trp Asp Gly Lys |     | 160 |
|                                                                 | 165 | 170 |
| Arg Ser Thr Ala Lys Asn Val Pro Pro Asn Ile Pro Arg Ser Asn Ser |     | 175 |
|                                                                 | 180 | 185 |
| Thr Val Asp Gln Leu Ile Lys Leu Phe Ala Ser Lys Gly Leu Thr Val |     | 190 |
|                                                                 | 195 | 200 |
| Glu Glu Leu Val Val Leu Ser Gly Ser His Thr Ile Gly Ser Pro Ile |     | 205 |
|                                                                 | 210 | 215 |
| Val Lys Ile Ser Leu Val Val Ser Thr Thr Thr Lys Ala Gln Asn Asp |     | 220 |
| 225                                                             | 230 | 235 |
| Pro Thr Arg Val Leu Thr Lys Asp Tyr                             |     | 240 |
|                                                                 | 245 |     |

(2) INFORMATION FOR SEQ ID NO:2325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..243

(D) OTHER INFORMATION: / Ceres Seq. ID 1572540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2325:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met His Val Ile Ser Leu Ser Leu Ser Ser Ile Phe Phe Leu Phe     |     |
| 1                                                               | 5   |
| Leu Thr Ser Thr Ile Leu Ile Ser Pro Val Gln Pro Thr Thr Ser Lys | 10  |
|                                                                 | 15  |
| Pro Pro Ala Pro Arg Pro His Arg Glu Leu Ser Ala Asp Tyr Tyr Ser | 20  |
|                                                                 | 25  |
| Lys Lys Cys Pro Gln Leu Glu Thr Leu Val Gly Ser Val Thr Ser Gln | 30  |
|                                                                 | 35  |
| Arg Phe Lys Glu Val Pro Ile Ser Ala Pro Ala Thr Ile Arg Leu Phe | 40  |
|                                                                 | 45  |
| Phe His Asp Cys Phe Val Glu Gly Cys Asp Gly Ser Ile Leu Ile Glu | 50  |
|                                                                 | 55  |
| Thr Lys Lys Gly Ser Lys Lys Leu Ala Glu Arg Glu Ala Tyr Glu Asn | 60  |
|                                                                 | 65  |
| Lys Glu Leu Arg Glu Glu Gly Phe Asp Ser Ile Ile Lys Ala Lys Ala | 70  |
|                                                                 | 75  |
| Leu Val Glu Ser His Cys Pro Ser Leu Val Ser Xaa Ser Asp Ile Leu | 80  |
|                                                                 | 85  |
| Ala Ile Ala Ala Arg Asp Phe Ile His Leu Ala Gly Gly Pro Tyr Tyr | 90  |
|                                                                 | 95  |
| Gln Val Lys Lys Gly Arg Trp Asp Gly Lys Arg Ser Thr Ala Lys Asn | 100 |
|                                                                 | 105 |
| Val Pro Pro Asn Ile Pro Arg Ser Asn Ser Thr Val Asp Gln Leu Ile | 110 |
|                                                                 | 115 |
| Lys Leu Phe Ala Ser Lys Gly Leu Thr Val Glu Glu Leu Val Val Leu | 120 |
|                                                                 | 125 |
| Ser Gly Ser His Thr Ile Gly Ser Pro Ile Val Lys Ile Ser Leu Val | 130 |
|                                                                 | 135 |
| Val Ser Thr Thr Thr Lys Ala Gln Asn Asp Pro Thr Arg Val Leu Thr | 140 |
| 225                                                             | 145 |
| Lys Asp Tyr                                                     | 150 |

(2) INFORMATION FOR SEQ ID NO:2326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1239 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1239

(D) OTHER INFORMATION: / Ceres Seq. ID 1572569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2326:

|             |             |             |             |            |            |      |
|-------------|-------------|-------------|-------------|------------|------------|------|
| acaattcaga  | ttccaaatttt | ctcaaaactct | aaaatcaatc  | tctcaaatct | ctcaaccgtg | 60   |
| atcaaggtag  | atttctgagt  | tcttattgta  | ttctctcgat  | ttgtttcggt | cgatcgcaat | 120  |
| ttaggctctg  | tcttttgatt  | tgatctcgt   | taatctctga  | tcggaggcaa | attacatagt | 180  |
| ttcatcggtta | gatctctctt  | tatttctcga  | ttagggttgg  | tatttttcgc | agatctgttt | 240  |
| attttcttgt  | tggttccctg  | tatttgatcc  | gatttgttga  | aagaatttgt | gtgttctcga | 300  |
| ttatttatgc  | tttgatctgt  | gattttttat  | tagatttggt  | gttagttttc | tgtttgtgcg | 360  |
| atcgaatttg  | tcgattaatc  | tcggtttttc  | tgattaacag  | atgcagatct | tcgttaagac | 420  |
| gtctaccgga  | aagactatca  | ccctcgaggt  | ggaaagctct  | gacaccatcg | acaacgtaa  | 480  |
| ggccaagatc  | caggataaag  | aaggtattcc  | tccggatcag  | cagagggtta | tcttcgcggg | 540  |
| aaagcagttg  | gaggatggcc  | gcacgttggc  | ggattacaat  | atccagaagg | aatccaccct | 600  |
| ccacttggtt  | ctcaggctcc  | gtggtgggtat | gcagattttc  | gttaaaaccc | taacgggaaa | 660  |
| gaagattact  | cttgagggtg  | agagctctga  | caccattgac  | aacgtcaagg | ccaagatcca | 720  |
| agataaggag  | ggatttctct  | cggaccagca  | gaggttgatc  | ttgcgcggaa | agcaactgtt | 780  |
| ggacggcaga  | accttggcgg  | attacaacat  | ccagaaggag  | tctacgcttc | atttggctt  | 840  |
| tcgctctgcg  | tggagggtatg | cagatcttcg  | taaaagacttt | gaacgggaa  | acatcactc  | 900  |
| ttgaagtgtg  | gagctccgag  | accattgata  | acgtgaagcg  | taagatccag | gacaaggaa  | 960  |
| cgattctctc  | ggaccagcag  | cgtctcatct  | tcgctggaaa  | gcagcttgag | gatggacgtg | 1020 |
| ctttggccga  | ctacaacatc  | cagaaggagt  | ctactcttca  | ctctgtctcc | cgctcccgta | 1080 |
| gtggttttcta | aaactgtgtc  | ctctctctta  | tggttactga  | accaagtcca | tgatctggtt | 1140 |
| catctagatc  | tttgggtggt  | tatgttttgg  | ggccatgtac  | agcctctgat | aaataatgtg | 1200 |
| tcgactatgt  | ttcgtttctt  | ttcatctctc  | ttttctttc   |            |            |      |

(2) INFORMATION FOR SEQ ID NO:2327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1572570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2327:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Ile | Phe | Val | Lys | Thr | Leu | Thr | Gly | Lys | Thr | Ile | Thr | Leu | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Glu | Ser | Ser | Asp | Thr | Ile | Asp | Asn | Val | Lys | Ala | Lys | Ile | Gln | Asp |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Glu | Gly | Ile | Pro | Pro | Asp | Gln | Gln | Arg | Leu | Ile | Phe | Ala | Gly | Lys |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Gln | Leu | Glu | Asp | Gly | Arg | Thr | Leu | Ala | Asp | Tyr | Asn | Ile | Gln | Lys | Glu |
|     |     |     |     | 50  |     |     |     | 55  |     |     | 60  |     |     |     |     |
| Ser | Thr | Leu | His | Leu | Val | Leu | Arg | Leu | Arg | Gly | Gly | Met | Gln | Ile | Phe |
|     |     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     | 80  |     |
| Val | Lys | Thr | Leu | Thr | Gly | Lys | Thr | Ile | Thr | Leu | Glu | Val | Glu | Ser | Ser |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asp | Thr | Ile | Asp | Asn | Val | Lys | Ala | Lys | Ile | Gln | Asp | Lys | Glu | Gly | Ile |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Pro | Asp | Gln | Gln | Arg | Leu | Ile | Phe | Ala | Gly | Lys | Gln | Leu | Glu | Asp |
|     |     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Arg | Thr | Leu | Ala | Asp | Tyr | Asn | Ile | Gln | Lys | Glu | Ser | Thr | Leu | His |
|     |     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |



Leu Val Phe Ala Ser Ala Trp Arg Tyr Ala Asp Leu Arg Lys Asp Phe  
145 150 155 160  
Asp Arg Lys Asp His His Ser  
165

(2) INFORMATION FOR SEQ ID NO:2328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1572571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2328:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Thr Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu |  |
| 1 5 10 15                                                       |  |
| Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp |  |
| 20 25 30                                                        |  |
| Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys |  |
| 35 40 45                                                        |  |
| Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu |  |
| 50 55 60                                                        |  |
| Ser Thr Leu His Leu Val Phe Ala Ser Ala Trp Arg Tyr Ala Asp Leu |  |
| 65 70 75 80                                                     |  |
| Arg Lys Asp Phe Asp Arg Lys Asp His His Ser                     |  |
| 85 90                                                           |  |

(2) INFORMATION FOR SEQ ID NO:2329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1597

(D) OTHER INFORMATION: / Ceres Seq. ID 1572576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2329:

|            |            |             |             |             |             |      |
|------------|------------|-------------|-------------|-------------|-------------|------|
| aaaaataaga | accttgacaa | cttctctaca  | acactcaatt  | tttctctcta  | atgggtggaag | 60   |
| caagaagcct | gaagaaacca | atccaattgg  | gtaataaaga  | agatcaaaaac | cctagaaaaat | 120  |
| tctactcttc | attcatcttt | aaagctcttta | tctctacogt  | gctctgcgac  | gtcgatccotg | 180  |
| tcttctcttc | tcagacacca | gagcttgcta  | accaaacaag  | actctcgag   | cttctccacc  | 240  |
| tgtgtttcgt | cggtatcgca | gtctcttaac  | gtctcttacc  | ccgcaggaag  | tacgacggag  | 300  |
| gaggaggttg | aggaacaacg | aatagtgatc  | acaacaagc   | tgatcatagt  | aataataatt  | 360  |
| cgcattcata | tgtgcctaa  | attcttgaag  | tatctctgt   | ttttacacgt  | gggtcacgaga | 420  |
| gtgaactcga | accgtccgat | gattctctcg  | gtgatcaacg  | taagtctcag  | acatggaaga  | 480  |
| acaagtacca | catgaaaatc | cccgagggtg  | agactcgttt  | cggtgatcga  | gttagttcag  | 540  |
| aaaacagaga | gaagcctctg | cttttgcggg  | ttcggagcgt  | gaattattct  | cgtgtttctc  | 600  |
| attcttccgg | cgataattcc | ggctgatggg  | agaaagtga   | attctaaaga  | gaacttctga  | 660  |
| agactcttat | cgatgataat | atgtagtgac  | ttccttctcc  | gattccatgg  | aggtcaagat  | 720  |
| catcttcttc | atcatcatca | tcatcaaaag  | aggttggaatc | tctaccgtcc  | gttaagaatc  | 780  |
| tgactacagt | tgaatcacag | ccggtgatca  | agaactctgac | accatcttct  | tctttctctt  | 840  |
| ctccaagaaa | gtcgaattct | atacctaata  | tgcgatctga  | gttccatcca  | tctccgcacc  | 900  |
| cgcctctctc | gccgcgcgca | ccactaccgg  | cgtttttata  | ctctctcgct  | agaaaagagt  | 960  |
| atcccggaat | ttacacgggt | gagagagagag | aatacatcgt  | tcacaagaag  | aaattttcag  | 1020 |
| gaggtgtagt | tcatctctcc | ccgcctctct  | ctccaccacc  | tcctggtggag | tattataagt  | 1080 |
| cacctctcgc | aaaattcaga | ctaagtaaac  | aacggagaaa  | gtctctcgag  | caaaagatgw  | 1140 |
| aaagaaacgc | tcctaaaaag | gtttggtggt  | ccgatccaat  | cgtggaatcg  | aaggaacaa   | 1200 |
| acacagagaa | gaatgatcaa | agaagtaact  | tgaggagcaa  | ggcagctgga  | gaatcccgaga | 1260 |

(2) INFORMATION FOR SEQ ID NO:2330:

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 473 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..473

(D) OTHER INFORMATION: / Ceres Seq. ID 1572577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2330:

|                     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| (A1) SEQUENCE BLOCK |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Met                 | Val | Glu | Ala | Arg | Ser | Leu | Lys | Lys | Pro | Ile | Gln | Leu | Gly | Asn | Lys | 15 |
| 1                   | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |     |     |    |
| Glu                 | Asp | Gln | Asn | Pro | Arg | Lys | Phe | Tyr | Ser | Arg | Phe | Ile | Phe | Lys | Ala |    |
| 20                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Leu                 | Ile | Leu | Thr | Val | Leu | Cys | Ala | Val | Val | Pro | Val | Phe | Leu | Ser | Gln |    |
| 25                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Thr                 | Pro | Glu | Leu | Ala | Asn | Gln | Thr | Arg | Leu | Leu | Glu | Leu | Leu | His | Leu |    |
| 30                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Val                 | Phe | Val | Gly | Ile | Ala | Val | Ser | Tyr | Gly | Leu | Phe | Ser | Arg | Arg | Asn |    |
| 35                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Tyr                 | Asp | Gly | Gly | Gly | Gly | Gly | Gly | Thr | Ser | Asn | Ser | Asp | His | Asn | Lys |    |
| 40                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Ala                 | Asp | His | Ser | Asn | Asn | Asn | Ser | His | Ser | Tyr | Val | Pro | Lys | Ile | Leu |    |
| 45                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Glu                 | Val | Ser | Ser | Val | Phe | Asn | Val | Gly | His | Glu | Ser | Glu | Ser | Glu | Pro |    |
| 50                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Ser                 | Asp | Asp | Ser | Ser | Gly | Asp | Gln | Arg | Lys | Phe | Gln | Thr | Trp | Lys | Asn |    |
| 55                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Lys                 | Tyr | His | Met | Lys | Ile | Pro | Glu | Val | Glu | Thr | Arg | Phe | Val | Asp | Arg |    |
| 60                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Val                 | Ser | Ser | Glu | Asn | Arg | Glu | Lys | Pro | Leu | Leu | Leu | Pro | Val | Arg | Ser |    |
| 65                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Leu                 | Asn | Tyr | Ser | Arg | Val | Ser | Asp | Ser | Ser | Gly | Asp | Asn | Ser | Gly | Arg |    |
| 70                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Trp                 | Glu | Lys | Val | Arg | Ser | Lys | Arg | Glu | Leu | Leu | Lys | Thr | Leu | Gly | Asp |    |
| 75                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Asp                 | Asn | Ser | Asp | Val | Leu | Pro | Ser | Pro | Ile | Pro | Trp | Arg | Ser | Arg | Ser |    |
| 80                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Ser                 | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Lys | Glu | Val | Glu | Ser | Leu | Pro | Ser |    |
| 85                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Val                 | Lys | Asn | Leu | Thr | Thr | Val | Glu | Ser |     |     |     |     |     |     |     |    |

340 345 350  
Asn Glu Arg Arg Lys Ser Ser Glu Gln Lys Met Xaa Arg Asn Ala Pro  
355 360 365  
Lys Lys Val Trp Trp Ser Asp Pro Ile Val Glu Ser Lys Glu Gln Asp  
370 375  
Thr Glu Lys Asn Asp Gln Arg Ser Asn Leu Gly Ser Lys Ala Val Glu  
385 390 395 400  
Glu Ser Glu Asn Gly Glu Gln Arg Arg Gly Glu Asn Glu Ile His Asp  
405 410 415  
Glu Val Glu Lys Lys Ile Val Glu Glu Glu Gly Val Ser Glu Ile Asn  
420 425 430  
Asn Gly Ser Asp Val Asp Lys Lys Ala Asp Glu Phe Ile Ala Lys Phe  
435 440 445  
Arg Glu Gln Ile Arg Leu Gln Arg Ile Glu Ser Ile Lys Arg Ser Thr  
450 455 460  
Asn Lys Ile Ser Ala Asn Ser Ser Arg  
465 470  
(2) INFORMATION FOR SEQ ID NO:2331:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 326 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..326  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572578  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2331:  
Met Lys Ile Pro Glu Val Glu Thr Arg Phe Val Asp Arg Val Ser Ser  
1 5 10 15  
Glu Asn Arg Glu Lys Pro Leu Leu Leu Pro Val Arg Ser Leu Asn Tyr  
20 25 30  
Ser Arg Val Ser Asp Ser Ser Gly Asp Asn Ser Gly Arg Trp Glu Lys  
35 40 45  
Val Arg Ser Lys Arg Glu Leu Leu Lys Thr Leu Gly Asp Asp Asn Ser  
50 55 60  
Asp Val Leu Pro Ser Pro Ile Pro Trp Arg Ser Arg Ser Ser Ser Ser  
65 70 75 80  
Ser Ser Ser Ser Ser Lys Glu Val Glu Ser Leu Pro Ser Val Lys Asn  
85 90 95  
Leu Thr Thr Val Glu Ser Gln Pro Leu Ile Lys Asn Leu Thr Pro Ser  
100 105 110  
Ser Ser Phe Ser Ser Pro Arg Lys Ser Asn Pro Ile Pro Asn Leu Ala  
115 120 125  
Ser Glu Phe His Pro Ser Pro Pro Pro Pro Pro Pro Pro Pro Pro  
130 135 140  
Leu Pro Ala Phe Tyr Asn Ser Ser Ser Arg Lys Asp His Pro Gly Ile  
145 150 155 160  
Tyr Arg Val Glu Arg Arg Glu Ser Ser Val His Lys Thr Lys Phe Ala  
165 170 175  
Gly Gly Glu Phe His Pro Pro Pro Pro Pro Pro Pro Pro Pro Val  
180 185 190  
Glu Tyr Tyr Lys Ser Pro Pro Thr Lys Phe Arg Leu Ser Asn Glu Arg  
195 200 205  
Arg Lys Ser Ser Glu Gln Lys Met Xaa Arg Asn Ala Pro Lys Lys Val  
210 215 220  
Trp Trp Ser Asp Pro Ile Val Glu Ser Lys Glu Gln Asp Thr Glu Lys  
225 230 235 240  
Asn Asp Gln Arg Ser Asn Leu Gly Ser Lys Ala Val Glu Glu Ser Glu  
245 250 255

Asn Gly Glu Gln Arg Arg Gly Glu Asn Glu Ile His Asp Glu Val Glu  
260 265 270  
Lys Lys Ile Val Glu Glu Gly Val Ser Glu Ile Asn Asn Gly Ser  
275 280 285  
Asp Val Asp Lys Lys Ala Asp Glu Phe Ile Ala Lys Phe Arg Glu Gln  
290 295 300  
Ile Arg Leu Gln Arg Ile Glu Ser Ile Lys Arg Ser Thr Asn Lys Ile  
305 310 315 320  
Ser Ala Asn Ser Ser Arg  
325

(2) INFORMATION FOR SEQ ID NO:2332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..783

(D) OTHER INFORMATION: / Ceres Seq. ID 1572627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2332:

|             |             |            |             |            |            |     |
|-------------|-------------|------------|-------------|------------|------------|-----|
| attgaagtct  | cgctctgtga  | gatacagctt | tagctttgtg  | gatgcagaat | tcgagactat | 60  |
| acattctttt  | ttaagtcttt  | gagcttgga  | caataacctt  | ttcactctat | ttgtttcttc | 120 |
| aactaaatgg  | atactgggtg  | gtttgttagt | gaaaaagggtg | agaacagatt | atatgttga  | 180 |
| aacctggatc  | ttagaataaa  | cgaggcttcg | ttgataaaaa  | tgttttctcc | atatgggaag | 240 |
| atcatatcag  | aagactctct  | ttggcacaca | cgcgggccaa  | agaagggaga | acctcggggt | 300 |
| tatgctttca  | ttcaatacac  | ccttaaaag  | tgagcataca  | ggaagctgaa | ttggcgaaag | 360 |
| agaagatgca  | tgggagatta  | gcttgttgta | ggcctttagt  | ggtgcgtcta | gctagtgaga | 420 |
| agcaactaga  | agattctctc  | catgatcaat | ccaaaagatc  | attaccagaa | ggaacagaa  | 480 |
| ccagatttgt  | aaacggggagc | agotcaggac | aaatgagccg  | agacgaaaaa | gtaactgcca | 540 |
| ttaaagaacaa | actcaaaagct | ttggaagaag | atgagaaaacg | tgatccCaag | aaacagaaaa | 600 |
| tttaagaaaa  | cggttttcaa  | acacacaact | ttgggtctat  | gtgactctgt | gactctgacc | 660 |
| atttttcagt  | tttggtttga  | tttgatttgg | tttacccggt  | taatcgaaac | caattttgat | 720 |
| ttaatatctt  | cggttggctc  | agtgatgat  | ataaaatttg  | taatggaaag | caaaagtga  | 780 |

cg

(2) INFORMATION FOR SEQ ID NO:2333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1572628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2333:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Thr | Gly | Gly | Phe | Val | Asp | Glu | Lys | Gly | Glu | Asn | Arg | Leu | Tyr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     | 15  |     |     |     |     |
| Val | Gly | Asn | Leu | Asp | Leu | Arg | Ile | Asn | Glu | Ala | Ser | Leu | Ile | Lys | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Ser | Pro | Tyr | Gly | Lys | Ile | Ile | Ser | Glu | Asp | Phe | Leu | Trp | His | Thr |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Arg | Gly | Pro | Lys | Lys | Gly | Glu | Pro | Arg | Gly | Tyr | Ala | Phe | Ile | Gln | Tyr |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Leu | Lys | Glu |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..79  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572629  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2334:  
Met His Gly Arg Leu Ala Cys Gly Arg Pro Leu Val Val Arg Leu Ala  
1 5 10 15  
Ser Glu Lys His Leu Glu Asp Ser Ser His Asp His Ser Lys Arg Ser  
20 25 30  
Leu Pro Glu Gly Asn Arg Thr Arg Phe Val Asn Gly Ser Ser Ser Gly  
35 40 45  
Gln Met Ser Arg Asp Glu Lys Val Thr Ala Ile Lys Asn Lys Leu Lys  
50 55 60  
Ala Leu Glu Glu Asp Glu Lys Arg Asp Pro Lys Lys Gln Lys Ile  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2335:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..58  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572630  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2335:  
Met Arg Asn Val Ile Pro Arg Asn Arg Lys Phe Lys Lys Thr Val Phe  
1 5 10 15  
Lys His Thr Thr Leu Gly Leu Cys Asp Ser Val Thr Leu Thr Ile Phe  
20 25 30  
Gln Phe Trp Phe Asp Leu Ile Trp Phe Thr Gly Leu Ile Glu Thr Asn  
35 40 45  
Phe Asp Leu Ile Phe Arg Phe Gly Ser Val  
50 55

(2) INFORMATION FOR SEQ ID NO:2336:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 910 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..910  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572643  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2336:  
atcaactctc tctctcaatt tcacaactct ccttttctat ttctctotct agaaaaatat 60  
catcatctat caattatata gaggacttat tttagattcat ttcatataaa tggagaaaag 120  
agaaagttagt ggtggttctg gatcaggaga tgcagagggt agaaaaagggc catggacgat 180  
ggaagaagat ttgatttcca tcaattatat cgccaatcat ggtgaagggt tttgaaactc 240  
tctgcacaaa tctgcaggac taaaacgcac cgggaaaagt tgcgcggtcc ggtggctgaa 300  
ctacctccga cctgatgtgc gacggggaaa tatcacacca gaagaacagc tcaccatcat 360  
ggaacttcat gcaaaatggg gaaatagggt gtcaaaaatt gcaaaagcatt taccaggaag 420  
gaccgacaat gagataaaga acttttgagg gactaagatc cagaaatata tcatcaagag 480  
cgagaaaacg acgaccgttg gatcacaaag ctccgagttt ataaaccatc atgcgacaac 540  
gagccatgtc atgaatgata ctcaagaaac Catggatgat tattctccaa cgacgtcgta 600

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| tcaacatgcc | agcaatatta | atcagcagct  | taattatggt | aattatgtgc | ctgaatccag | 660 |
| ttcgatcatg | atgccattat | ctgttgatca  | atccgaacaa | aactattgga | gcgtcgatga | 720 |
| tccttggccc | atgaatatat | ataatggtaa  | ttaataaata | agttcggtaa | aacttatata | 780 |
| taattacggt | ccaagagggt | ttctatatata | acagagtact | gtatgggttt | gcctcattgt | 840 |
| ttagaggtag | gtacttaata | taaggttgga  | gatcttatat | gaattaataa | ataactcga  | 900 |
| tttactagat |            |             |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1572644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2337:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Lys | Arg | Glu | Glu | Ser | Ser | Gly | Gly | Ser | Gly | Ser | Ala | Glu |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Val | Arg | Lys | Gly | Pro | Trp | Thr | Met | Glu | Glu | Asp | Leu | Ile | Leu | Ile | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Ile | Ala | Asn | His | Gly | Glu | Gly | Val | Trp | Asn | Ser | Leu | Ala | Lys | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Gly | Leu | Lys | Arg | Thr | Gly | Lys | Ser | Cys | Arg | Leu | Arg | Trp | Leu | Asn |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Tyr | Leu | Arg | Pro | Asp | Val | Arg | Arg | Gly | Asn | Ile | Thr | Pro | Glu | Glu | Gln |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Thr | Ile | Met | Glu | Leu | His | Ala | Lys | Trp | Gly | Asn | Arg | Trp | Ser | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Ala | Lys | His | Leu | Pro | Gly | Arg | Thr | Asp | Asn | Glu | Ile | Lys | Asn | Phe |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Trp | Arg | Thr | Lys | Ile | Gln | Lys | Tyr | Ile | Ile | Lys | Ser | Gly | Glu | Thr | Thr |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Thr | Val | Gly | Ser | Gln | Ser | Ser | Glu | Phe | Ile | Asn | His | His | Ala | Thr | Thr |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Ser | His | Val | Met | Asn | Asp | Thr | Gln | Glu | Thr | Met | Asp | Met | Tyr | Ser | Pro |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Thr | Thr | Ser | Tyr | Gln | His | Ala | Ser | Asn | Ile | Asn | Gln | Gln | Leu | Asn | Tyr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Gly | Asn | Tyr | Val | Pro | Glu | Ser | Ser | Ser | Ile | Met | Met | Pro | Leu | Ser | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | Gln | Ser | Glu | Gln | Asn | Tyr | Trp | Ser | Val | Asp | Asp | Leu | Trp | Pro | Met |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | Ile | Tyr | Asn | Gly | Asn |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 210 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1572645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2338:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Glu | Asp | Leu | Ile | Leu | Ile | Asn | Tyr | Ile | Ala | Asn | His | Gly | Glu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gly | Val | Trp | Asn | Ser | Leu | Ala | Lys | Ser | Ala | Gly | Leu | Lys | Arg | Thr | Gly |

(B) LOCATION: 1..1928

(D) OTHER INFORMATION: / Ceres Seq. ID 1572647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2340:

|            |             |             |             |            |            |      |
|------------|-------------|-------------|-------------|------------|------------|------|
| ttctctcttc | ttccattctc  | acaaattcca  | aacatctctc  | ttcttttctc | totcacacac | 60   |
| aaaattgcag | aagaagaaga  | gtcatgaatg  | gtgaagaaga  | ctttgtagaa | gattgtctgc | 120  |
| ttttttgtga | gattgatctc  | tctggaagat  | atggaagata  | cgatgaaata | cttggcaaa  | 180  |
| gagcttcaaa | gacagtatac  | agagcatttg  | atgagtagta  | aggtagatga | gtagcatgga | 240  |
| accaagtaaa | gcttcgaaat  | ttcacaagga  | atcctgagga  | attagagaag | tttttcagag | 300  |
| agattcatct | ttccaagact  | ttgaatcctc  | aaaacattat  | gaaattctac | actctctggg | 360  |
| ttgataccaa | caatttatca  | atcaattttg  | tcaactgaact | cttcacacct | ggtagcttca | 420  |
| gacagtatag | gttgagacat  | agaagagtag  | atattagagc  | agtgaagcaa | tgggtgcaag | 480  |
| agatttttaa | agggctcttc  | tattttacata | ctgcgttctc  | accaattata | catagagatc | 540  |
| tcaaatgtga | taacattttt  | atcaatggaa  | accaaggtga  | agtcgaagtc | ggtagacctg | 600  |
| gactcgctgc | gattctctgc  | aaatcacatg  | ccgttcgttg  | cggttggaac | cctgagttta | 660  |
| tggtctcaga | agtgtagatg  | gaggaatata  | atgagttggg  | tgatgtatat | gcttttggca | 720  |
| tgtgtgtgtt | ggagatgggt  | acttttgatt  | atccttacag  | tgaatgtact | caaccggcac | 780  |
| aaatctacaa | gaaagttaac  | tccgggaaaa  | agcctgaagc  | tttttactta | gtgaaggatc | 840  |
| ctgaggttgc | tgaagtttgt  | gagaagtgtt  | tagctaacgt  | gacgtgtagg | ctaacggcat | 900  |
| tgtagctttt | acaagaccct  | tttctacaa   | atgataatat  | ggatggattt | gttatgagac | 960  |
| ctattgatta | ctacaatgtg  | tatgatgaaa  | ctgggtgtgt  | ccttagacat | cctttgattg | 1020 |
| ctagctctct | ttaccatgat  | cagtttgagt  | cgtcacagat  | atgtgagatc | gatctttctg | 1080 |
| ctaagcatga | tgaagatcat  | gtcgacattt  | cgattaaagg  | gaagagaaac | ggtagctgat | 1140 |
| ggatattctt | gagactttga  | atatctgatg  | ctgaaggacg  | gataaggaa  | atttactctc | 1200 |
| cgtttgagac | ggctattgtg  | actgcgatga  | gtgtagcggt  | tgagatgggt | ctcagagctc | 1260 |
| acataacgaa | tcaagatgat  | gcgaaaatcg  | cggagatgat  | cgatgcagag | attgtcgc   | 1320 |
| tggtgctgta | ttggaaaaat  | gatacagaaa  | gtTccaaaa   | tgtaaaaca  | acaaagaaca | 1380 |
| acaaactctc | aggattctct  | ggagagtggt  | cttcaaacgg  | gtatatacaa | gagactgtat | 1440 |
| catcaggaga | aaaattctct  | cataatcctc  | atgagttcga  | tagttctgaa | gacaagagct | 1500 |
| ttctctcggt | tcaaggtagg  | tttgccgata  | tgtgggggtt  | gcgagaatca | tattctgatg | 1560 |
| atggagaaaa | acagagctca  | aggaaggtta  | gaagtggacg  | gtggctggag | aatgagatga | 1620 |
| gacgagaact | gagatggcct  | aaggcaagcg  | acaaagtcca  | acttatgaaa | attagagagc | 1680 |
| aaaacgatct | cgagacacgc  | atagagatct  | ctcttacacc  | gggaacttca | gtttcgctac | 1740 |
| ctcttcttta | cagggcctata | tcacttctct  | tggatgccgt  | ggatatgtga | cattattgtg | 1800 |
| aagtctgatg | atagttatca  | cttatatttg  | tatgtttcga  | catttttaac | ttttgttaag | 1860 |
| ttaaaagtta | atgacatagt  | gtactttatt  | taaagagaag  | aagagtaaac | gaaaaacata | 1920 |
| aattagtc   |             |             |             |            |            |      |

(2) INFORMATION FOR SEQ ID NO:2341:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 595 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..595

(D) OTHER INFORMATION: / Ceres Seq. ID 1572648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2341:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Ser | Ser | Ile | Ser | Thr | Asn | Ser | Lys | His | Leu | Ser | Leu | Phe | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | His | Thr | Gln | Asn | Cys | Ser | Arg | Arg | Arg | Val | Met | Asn | Gly | Glu | Glu |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Ser | Phe | Val | Glu | Asp | Cys | Ser | Val | Phe | Val | Glu | Ile | Asp | Pro | Ser | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Tyr | Gly | Arg | Tyr | Asp | Glu | Ile | Leu | Gly | Lys | Gly | Ala | Ser | Lys | Thr |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Tyr | Arg | Ala | Phe | Asp | Glu | Tyr | Glu | Gly | Ile | Glu | Val | Ala | Trp | Asn |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Gln | Val | Lys | Leu | Arg | Asn | Phe | Thr | Arg | Asn | Pro | Glu | Glu | Leu | Glu | Lys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Phe | Thr | Arg | Glu | Ile | His | Leu | Leu | Lys | Thr | Leu | Asn | His | Gln | Asn | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Phe | Tyr | Thr | Ser | Trp | Val | Asp | Thr | Asn | Asn | Leu | Ser | Ile | Asn |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Val | Thr | Glu | Leu | Phe | Thr | Ser | Gly | Thr | Leu | Arg | Gln | Tyr | Arg | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | His | Arg | Arg | Val | Asn | Ile | Arg | Ala | Val | Lys | Gln | Trp | Cys | Lys | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Leu | Lys | Gly | Leu | Leu | Tyr | Leu | His | Ser | Arg | Ser | Pro | Pro | Ile | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Arg | Asp | Leu | Lys | Cys | Asp | Asn | Ile | Phe | Ile | Asn | Gly | Asn | Gln | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Val | Lys | Ile | Gly | Asp | Leu | Gly | Leu | Ala | Ala | Ile | Leu | Arg | Lys | Ser |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| His | Ala | Val | Arg | Cys | Val | Gly | Thr | Pro | Glu | Phe | Met | Ala | Pro | Glu | Val |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Tyr | Asp | Glu | Glu | Tyr | Asn | Glu | Leu | Val | Asp | Val | Tyr | Ala | Phe | Gly | Met |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Cys | Val | Leu | Glu | Met | Val | Thr | Phe | Asp | Tyr | Pro | Tyr | Ser | Glu | Cys | Thr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| His | Pro | Ala | Gln | Ile | Tyr | Lys | Lys | Val | Thr | Ser | Gly | Lys | Lys | Pro | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ala | Phe | Tyr | Leu | Val | Lys | Asp | Pro | Glu | Val | Arg | Glu | Phe | Val | Glu | Lys |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Cys | Leu | Ala | Asn | Val | Thr | Cys | Arg | Leu | Thr | Ala | Leu | Glu | Leu | Leu | Gln |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asp | Pro | Phe | Leu | Gln | Asp | Asn | Met | Asp | Gly | Phe | Val | Met | Arg | Pro |     |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |     |
| Ile | Asp | Tyr | Tyr | Asn | Gly | Tyr | Asp | Glu | Thr | Gly | Val | Phe | Leu | Arg | His |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Pro | Leu | Ile | Asp | Asp | Pro | Leu | Tyr | His | Asp | Gln | Phe | Glu | Ser | Ser | Gln |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ile | Cys | Glu | Ile | Asp | Leu | Phe | Ala | Asn | Asp | Asp | Glu | Asp | His | Val | Asp |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ile | Ser | Ile | Lys | Gly | Lys | Arg | Asn | Gly | Asp | Asp | Gly | Ile | Phe | Leu | Arg |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Leu | Arg | Ile | Ser | Asp | Ala | Glu | Gly | Arg | Ile | Arg | Asn | Ile | Tyr | Phe | Pro |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Phe | Glu | Thr | Ala | Ile | Asp | Thr | Ala | Trp | Ser | Val | Ala | Val | Glu | Met | Val |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Ser | Glu | Leu | Asp | Ile | Thr | Asn | Gln | Asp | Val | Ala | Lys | Ile | Ala | Glu | Met |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Ile | Asp | Ala | Glu | Ile | Ala | Ala | Leu | Val | Pro | Asp | Trp | Lys | Asn | Asp | Thr |
|     | 435 |     |     |     |     | 440 |     |     |     |     |     | 445 |     |     |     |
| Glu | Ser | Ser | Gln | Asn | Val | Asn | Asn | Asn | Lys | Asn | Asn | Asn | Thr | Ala | Gly |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Phe | Cys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

595

(2) INFORMATION FOR SEQ ID NO:2342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..568
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2342:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Gly | Glu | Glu | Ser | Phe | Val | Glu | Asp | Cys | Ser | Val | Phe | Val | Glu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Asp | Pro | Ser | Gly | Arg | Tyr | Gly | Arg | Tyr | Asp | Glu | Ile | Leu | Gly | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ala | Ser | Lys | Thr | Val | Tyr | Arg | Ala | Phe | Asp | Glu | Tyr | Glu | Gly | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Val | Ala | Trp | Asn | Gln | Val | Lys | Leu | Arg | Asn | Phe | Thr | Arg | Asn | Pro |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Glu | Glu | Leu | Glu | Lys | Phe | Phe | Arg | Glu | Ile | His | Leu | Leu | Lys | Thr | Leu |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |
| Asn | His | Gln | Asn | Ile | Met | Lys | Phe | Tyr | Thr | Ser | Trp | Val | Asp | Thr | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Leu | Ser | Ile | Asn | Phe | Val | Thr | Glu | Leu | Phe | Thr | Ser | Gly | Thr | Leu |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Gln | Tyr | Arg | Leu | Arg | His | Arg | Arg | Val | Asn | Ile | Arg | Ala | Val | Lys |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Gln | Trp | Cys | Lys | Gln | Ile | Leu | Lys | Gly | Leu | Leu | Tyr | Leu | His | Ser | Arg |
|     |     |     |     | 130 |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Ser | Pro | Pro | Ile | Ile | His | Arg | Asp | Leu | Lys | Cys | Asp | Asn | Ile | Phe | Ile |
|     |     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |
| Asn | Gly | Asn | Gln | Gly | Glu | Val | Lys | Ile | Gly | Asp | Leu | Gly | Leu | Ala | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Leu | Arg | Lys | Ser | His | Ala | Val | Arg | Cys | Val | Gly | Thr | Pro | Glu | Phe |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Met | Ala | Pro | Glu | Val | Tyr | Asp | Glu | Glu | Tyr | Asn | Glu | Leu | Val | Asp | Val |
|     |     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Tyr | Ala | Phe | Gly | Met | Cys | Val | Leu | Glu | Met | Val | Thr | Phe | Asp | Tyr | Pro |
|     |     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Tyr | Ser | Glu | Cys | Thr | His | Pro | Ala | Gln | Ile | Tyr | Lys | Lys | Val | Thr | Ser |
|     |     |     |     | 225 |     |     | 230 |     |     |     | 235 |     |     |     | 240 |
| Gly | Lys | Lys | Pro | Glu | Ala | Phe | Tyr | Leu | Val | Lys | Asp | Pro | Glu | Val | Arg |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Phe | Val | Glu | Lys | Cys | Leu | Ala | Asn | Val | Thr | Cys | Arg | Leu | Thr | Ala |
|     |     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Glu | Leu | Leu | Gln | Asp | Pro | Phe | Leu | Gln | Asp | Asp | Asn | Met | Asp | Gly |
|     |     |     |     | 275 |     |     |     | 280 |     |     |     | 285 |     |     |     |
| Phe | Val | Met | Arg | Pro | Ile | Asp | Tyr | Tyr | Asn | Gly | Tyr | Asp | Glu | Thr | Gly |
|     |     |     |     | 290 |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Val | Phe | Leu | Arg | His | Pro | Leu | Ile | Asp | Asp | Pro | Leu | Tyr | His | Asp | Gln |
|     |     |     |     | 305 |     |     | 310 |     |     |     | 315 |     |     |     | 320 |
| Phe | Glu | Ser | Ser | Gln | Ile | Cys | Glu | Ile | Asp | Leu | Phe | Ala | Asn | Asp | Asp |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Glu | Asp | His | Val | Asp | Ile | Ser | Ile | Lys | Gly | Lys | Arg | Asn | Gly | Asp | Asp |
|     |     |     |     | 340 |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gly | Ile | Phe | Leu | Arg | Leu | Arg | Ile | Ser | Asp | Ala | Glu | Gly | Arg | Ile | Arg |
|     |     |     |     | 355 |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Asn | Ile | Tyr | Phe | Pro | Phe | Glu | Thr | Ala | Ile | Asp | Thr | Ala | Trp | Ser | Val |
|     |     |     |     | 370 |     |     | 375 |     |     |     |     | 380 |     |     |     |

Ala Val Glu Met Val Ser Glu Leu Asp Ile Thr Asn Gln Asp Val Ala  
385 390 395 400  
Lys Ile Ala Glu Met Ile Asp Ala Glu Ile Ala Leu Val Pro Asp  
405 410 415  
Trp Lys Asn Asp Thr Glu Ser Ser Gln Asn Val Asn Asn Asn Lys Asn  
420 425 430  
Asn Asn Thr Ala Gly Phe Cys Gly Glu Cys Ala Ser Asn Gly Tyr Ile  
435 440 445  
Gln Glu Thr Val Ser Ser Gly Glu Lys Ser His His Asn His His Glu  
450 455 460  
Phe Asp Ser Ser Glu Asp Lys Ser Cys Ser Ser Val His Gly Arg Phe  
465 470 475 480  
Ala Asp Met Trp Gly Leu Arg Glu Ser Tyr Ser Asp Asp Gly Glu Lys  
485 490 495  
Gln Ser Ser Arg Lys Val Arg Ser Gly Arg Trp Ser Glu Asn Glu Met  
500 505 510  
Arg Arg Glu Leu Arg Trp Leu Lys Ala Arg His Lys Ile Gln Leu Met  
515 520 525  
Lys Met Arg Gly Gln Thr Ile Cys Glu Thr Pro Ile Glu Ile Ser Leu  
530 535 540  
Thr Pro Gly Thr Ser Val Ser Leu Pro Leu Leu Tyr Arg Ala Ile Ser  
545 550 555 560  
Leu Pro Val Asp Ala Val Asp Met  
565

(2) INFORMATION FOR SEQ ID NO:2343:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 483 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..483

(D) OTHER INFORMATION: / Ceres Seq. ID 1572650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2343:

Met Lys Phe Tyr Thr Ser Trp Val Asp Thr Asn Asn Leu Ser Ile Asn  
1 5 10 15  
Phe Val Thr Glu Leu Phe Thr Ser Gly Thr Leu Arg Gln Tyr Arg Leu  
20 25 30  
Arg His Arg Arg Val Asn Ile Arg Ala Val Lys Gln Trp Cys Lys Gln  
35 40 45  
Ile Leu Lys Gly Leu Leu Tyr Leu His Ser Arg Ser Pro Pro Ile Ile  
50 55 60  
His Arg Asp Leu Lys Cys Asp Asn Ile Phe Ile Asn Gly Asn Gln Gly  
65 70 75 80  
Glu Val Lys Ile Gly Asp Leu Gly Leu Ala Ile Leu Arg Lys Ser  
85 90 95  
His Ala Val Arg Cys Val Gly Thr Pro Glu Phe Met Ala Pro Glu Val  
100 105 110  
Tyr Asp Glu Glu Tyr Asn Glu Leu Val Asp Val Tyr Ala Phe Gly Met  
115 120 125  
Cys Val Leu Glu Met Val Thr Phe Asp Tyr Pro Tyr Ser Glu Cys Thr  
130 135 140  
His Pro Ala Gln Ile Tyr Lys Lys Val Thr Ser Gly Lys Lys Pro Glu  
145 150 155 160  
Ala Phe Tyr Leu Val Lys Asp Pro Glu Val Arg Glu Phe Val Glu Lys  
165 170 175  
Cys Leu Ala Asn Val Thr Cys Arg Leu Thr Ala Leu Glu Leu Leu Gln  
180 185 190  
Asp Pro Phe Leu Gln Asp Asp Asn Met Asp Gly Phe Val Met Arg Pro

**SECRET**

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 931 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(A) NAME/KEY: -

(B) LOCATION: 1..931

(D) OTHER INFORMATION: / Ceres Seq. ID 1572662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2344:

|              |             |             |            |            |            |     |
|--------------|-------------|-------------|------------|------------|------------|-----|
| aagatgtgggga | cgaaaattgag | ctggatatag  | aagctgtcga | caatgagact | ctatgggagc | 60  |
| ttgctagcttt  | tgtgcagaac  | tacaagaata  | tggctagcaa | aatcacaagc | caagggttta | 120 |
| cgaggaaagc   | gtcacaatcca | cttaggaaga  | tggcttcggt | agcagaaatg | ggtagtgcgg | 180 |
| caatgagaac   | aatgagagga  | gatcgacggg  | aagaaagtgt | tgcactgcgt | gaggcacata | 240 |
| cgaatcgaag   | ttatccatct  | stagagatgt  | aaagagatgg | gtactgcagt | tgcagttcgt | 300 |
| gctagtattg   | gtttcagttc  | ttcaggtcagt | tcaggttcta | gtgtgggtag | ttcttcgtct | 360 |
| agctagcttag  | ggtcagggtg  | gagtcacata  | ggtagtgatt | ctgatgcaga | tagtgttcaa | 420 |
| tgtccatttt   | tggaaagcaa  | agagccccaa  | tggtaaaaat | atttgggaat | ttaacgggtt | 480 |
| attctgtctc   | gaagttaact  | gaactggttag | ctgaggggtg | aaagggaaga | atgaacggga | 540 |
| aaactgagga   | aaaggatttg  | ttttttcttc  | cgatgataaa | cttaggaaga | agatgtagtt | 600 |
| agaagatmaa   | aattgtaatg  | atagatagata | agagaatgtc | agtttaagca | agaagaagag | 660 |
| tttcgttatt   | ataactcttt  | gcatttaaga  | gttgtttagt | gtattttgta | gatctgaac  | 720 |



Met Gln Gly Gly Gly Gly Arg Asp Pro Phe Gly Gly Gly Phe Gly Gly  
1 5 10 15  
Pro Phe Gly Gly Phe Gly Gly Gly Ser Phe Gly Gly Phe Gly Arg Gly  
20 25 30

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Ser Phe Gly Gly Phe Gly Gly Pro Asn Gly Pro Pro Ser Leu Met Ser
 35 40 45
Asn Phe Phe Gly Gly Arg Asp Pro Phe Asp Asp Pro Phe Phe Thr Gln
 50 55 60
Pro Phe Gly Gly Gly Met Phe Gln Ser Asn Phe Phe Gly Pro Ser Met
 65 70 75 80
Asn Pro Phe Ala Glu Met His Arg Leu Pro Gln Gly Phe Ile Glu Asn
 85 90 95
Asn Gln Pro Pro Gly Pro Ser Arg Ser Arg Gly Pro Val Ile Glu Glu
 100 105 110
Ile Asp Ser Asp Asp Glu Lys Glu Gly Glu Gly Asp Lys Glu Lys Lys
 115 120 125
Gly Ser Leu Gly Lys His Gly Arg Ser Ser Ser Glu Ala Glu Thr Glu
 130 135 140
Asp Ala Arg Val Arg Glu Arg Arg Asn Arg Gln Met Gln Ser Met Asn
 145 150 155 160
Val Asn Ala Glu Arg Arg Asn Arg Glu Met Gln Asn Met Asn Val Asn
 165 170 175
Ala Glu Arg Arg Asn Pro Gln Met Gln Asn Met Asn Val Asn Ala Met
 180 185 190
Val Asn Asn Gly Gln Trp Gln Pro Gln Thr Gly Ser Tyr Ser Phe Gln
 195 200 205
Ser Ser Thr Val Thr Tyr Gly Gly Gln Asn Gly Asn Tyr Tyr Thr Ser
 210 215 220
Ser Lys Thr Arg Arg Thr Gly Ser Asp Gly Leu Thr Leu Glu Glu Ser
 225 230 235 240
Arg Glu Ala Asn Thr Ala Thr Arg Glu Ala Ala His Met Ile Ser Arg
 245 250 255
Gly Leu His Asn Lys Gly His Thr Val Ala Arg Lys Leu Asn Ser Asp
 260 265 270
Gly Arg Val Asp Thr Thr Gln Thr Leu His Asn Leu Asn Glu Asp Glu
 275 280 285
Leu Ala Gly Phe Glu Gln Ser Trp Ser Gly Asn Ala Arg Arg Gln Met
 290 295 300
Gln Leu Pro Ser Arg Ser Gly Ser Phe Gly Ser Gly Leu Val Asn Arg
 305 310 315 320
Glu Gln Pro Met Leu Leu Pro Xaa Thr Asp Pro Ser Pro Ser His Ala
 325 330 335
Arg Ala Glu Ser Ser Arg Arg Pro Xaa Ala Ala Met Asn Val Arg Gly
 340 345 350
His Gly Thr Asn
 355

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(2) INFORMATION FOR SEQ ID NO:2350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..310
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2350:

```

Met Ser Asn Phe Phe Gly Gly Arg Asp Pro Phe Asp Asp Pro Phe Phe
1 5 10 15
Thr Gln Pro Phe Gly Gly Gly Met Phe Gln Ser Asn Phe Phe Gly Pro
 20 25 30
Ser Met Asn Pro Phe Ala Glu Met His Arg Leu Pro Gln Gly Phe Ile
 35 40 45
Glu Asn Asn Gln Pro Pro Gly Pro Ser Arg Ser Arg Gly Pro Val Ile

```

|                                                                     |     |     |
|---------------------------------------------------------------------|-----|-----|
| 50                                                                  | 55  | 60  |
| Glu Glu Ile Asp Ser Asp Asp Glu Lys Glu Gly Glu Gly Asp Lys Glu     |     |     |
| 65                                                                  | 70  | 75  |
| Lys Lys Gly Ser Leu Gly Lys His Gly Arg Ser Ser Ser Glu Ala Glu     |     |     |
|                                                                     | 85  | 90  |
| Thr Glu Asp Ala Arg Val Arg Glu Arg Arg Asn Arg Gln Met Gln Ser     |     |     |
|                                                                     | 100 | 105 |
| Met Asn Val Asn Ala Glu Arg Arg Asn Arg Glu Met Gln Asn Met Asn     |     |     |
|                                                                     | 115 | 120 |
| Val Asn Ala Glu Arg Arg Asn Pro Gln Met Gln Asn Met Asn Val Asn     |     |     |
|                                                                     | 130 | 135 |
| Ala Met Val Asn Asn Gly Gln Trp Gln Pro Gln Thr Gly Ser Tyr Ser     |     |     |
| 145                                                                 | 150 | 155 |
| Phe Gln Ser Ser Thr Val Thr Tyr Gly Gly Gln Asn Gly Asn Tyr Tyr     |     |     |
|                                                                     | 165 | 170 |
| Thr Ser Ser Lys Thr Arg Arg Thr Gly Ser Asp Gly Leu Thr Leu Glu     |     |     |
|                                                                     | 180 | 185 |
| Glu Ser Arg Glu Ala Asn Thr Ala Thr Arg Glu Ala Ala His Met Ile     |     |     |
|                                                                     | 195 | 200 |
| Ser Arg Gly Leu His Asn Lys Lys Gly His Thr Val Ala Arg Lys Leu Asn |     |     |
|                                                                     | 210 | 215 |
| Ser Asp Gly Arg Val Asp Thr Thr Gln Thr Leu His Asn Leu Asn Glu     |     |     |
| 225                                                                 | 230 | 235 |
| Asp Glu Leu Ala Gly Phe Glu Gln Ser Trp Ser Gly Asn Ala Arg Arg     |     |     |
|                                                                     | 245 | 250 |
| Gln Met Gln Leu Pro Ser Arg Ser Gly Ser Phe Gly Ser Gly Leu Val     |     |     |
|                                                                     | 260 | 265 |
| Asn Arg Glu Gln Pro Met Leu Leu Pro Xaa Thr Asp Pro Ser Pro Ser     |     |     |
|                                                                     | 275 | 280 |
| His Ala Arg Ala Glu Ser Ser Arg Arg Pro Xaa Ala Ala Met Asn Val     |     |     |
|                                                                     | 290 | 295 |
| Arg Gly His Gly Thr Asn                                             |     | 300 |
| 305                                                                 | 310 |     |

(2) INFORMATION FOR SEQ ID NO:2351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..287
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2351:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| Met Phe Gln Ser Asn Phe Phe Gly Pro Ser Met Asn Pro Phe Ala Glu     |     |
| 1                                                                   | 5   |
| Met His Arg Leu Pro Gln Gly Phe Ile Glu Asn Asn Gln Pro Pro Gly     |     |
|                                                                     | 20  |
| Pro Ser Arg Ser Arg Gly Pro Val Ile Glu Glu Ile Asp Ser Asp Asp     |     |
|                                                                     | 35  |
| Glu Lys Glu Gly Glu Gly Asp Lys Glu Lys Lys Gly Ser Leu Gly Lys     |     |
|                                                                     | 50  |
| His Gly Arg Ser Ser Ser Ser Glu Ala Glu Thr Glu Asp Ala Arg Val Arg |     |
| 65                                                                  | 70  |
| Glu Arg Arg Asn Arg Gln Met Gln Ser Met Asn Val Asn Ala Glu Arg     |     |
|                                                                     | 85  |
| Arg Asn Arg Glu Met Gln Asn Met Asn Val Asn Ala Glu Arg Arg Asn     |     |
|                                                                     | 100 |
| Pro Gln Met Gln Asn Met Asn Val Asn Ala Met Val Asn Asn Gly Gln     |     |
|                                                                     | 115 |
|                                                                     | 120 |
|                                                                     | 125 |



Trp Gln Pro Gln Thr Gly Ser Tyr Ser Phe Gln Ser Ser Thr Val Thr  
130 135 140  
Tyr Gly Gly Gln Asn Gly Asn Tyr Tyr Thr Ser Ser Lys Thr Arg Arg  
145 150 155 160  
Thr Gly Ser Asp Gly Leu Thr Leu Glu Glu Ser Arg Glu Ala Asn Thr  
165 170 175  
Ala Thr Arg Glu Ala Ala His Met Ile Ser Arg Gly Leu His Asn Lys  
180 185 190  
Gly His Thr Val Ala Arg Lys Leu Asn Ser Asp Gly Arg Val Asp Thr  
195 200 205  
Thr Gln Thr Leu His Asn Leu Asn Glu Asp Glu Leu Ala Gly Phe Glu  
210 215 220  
Gln Ser Trp Ser Gly Asn Ala Arg Arg Gln Met Gln Leu Pro Ser Arg  
225 230 235 240  
Ser Gly Ser Phe Gly Ser Gly Leu Val Asn Arg Glu Gln Pro Met Leu  
245 250 255  
Leu Pro Xaa Thr Asp Pro Ser Pro Ser His Ala Arg Ala Glu Ser Ser  
260 265 270  
Arg Arg Pro Xaa Ala Ala Met Asn Val Arg Gly His Gly Thr Asn  
275 280 285

(2) INFORMATION FOR SEQ ID NO:2352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 629 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..629
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2352:

|            |             |             |            |             |             |     |
|------------|-------------|-------------|------------|-------------|-------------|-----|
| tccacacttt | catatccaca  | aaataaaata  | aaaaaatggc | ctcaagagc   | tcaaccacca  | 60  |
| tttccctcat | catecatcctc | ctcatcagcc  | tcgcagaagc | aaatctctta  | agctcgccca  | 120 |
| caccgaccaa | caacttttggc | tcattgtccca | gaacccatt  | gcaactagcc  | gtatgtgccca | 180 |
| acgtccttgg | cctagccaat  | gttacagctg  | gcgacccag  | agcacgacag  | tgttgcactg  | 240 |
| ccctcaatgg | cctcactaat  | gttcaagtaa  | ccgattgtct | ctgttttacc  | tccaggccga  | 300 |
| ttccgttggt | tttcggtatt  | gatgtggccg  | ttagagaaat | cttttttgc   | tgcaataggg  | 360 |
| tttttccat  | cggtttccag  | tgtccaccac  | cacagtaact | actacttaat  | tcccctaaat  | 420 |
| aagagcccta | tcgggtgttt  | ccttgcaacta | taagtttgc  | ggtaccacaaa | gtatgggttt  | 480 |
| atctattaat | gttttacagt  | gttggtgtgt  | gtttcgttgt | tgattagaac  | gtaattataa  | 540 |
| ggactatcga | tgcttactaa  | aaagttgtta  | agcatatcta | ttaatgtcta  | Mtgaagaata  | 600 |
| atattaaata | aagtataaca  | ctttgtgtc   |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2353:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Lys | Ser | Ser | Thr | Thr | Ile | Ser | Leu | Ile | Ile | Ile | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Ser | Leu | Ala | Glu | Ala | Asn | Leu | Leu | Ser | Ser | Pro | Thr | Pro | Thr | Asn |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asn | Phe | Gly | Ser | Cys | Pro | Arg | Asn | Pro | Leu | Gln | Leu | Gly | Val | Cys | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Asn Val Leu Gly Leu Ala Asn Val Thr Ala Gly Asp Pro Arg Ala Arg  
50 55 60  
Gln Cys Cys Thr Ala Leu Asn Gly Leu Thr Asn Val Gln Val Thr Asp  
65 70 75 80  
Cys Leu Cys Phe Ile Phe Arg Pro Ile Pro Leu Val Phe Gly Ile Asp  
85 90 95  
Val Ala Val Arg Glu Ile Phe Phe Ala Cys Asn Arg Val Phe Pro Ile  
100 105 110  
Gly Phe Gln Cys Pro Pro Pro Gln  
115 120

(2) INFORMATION FOR SEQ ID NO:2354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..954
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2354:

|             |             |             |             |             |            |     |
|-------------|-------------|-------------|-------------|-------------|------------|-----|
| acattaccgaa | aagtactagt  | ttattggtgt  | tattcatcgc  | tgctcaagggt | ggcaaaccaa | 60  |
| ggagaacaag  | aagagtcag   | ggccaatgag  | cotgagggta  | tcaaatcagt  | gattgatgac | 120 |
| atctacaatt  | ttgaagacga  | cctgtggtt   | gatagattca  | atagatttgg  | aacggagatg | 180 |
| tttgccatgg  | ttctggcctt  | gacacagggt  | gtttctgctc  | gctctcagac  | tgaagctgaa | 240 |
| gggtctcaact | cttcttcttc  | ctcggctgga  | cataagagag  | aatggcttgg  | aatcgattct | 300 |
| gttctctattc | ctctcatcatt | tgctctgtgt  | gactcttcac  | ataatccgat  | cgaagaatcc | 360 |
| ataagaaagg  | catttccaga  | ggaagcaagg  | gagaaaaaaa  | ggaggtagac  | aggagtaggt | 420 |
| cagagaccat  | ggggcaaatg  | ggcagctgag  | atacgtgatc  | cacatagagc  | cgctaRggtt | 480 |
| tggctcgggg  | cgtttgatac  | agcggaggcc  | goggtctagag | cctacgacga  | ggctgcactc | 540 |
| cggttccgtg  | gaaataaagg  | aaagctaaat  | ttcccagagg  | atgtaaggat  | ttctctcctt | 600 |
| ccccctcttc  | ttcttctgtt  | accagctgac  | acggtggcga  | ataaagcaga  | agaggatctg | 660 |
| ataaaattatt | ggagtttata  | aaagttgttg  | caaagtctag  | gccaacggtc  | atttctcgag | 720 |
| cgaggacaag  | aagagagtaa  | taacataatt  | gaacatttcac | caatggaaca  | acctctgcct | 780 |
| ccttcaagtt  | ctgggtccaa  | ttctcttaatt | tttctctgac  | cttctctacc  | taatacatag | 840 |
| tttctacttt  | attaaagctc  | tacaaataca  | attaaataca  | tagctaaatg  | aaaatgattt | 900 |
| ctttgtctgt  | ataccttctt  | aagtgtctaaa | caatatattg  | tactctttgt  | ttcc       |     |

(2) INFORMATION FOR SEQ ID NO:2355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..279
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2355:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Leu | Arg | Lys | Val | Leu | Val | Tyr | Trp | Cys | Tyr | Ser | Ser | Leu | Leu | Lys |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |
| Val | Ala | Asn | Gln | Gly | Glu | Gln | Glu | Glu | Ser | Arg | Ala | Asn | Glu | Pro | Glu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Gly | Ile | Lys | Ser | Val | Ile | Asp | Asp | Ile | Tyr | Asn | Phe | Glu | Asp | Asp | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Val | Asp | Arg | Phe | Asn | Arg | Phe | Gly | Thr | Glu | Met | Ser | Ala | Met | Val |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ser | Ala | Leu | Thr | Gln | Val | Val | Ser | Ala | Arg | Ser | Gln | Thr | Glu | Ala | Glu |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Gly | Ala | His | Ser | Ser | Ser | Ser | Ala | Gly | His | Lys | Arg | Glu | Trp | Leu |     |

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(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..220

- (D) OTHER INFORMATION: / Ceres Seq. ID 1572752

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ala | Met | Val | Ser | Ala | Leu | Thr | Gln | Val | Val | Ser | Ala | Arg | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gln | Thr | Glu | Ala | Glu | Gly | Ala | His | Ser | Ser | Ser | Ser | Ser | Ala | Gly | His |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Arg | Glu | Trp | Leu | Gly | Ile | Asp | Ser | Val | Pro | Ile | Pro | Ser | Ser | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Arg | Val | Asp | Ser | Ser | His | Asn | Pro | Ile | Glu | Glu | Ser | Ile | Arg | Lys |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Phe | Pro | Glu | Glu | Ala | Arg | Glu | Lys | Lys | Arg | Glu | Tyr | Arg | Gly | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Gln | Arg | Pro | Trp | Gly | Lys | Trp | Ala | Ala | Glu | Ile | Arg | Asp | Pro | His |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | Ala | Ala | Xaa | Val | Trp | Leu | Gly | Thr | Phe | Asp | Thr | Ala | Glu | Ala | Ala |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Arg | Ala | Tyr | Asp | Glu | Ala | Ala | Leu | Arg | Phe | Arg | Gly | Asn | Lys | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Leu | Asn | Phe | Pro | Glu | Asp | Val | Arg | Ile | Leu | Pro | Pro | Pro | Pro | Pro |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Leu | Arg | Ser | Pro | Ala | Asp | Thr | Val | Ala | Asn | Lys | Ala | Glu | Glu | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Ile | Asn | Tyr | Trp | Ser | Tyr | Thr | Lys | Leu | Leu | Gln | Ser | Ile | Gly | Gln |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | Ser | Phe | Leu | Glu | Arg | Gly | Gln | Glu | Glu | Ser | Asn | Asn | Ile | Phe | Glu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

His Ser Pro Met Glu Gln Pro Leu Pro Pro Ser Ser Ser Gly Pro Ser  
195 200 205  
Ser Ser Asn Phe Pro Ala Pro Ser Leu Pro Asn Thr  
210 215 220

(2) INFORMATION FOR SEQ ID NO:2357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1572753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2357:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ser | Ala | Leu | Thr | Gln | Val | Val | Ser | Ala | Arg | Ser | Gln | Thr | Glu |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Ala | Glu | Gly | Ala | His | Ser | Ser | Ser | Ser | Ser | Ala | Gly | His | Lys | Arg | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp | Leu | Gly | Ile | Asp | Ser | Val | Pro | Ile | Pro | Ser | Ser | Phe | Ala | Arg | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Asp | Ser | Ser | His | Asn | Pro | Ile | Glu | Glu | Ser | Ile | Arg | Lys | Ala | Phe | Pro |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Glu | Ala | Arg | Glu | Lys | Lys | Arg | Arg | Tyr | Arg | Gly | Val | Arg | Gln | Arg |
|     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Trp | Gly | Lys | Trp | Ala | Ala | Glu | Ile | Arg | Asp | Pro | His | Arg | Ala | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Xaa | Val | Trp | Leu | Gly | Thr | Phe | Asp | Thr | Ala | Glu | Ala | Ala | Ala | Arg | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Asp | Glu | Ala | Ala | Leu | Arg | Phe | Arg | Gly | Asn | Lys | Ala | Lys | Leu | Asn |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Phe | Pro | Glu | Asp | Val | Arg | Ile | Leu | Pro | Pro | Pro | Pro | Pro | Leu | Leu | Arg |
|     |     |     | 130 |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Ser | Pro | Ala | Asp | Thr | Val | Ala | Asn | Lys | Ala | Glu | Glu | Asp | Leu | Ile | Asn |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Tyr | Trp | Ser | Tyr | Thr | Lys | Leu | Leu | Gln | Ser | Ser | Gly | Gln | Arg | Ser | Phe |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Leu | Glu | Arg | Gly | Gln | Glu | Ser | Asn | Asn | Ile | Phe | Glu | His | Ser | Ser | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Met | Glu | Gln | Pro | Leu | Pro | Pro | Ser | Ser | Ser | Gly | Pro | Ser | Ser | Ser | Asn |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Phe | Pro | Ala | Pro | Ser | Leu | Pro | Asn | Thr |     |     |     |     |     |     |     |
|     |     |     | 210 |     |     | 215 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1072 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1072

(D) OTHER INFORMATION: / Ceres Seq. ID 1572762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2358:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| acacatctca | ctgctcacta | ctctcactgt | aatcccttag | atcttctttt | caaatctcaa | 60  |
| tggcgctcgg | tgatgttgag | tatcggtgct | tcgttgagg  | tctagcatgg | gccactgatg | 120 |
| acagagctct | tgagactgcc | tctgctcaat | acggcgacgt | tattgattcc | aaggtctgtt | 180 |
| acacgcagag | atcgactacc | gagtgatata | gatgatctca | tctcgaagg  | atctgttccg | 240 |
| atcttgtgtt | tctctgttac | ttgattcgat | tactctgtta | ctattctcgt | tctttgttac | 300 |

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| tactactact  | actactgtta  | cttgatattt | cccaaatcgg  | tacgttcac   | ttcctgcttc  | 360  |
| tgtgagcccg  | gagatcgatc  | ggattttttt | gtatttttga  | tattttgtgt  | agatcataat  | 420  |
| gctttttgtt  | agttttgttg  | gattgttttg | ctgatctggg  | ttttgtatta  | tttggaatac  | 480  |
| agatcattaa  | cgatcgtgag  | actggaagat | caaggggatt  | cggattcgtc  | acctccaagg  | 540  |
| atgagaaagc  | catgaaggat  | gcgattgagg | gaatgaacgg  | acaagatctc  | gatggccgta  | 600  |
| gcatacactgt | taacgaggct  | cagtcacgag | gaagcgggtg  | cgccggaggc  | caccgtggag  | 660  |
| gtggtggcgg  | tggatacgcg  | agcggcggtg | gtggagggtta | ctccggtgga  | ggtggtagct  | 720  |
| acggaggttg  | cggcggttaga | cgcgagggtg | gaggaggata  | cagcggcgcc  | ggcggttaact | 780  |
| cctcaagagg  | tgggtgtggc  | ggaagctacg | gtggtggaag  | acgtgaggga  | ggaggaggat  | 840  |
| acgggtgttg  | tgaaggagga  | ggttacggag | gaagcgggtg  | tggtggagga  | tggtaattcc  | 900  |
| tttaattagg  | tttgggatta  | ccaatgaatg | ttctctctct  | cgcttgttat  | gcttctactt  | 960  |
| ggttttgtgt  | gttctctatt  | ttgttctggt | tctgctttag  | atttgatga   | acagttcgtg  | 1020 |
| attaggtatt  | ttgtatctct  | gaaacgtaat | gttaagtcac  | ttgtcaattct | cc          |      |

(2) INFORMATION FOR SEQ ID NO:2359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2359:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Asp | Ala | Ile | Glu | Gly | Met | Asn | Gly | Gln | Asp | Leu | Asp | Gly | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ile | Thr | Val | Asn | Glu | Ala | Gln | Ser | Arg | Gly | Ser | Gly | Gly | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Gly | His | Arg | Gly | Gly | Gly | Gly | Gly | Tyr | Arg | Ser | Gly | Gly | Gly | Gly | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Gly | Tyr | Ser | Gly | Gly | Gly | Ser | Tyr | Gly | Gly | Gly | Gly | Gly | Arg | Arg |     |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Gly | Gly | Gly | Gly | Tyr | Ser | Gly | Gly | Gly | Tyr | Ser | Ser | Arg | Gly |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Gly | Gly | Gly | Ser | Tyr | Gly | Gly | Gly | Arg | Glu | Gly | Gly | Gly | Gly |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Tyr | Gly | Gly | Gly | Glu | Gly | Gly | Gly | Tyr | Gly | Gly | Ser | Gly | Gly | Gly | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Gly Trp

(2) INFORMATION FOR SEQ ID NO:2360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2360:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Gly | Gln | Asp | Leu | Asp | Gly | Arg | Ser | Ile | Thr | Val | Asn | Glu | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Ser | Arg | Gly | Ser | Gly | Gly | Gly | Gly | Gly | His | Arg | Gly | Gly | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Gly | Tyr | Arg | Ser | Gly | Gly | Gly | Gly | Gly | Tyr | Ser | Gly | Gly | Gly | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Ser | Tyr | Gly | Gly | Gly | Gly | Gly | Arg | Arg | Glu | Gly | Gly | Gly | Gly | Tyr | Ser |
|     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |

Gly Gly Gly Gly Tyr Ser Ser Arg Gly Gly Gly Gly Ser Tyr Gly  
65 70 75 80  
Gly Gly Arg Arg Glu Gly Gly Gly Tyr Gly Gly Glu Gly Gly  
85 90 95  
Gly Tyr Gly Gly Ser Gly Gly Gly Gly Trp  
100 105

(2) INFORMATION FOR SEQ ID NO:2361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1572765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2361:

Met Ala Val Ala Ser Leu Leu Thr Arg Leu Ser His Glu Glu Ala Val  
1 5 10 15  
Ala Ala Glu Ala Thr Val Glu Val Val Ala Val Asp Thr Ala Ala Ala  
20 25 30  
Val Val Glu Val Thr Pro Val Glu Val Val Ala Thr Glu Val Ala Ala  
35 40 45  
Val Asp Ala Arg Val Glu Glu Asp Thr Ala Ala Ala Val Thr Pro  
50 55 60  
Gln Glu Val Val Val Ala Glu Ala Thr Val Val Glu Asp Val Arg Glu  
65 70 75 80  
Glu Glu Asp Thr Val Val Lys Glu Glu Val Thr Glu Glu Ala Val  
85 90 95  
Val Val Glu Asp Gly Asn Ser Phe Asn  
100 105

(2) INFORMATION FOR SEQ ID NO:2362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 629 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..629

(D) OTHER INFORMATION: / Ceres Seq. ID 1572774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2362:

ggtttctctag ggtttcagcg accagactca aacagagagt gaaaatgccg gcgggacacg 60  
gagtgagggc gagaacaaga gatctgttcg cgagaccatt gaggagaag gggtatatc 120  
cactctccac ttacctcaga acctccaagg tcggcgatta cgtcgatgct aagggttaag 180  
gagctatcca caagggtatg cctcataagt tctaccatgg tegtactggt cgcactctgga 240  
atgtcactaa gcgtgccgtt ggtgttgaag tcaacaaaca gattgggaac agaatacataa 300  
ggaagaggat acatgtgcgt gtggagcatg tgcaacagtc aaggtgtgct gaggagtta 360  
aactcagaaa gaagcagaac gatgtgctta aggcgtatgc taaagccaga ggagagacta 420  
tcagcaccaa gagacagcct aaaggtccta aaccgggttt catggctgaa ggtatgacat 480  
tggagactgt cactccatt ccttacgatg ttgtcaacga tctcaagggt ggttattgag 540  
tttttccat tttattatca ttctttactc agaatttttg cacttgcttt tttaatgatg 600  
ttttgtatc aattaagact aattBStct

(2) INFORMATION FOR SEQ ID NO:2363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1572775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2363:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ser | Arg | Val | Ser | Ala | Thr | Arg | Leu | Lys | Gln | Arg | Val | Lys | Met | Pro |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Gly | His | Gly | Val | Arg | Ala | Arg | Thr | Arg | Asp | Leu | Phe | Ala | Arg | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Phe | Arg | Lys | Lys | Gly | Tyr | Ile | Pro | Leu | Ser | Thr | Tyr | Leu | Arg | Thr | Phe |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Lys | Val | Gly | Asp | Tyr | Val | Asp | Val | Lys | Val | Asn | Gly | Ala | Ile | His | Lys |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Gly | Met | Pro | His | Lys | Phe | Tyr | His | Gly | Arg | Thr | Gly | Arg | Ile | Trp | Asn |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     |     | 75  |     |
| Val | Thr | Lys | Arg | Ala | Val | Gly | Val | Glu | Val | Asn | Lys | Gln | Ile | Gly | Asn |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | Ile | Ile | Arg | Lys | Arg | Ile | His | Val | Arg | Val | Glu | His | Val | Gln | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Ser | Arg | Cys | Ala | Glu | Glu | Phe | Lys | Leu | Arg | Lys | Lys | Gln | Asn | Asp | Val |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Leu | Lys | Ala | Asp | Ala | Lys | Ala | Arg | Gly | Glu | Thr | Ile | Ser | Thr | Lys | Arg |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |
| Gln | Pro | Lys | Gly | Pro | Lys | Pro | Gly | Phe | Met | Val | Glu | Gly | Met | Thr | Leu |
|     |     |     | 145 |     |     |     |     | 150 |     |     |     |     |     | 155 |     |
| Glu | Thr | Val | Thr | Pro | Ile | Pro | Tyr | Asp | Val | Val | Asn | Asp | Leu | Lys | Gly |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |

Gly Tyr

(2) INFORMATION FOR SEQ ID NO:2364:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1572776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2364:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Ala | Gly | His | Gly | Val | Arg | Ala | Arg | Thr | Arg | Asp | Leu | Phe | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Pro | Phe | Arg | Lys | Lys | Gly | Tyr | Ile | Pro | Leu | Ser | Thr | Tyr | Leu | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Thr | Phe | Lys | Val | Gly | Asp | Tyr | Val | Asp | Val | Lys | Val | Asn | Gly | Ala | Ile |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| His | Lys | Gly | Met | Pro | His | Lys | Phe | Tyr | His | Gly | Arg | Thr | Gly | Arg | Ile |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Trp | Asn | Val | Thr | Lys | Arg | Ala | Val | Gly | Val | Glu | Val | Asn | Lys | Gln | Ile |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     |     | 75  |     |
| Gly | Asn | Arg | Ile | Ile | Arg | Lys | Arg | Ile | His | Val | Arg | Val | Glu | His | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gln | Gln | Ser | Arg | Cys | Ala | Glu | Glu | Phe | Lys | Leu | Arg | Lys | Lys | Gln | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Asp | Val | Leu | Lys | Ala | Asp | Ala | Lys | Ala | Arg | Gly | Glu | Thr | Ile | Ser | Thr |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Lys | Arg | Gln | Pro | Lys | Gly | Pro | Lys | Pro | Gly | Phe | Met | Val | Glu | Gly | Met |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |

Thr Leu Glu Thr Val Thr Pro Ile Pro Tyr Asp Val Val Asn Asp Leu

145 150 155 160  
Lys Gly Gly Tyr

(2) INFORMATION FOR SEQ ID NO:2365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2365:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | His | Lys | Phe | Tyr | His | Gly | Arg | Thr | Gly | Arg | Ile | Trp | Asn | Val |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Thr | Lys | Arg | Ala | Val | Gly | Val | Glu | Val | Asn | Lys | Gln | Ile | Gly | Asn | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ile | Arg | Lys | Arg | Ile | His | Val | Arg | Val | Glu | His | Val | Gln | Gln | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Cys | Ala | Glu | Glu | Phe | Lys | Leu | Arg | Lys | Lys | Gln | Asn | Asp | Val | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Lys | Ala | Asp | Ala | Lys | Ala | Arg | Gly | Glu | Thr | Ile | Ser | Thr | Lys | Arg | Gln |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |
| Pro | Lys | Gly | Pro | Lys | Pro | Gly | Phe | Met | Val | Glu | Gly | Met | Thr | Leu | Glu |
|     |     |     |     |     |     |     | 85  |     |     |     | 90  |     |     | 95  |     |
| Thr | Val | Thr | Pro | Ile | Pro | Tyr | Asp | Val | Val | Asn | Asp | Leu | Lys | Gly | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Tyr

(2) INFORMATION FOR SEQ ID NO:2366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1472
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2366:

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| aaaaaagtca  | atcatatcaa  | atccaaaatc  | ctccagatg  | tttttatcat  | cttcttcttc  | 60   |
| ctgaagattt  | gatttcattt  | tctctctttt  | cagatcccta | ttctcatggc  | ttctggattc  | 120  |
| tactgggtgc  | atagtttgtt  | cagattcgtt  | tgggtttccg | attcaatctc  | ttgccttgat  | 180  |
| tgcgacggtg  | gttttctcga  | actcatccaa  | gagcctctcg | atttcacacc  | ttccgattcc  | 240  |
| ttcaccacca  | ccaccaccac  | tcaacatcgc  | agccccaact | gcttccctcc  | tctctctctc  | 300  |
| tctctctcca  | ccccatccgc  | ttctatgcac  | gccgataaca | gtcccaactc  | taccatcggt  | 360  |
| actcgtacac  | gaagcaatcg  | atctcctaatt | ccagttattg | ttctccgtgg  | atctcgtcgt  | 420  |
| gctccttctt  | ctgatgttgt  | ttccgaaggt  | ttagatcgat | ctgcttttca  | gatgtattac  | 480  |
| gatgatggta  | ctgattctgt  | tcttagacct  | ttaccaccga | gtatgactga  | gtttttgtta  | 540  |
| ggttctggat  | ttgatcgttt  | gttagatcag  | atctctcaga | tcgagcttaa  | caccaatcgg  | 600  |
| aatctctggt  | cttgtgaaca  | tccaccggct  | tctaaatcgg | ccattgaagc  | tttgccctcg  | 660  |
| attgaaatcg  | atccgactca  | tctcttatcg  | gattctcaat | ctcattgcgc  | gttttgcaaa  | 720  |
| gagaaatttc  | ttttgaaatc  | atctgctcgc  | gagatgcctt | gtaatcacat  | ctatcatcct  | 780  |
| gattgtattc  | ttccttggtt  | tcggaatcgt  | aactcttgtc | cggtttgcgc  | tcattgageta | 840  |
| ccggcggagg  | atctcaccga  | cggaaaccgg  | gctgctttga | ctgctgtttac | cgctactcga  | 900  |
| gaggaaagagg | aagactcagc  | tcgcgggtta  | acgatttgga | ggttacacgg  | tgaggatttc  | 960  |
| gctgtaggga  | gaatccctcg  | tgggtggaga  | ggtggagata | gaatgatgcc  | gggtggtttac | 1020 |
| acggagggttg | atgggtggtag | actcgggtgat | gagagacttc | cgagaagagt  | agcttgggggt | 1080 |



|             |             |            |            |             |            |      |
|-------------|-------------|------------|------------|-------------|------------|------|
| tcgagaagag  | gtggaagaga  | tggtggaggt | agtagagagC | agaggtgggtg | gctttgcggg | 1140 |
| tcggatcatg  | aggtcttttcg | gatgttttag | tgatcatct  | ggatccattg  | ctgctgctgc | 1200 |
| tgctgcatca  | tcgggtgccg  | ggtccagaat | tcgggttact | cgtagaacca  | ggtcgtcttc | 1260 |
| tatgttcagt  | acggcgctcg  | cttcgtcaa  | gagacgaaat | tggttagcgt  | gattactaga | 1320 |
| attaccaagc  | tctctttcca  | ggtgaaaaat | aaacacgaaa | gaacacactc  | ttctcttggt | 1380 |
| taaaatttttc | ctatgttctc  | tattaagttt | ttgtctattt | cagtgtaatg  | attatattca | 1440 |
| ttctctaaat  | ttgaatctat  | gcgagtaaat | tg         |             |            |      |

(2) INFORMATION FOR SEQ ID NO:2367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..354

(D) OTHER INFORMATION: / Ceres Seq. ID 1572786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2367:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Gly | Ser | Tyr | Trp | Cys | Tyr | Ser | Cys | Ser | Arg | Phe | Val | Trp |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |
| Val | Ser | Asp | Ser | Ile | Ser | Cys | Pro | Asp | Cys | Asp | Gly | Gly | Phe | Leu | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ile | Gln | Glu | Pro | Leu | Asp | Phe | Thr | Pro | Ser | Asp | Ser | Phe | Thr | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Thr | Thr | Thr | Gln | His | Arg | Ser | Pro | Thr | Arg | Phe | Pro | Pro | Pro | Ser |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ser | Ser | Ser | Thr | Pro | Ser | Ala | Ser | Met | His | Ala | Asp | Asn | Ser | Pro |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Pro | Thr | Ile | Val | Thr | Arg | Thr | Arg | Ser | Asn | Arg | Ser | Pro | Asn | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Val | Ile | Val | Leu | Arg | Gly | Ser | Ala | Ala | Ala | Pro | Ser | Ser | Asp | Val | Val |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ser | Glu | Gly | Leu | Asp | Arg | Ser | Ala | Phe | Gln | Met | Tyr | Tyr | Asp | Asp | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Asp | Ser | Gly | Leu | Arg | Pro | Leu | Pro | Pro | Ser | Met | Thr | Glu | Phe | Leu |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Gly | Ser | Gly | Phe | Asp | Arg | Leu | Leu | Asp | Gln | Ile | Ser | Gln | Ile | Glu |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Asn | Thr | Asn | Arg | Asn | Leu | Arg | Ser | Cys | Glu | His | Pro | Pro | Ala | Ser |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     |     | 175 |
| Lys | Ser | Ala | Ile | Glu | Ala | Leu | Pro | Leu | Ile | Glu | Ile | Asp | Pro | Thr | His |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     | 190 |
| Leu | Leu | Ser | Asp | Ser | Gln | Ser | His | Cys | Ala | Val | Cys | Lys | Glu | Asn | Phe |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Leu | Lys | Ser | Ser | Ala | Arg | Glu | Met | Pro | Cys | Asn | His | Ile | Tyr | His |
|     |     |     | 210 |     |     | 215 |     |     |     | 220 |     |     |     |     |     |
| Pro | Asp | Cys | Ile | Leu | Pro | Trp | Leu | Ala | Ile | Arg | Asn | Ser | Cys | Pro | Val |
|     |     |     | 225 |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |
| Cys | Arg | His | Glu | Leu | Pro | Ala | Glu | Asp | Leu | Thr | Asp | Gly | Thr | Gly | Ala |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Leu | Thr | Ala | Val | Thr | Ala | Thr | Ala | Glu | Glu | Glu | Glu | Asp | Ser | Ala |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Ala | Gly | Leu | Thr | Ile | Trp | Arg | Leu | Pro | Gly | Gly | Gly | Phe | Ala | Val | Gly |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Arg | Ile | Pro | Gly | Gly | Trp | Arg | Gly | Gly | Asp | Arg | Met | Met | Pro | Val | Val |
|     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Tyr | Thr | Glu | Val | Asp | Gly | Gly | Arg | Leu | Gly | Asp | Glu | Arg | Leu | Pro | Arg |
|     |     |     | 305 |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |
| Arg | Val | Ala | Trp | Gly | Ser | Arg | Arg | Gly | Gly | Arg | Asp | Gly | Gly | Gly | Ser |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     |     |     |

Arg Glu Gln Arg Trp Trp Leu Cys Gly Ser Asp His Glu Ala Phe Arg  
340 345 350  
Met Phe

(2) INFORMATION FOR SEQ ID NO:2368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..281
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2368:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | His | Ala | Asp | Asn | Ser | Pro | Thr | Pro | Thr | Ile | Val | Thr | Arg | Thr | Arg |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser | Asn | Arg | Ser | Pro | Asn | Pro | Val | Ile | Val | Leu | Arg | Gly | Ser | Ala | Ala |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Ala | Pro | Ser | Ser | Asp | Val | Val | Ser | Glu | Gly | Leu | Asp | Arg | Ser | Ala | Phe |  |
|     |     | 35  |     |     |     | 40  |     |     | 45  |     |     |     |     |     |     |  |
| Gln | Met | Tyr | Tyr | Asp | Asp | Gly | Thr | Asp | Ser | Gly | Leu | Arg | Pro | Leu | Pro |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Pro | Ser | Met | Thr | Glu | Phe | Leu | Leu | Gly | Ser | Gly | Phe | Asp | Arg | Leu | Leu |  |
|     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Asp | Gln | Ile | Ser | Gln | Ile | Glu | Leu | Asn | Thr | Asn | Arg | Asn | Leu | Arg | Ser |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Cys | Glu | His | Pro | Pro | Ala | Ser | Lys | Ser | Ala | Ile | Glu | Ala | Leu | Pro | Leu |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Ile | Glu | Ile | Asp | Pro | Thr | His | Leu | Leu | Ser | Asp | Ser | Gln | Ser | His | Cys |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Ala | Val | Cys | Lys | Glu | Asn | Phe | Val | Leu | Lys | Ser | Ser | Ala | Arg | Glu | Met |  |
|     | 130 |     |     |     | 135 |     |     |     |     |     |     | 140 |     |     |     |  |
| Pro | Cys | Asn | His | Ile | Tyr | His | Pro | Asp | Cys | Ile | Leu | Pro | Trp | Leu | Ala |  |
|     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Ile | Arg | Asn | Ser | Cys | Pro | Val | Cys | Arg | His | Glu | Leu | Pro | Ala | Glu | Asp |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |
| Leu | Thr | Asp | Gly | Thr | Gly | Ala | Ala | Leu | Thr | Ala | Val | Thr | Ala | Thr | Ala |  |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |
| Glu | Glu | Glu | Glu | Asp | Ser | Ala | Ala | Gly | Leu | Thr | Ile | Trp | Arg | Leu | Pro |  |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |
| Gly | Gly | Gly | Phe | Ala | Val | Gly | Arg | Ile | Pro | Gly | Gly | Trp | Arg | Gly | Gly |  |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |  |
| Asp | Arg | Met | Met | Pro | Val | Val | Tyr | Thr | Glu | Val | Asp | Gly | Gly | Arg | Leu |  |
|     | 225 |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |  |
| Gly | Asp | Glu | Arg | Leu | Pro | Arg | Arg | Val | Ala | Trp | Gly | Ser | Arg | Arg | Gly |  |
|     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |     |  |
| Gly | Arg | Asp | Gly | Gly | Gly | Ser | Arg | Glu | Gln | Arg | Trp | Trp | Leu | Cys | Gly |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Ser | Asp | His | Glu | Ala | Phe | Arg | Met | Phe |     |     |     |     |     |     |     |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..232

(D) OTHER INFORMATION: / Ceres Seq. ID 1572788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2369:

```
Met Tyr Tyr Asp Asp Gly Thr Asp Ser Gly Leu Arg Pro Leu Pro Pro
1 5 10 15
Ser Met Thr Glu Phe Leu Leu Gly Ser Gly Phe Asp Arg Leu Leu Asp
20 25 30
Gln Ile Ser Gln Ile Glu Leu Asn Thr Asn Arg Asn Leu Arg Ser Cys
35 40 45
Glu His Pro Pro Ala Ser Lys Ser Ala Ile Glu Ala Leu Pro Leu Ile
50 55 60
Glu Ile Asp Pro Thr His Leu Ser Asp Ser Gln Ser His Cys Ala
65 70 75 80
Val Cys Lys Glu Asn Phe Val Leu Lys Ser Ser Ala Arg Glu Met Pro
85 90 95
Cys Asn His Ile Tyr His Pro Asp Cys Ile Leu Pro Trp Leu Ala Ile
100 105 110
Arg Asn Ser Cys Pro Val Cys Arg His Glu Leu Pro Ala Glu Asp Leu
115 120 125
Thr Asp Gly Thr Gly Ala Ala Leu Thr Ala Val Thr Ala Thr Ala Glu
130 135 140
Glu Glu Glu Asp Ser Ala Ala Gly Leu Thr Ile Trp Arg Leu Pro Gly
145 150 155 160
Gly Gly Phe Ala Val Gly Arg Ile Pro Gly Gly Trp Arg Gly Gly Asp
165 170 175
Arg Met Met Pro Val Val Tyr Thr Glu Val Asp Gly Gly Arg Leu Gly
180 185 190
Asp Glu Arg Leu Pro Arg Arg Val Ala Trp Gly Ser Arg Arg Gly Gly
195 200 205
Arg Asp Gly Gly Gly Ser Arg Glu Gln Arg Trp Trp Leu Cys Gly Ser
210 215 220
Asp His Glu Ala Phe Arg Met Phe
225 230
```

(2) INFORMATION FOR SEQ ID NO:2370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 944 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..944

(D) OTHER INFORMATION: / Ceres Seq. ID 1572796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2370:

```
acagtcgtcaca ctcaccacct caccgacctc accgttcctt atccatttgg ctgacgcaaaa 60
atcgaaatcgg aaccctaaaa tctctccgaa agccatgtct cctcctcctg ctgtagtcaac 120
tgaatctgcgc gatggacaac ctgagcaacc accggttacc gccattgctg aagagctgcac 180
gaaaagcttcca gactgatgaa ccgattgtag aagatgttaa agatgatgaa gacgatgatg 240
atgatgacga agaagaggaa gacgacgatg ctcaagggtg aagtggaaagt tcaaagcaga 300
tagaagatga aaagaagagt aggaagcgca tggttgaagct cggtatgaaa cctgtcactg 360
gtgttagtcg agtaaccatc aagagaacga aaaacgttct ctcttatttc tctaagcctg 420
atgtcttttaa gagcccgcat tcagaaaacct atgttatatt cggtgaggcc aagatcgagg 480
atttgagctc tcagcttcaa acgcaagcgt ctcaacagtt taggatgcct gMaattggag 540
ccacatctca gagagcagag gcattcgacag ccactgtaga agcacagggt gaagaagatg 600
aagaggaatat cgatgagacc ggtgtggagg ctgcgtgacat tgacttggct atgactcagg 660
ctggaggttcc gcgtagcaaa gcggtttaaag cactcaagag tcacgatgga gacattgttaa 720
gtgcaataat ggaactcact acttaagagt taagagagat tgagtctcta tgccttattc 780
actctgcagat tgttttcaaa tacttttggg tttatcagga aattgatta ttgttgtctc 840
taccgagtac taatctagtt tgtttgttat gatgcttatg cagtatctga gttgtactgt 900
gtttttcacg acaatgtatt ggagaaaaa catatcaaaa ttcg
```

(2) INFORMATION FOR SEQ ID NO:2371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1572797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2371:

```
Met Asp Asn Leu Ser Asn His Arg Leu Pro Leu Leu Lys Ser Trp
1 5 10 15
Arg Lys Leu Gln Thr Asp Glu Pro Ile Val Glu Asp Val Lys Asp Asp
20 25 30
Glu Asp Asp Asp Asp Asp Asp Glu Glu Glu Asp Asp Ala Gln
35 40 45
Gly Val Ser Gly Ser Ser Lys Gln Ser Arg Ser Glu Lys Lys Ser Arg
50 55 60
Lys Ala Met Leu Lys Leu Gly Met Lys Pro Val Thr Gly Val Ser Arg
65 70 75 80
Val Thr Ile Lys Arg Thr Lys Asn Val Leu Phe Ile Ser Lys Pro
85 90 95
Asp Val Phe Lys Ser Pro His Ser Glu Thr Tyr Val Ile Phe Gly Glu
100 105 110
Ala Lys Ile Glu Asp Leu Ser Ser Gln Leu Gln Thr Gln Ala Ala Gln
115 120 125
Gln Phe Arg Met Pro Xaa Ile Gly Ala Thr Ser Gln Arg Ala Glu Ala
130 135 140
Ser Thr Ala Thr Val Glu Ala Gln Val Glu Glu Asp Glu Glu Glu Ile
145 150 155 160
Asp Glu Thr Gly Val Glu Ala Arg Asp Ile Asp Leu Val Met Thr Gln
165 170 175
Ala Gly Val Ser Arg Ser Lys Ala Val Lys Ala Leu Lys Ser His Asp
180 185 190
Gly Asp Ile Val Ser Ala Ile Met Glu Leu Thr Thr
195 200
```

(2) INFORMATION FOR SEQ ID NO:2372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1572798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2372:

```
Met Leu Lys Leu Gly Met Lys Pro Val Thr Gly Val Ser Arg Val Thr
1 5 10 15
Ile Lys Arg Thr Lys Asn Val Leu Phe Phe Ile Ser Lys Pro Asp Val
20 25 30
Phe Lys Ser Pro His Ser Glu Thr Tyr Val Ile Phe Gly Glu Ala Lys
35 40 45
Ile Glu Asp Leu Ser Ser Gln Leu Gln Thr Gln Ala Ala Gln Gln Phe
50 55 60
Arg Met Pro Xaa Ile Gly Ala Thr Ser Gln Arg Ala Glu Ala Ser Thr
65 70 75 80
Ala Thr Val Glu Ala Gln Val Glu Glu Asp Glu Glu Glu Ile Asp Glu
```

85 90 95  
Thr Gly Val Glu Ala Arg Asp Ile Asp Leu Val Met Thr Gln Ala Gly  
100 105 110  
Val Ser Arg Ser Lys Ala Val Lys Ala Leu Lys Ser His Asp Gly Asp  
115 120 125  
Ile Val Ser Ala Ile Met Glu Leu Thr Thr  
130 135

(2) INFORMATION FOR SEQ ID NO:2373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..133
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2373:

Met Lys Pro Val Thr Gly Val Ser Arg Val Thr Ile Lys Arg Thr Lys  
1 5 10 15  
Asn Val Leu Phe Phe Ile Ser Lys Pro Asp Val Phe Lys Ser Pro His  
20 25 30  
Ser Glu Thr Tyr Val Ile Phe Gly Glu Ala Lys Ile Glu Asp Leu Ser  
35 40 45  
Ser Gln Leu Gln Thr Gln Ala Ala Gln Gln Phe Arg Met Pro Xaa Ile  
50 55 60  
Gly Ala Thr Ser Gln Arg Ala Glu Ala Ser Thr Ala Thr Val Glu Ala  
65 70 75 80  
Gln Val Glu Glu Asp Glu Glu Glu Ile Asp Glu Thr Gly Val Glu Ala  
85 90 95  
Arg Asp Ile Asp Leu Val Met Thr Gln Ala Gly Val Ser Arg Ser Lys  
100 105 110  
Ala Val Lys Ala Leu Lys Ser His Asp Gly Asp Ile Val Ser Ala Ile  
115 120 125  
Met Glu Leu Thr Thr  
130

(2) INFORMATION FOR SEQ ID NO:2374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1793
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2374:

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| ctctcgatt   | tttatttctt | atatacaat  | ccctaaaacc | ctatagccct | ctttcttcac  | 60  |
| caactactac  | taactccaag | ctcaagcccc | tctgttttct | ctgctttgtg | ttaaaaatca  | 120 |
| tttcagacac  | agtgcctttg | atgactctct | gcaacaaaac | acagcagctg | cagacaaaagc | 180 |
| ttatacgaag  | ctgtatctac | tgactttgat | ggtgaaatat | caaaaaccct | aaattaaatt  | 240 |
| aaaaaataaaa | aacacatttt | ttttcttctt | ttgtgttttc | ctctgagggg | attcatcatc  | 300 |
| aatgcttaca  | aagtacagtg | ggtaaacaaa | acaaaaacaa | aaaaccattt | ttttctctct  | 360 |
| tcctttaaact | ccaaactccc | ctaaaggatt | tgatttttaa | ttttgggggt | accacaaaaa  | 420 |
| aaacaaaacc  | ccaatttttt | ttcttttagt | atgagattat | tggtgatgat | gaaatgattg  | 480 |
| gagatctaat  | gaagaataac | aacaatggcg | acgttgttga | taacgaagtg | aacacccggg  | 540 |
| taagccgggt  | gcatacaact | tcttcocgga | taattagggt | ttcacgagct | tcgggttgta  | 600 |
| aagatcgaca  | cagcaaaatc | ttgacttcta | aaggaccacg | tgaccgtcgt | gtccgtttat  | 660 |
| cagttctccac | cgcttctcaa | ttctatgatc | ttcaagatcg | gttaggttat | gatcaacctc  | 720 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| gcaaagctgt | tgaatgggta | atcaaagctg | ctgaagattc | aatctbtgag | cttccttcac | 780  |
| tcaacaacac | ttcttttccg | accgatgacg | agaatcacca | gaatcagaca | ttacaacacg | 840  |
| ttgtgctgt  | ttctttgtct | aaatctgctt | gtagtaccaa | ttcagacacg | agcaagaact | 900  |
| cttttgctt  | YYtthatcaa | gatcggagct | tagagataaa | gctagagaga | gagctagaga | 960  |
| gagaacagct | aaagagacca | aggagagaga | tcataaccac | acttcgttta | cogatttgtt | 1020 |
| aaattccggt | tcagatccgg | ttaaactcaa | ccggcaatgg | atggctttct | ctcctttctt | 1080 |
| atctccaatg | gagtatttta | gttcgggttt | aattctcggg | tcgggtcaac | aaacccattt | 1140 |
| cccgatttcg | acaaattctc | atcctttctc | atcaatctcc | gatcatcatc | atcctcatca | 1200 |
| tcagacccaa | gagttttcat | tcgttcccca | ccatttgata | tcaccgcgag | aatccaacgg | 1260 |
| cgagacattc | aatcttgatt | ttaatatgtc | gacacccctc | ggcgccggag | ctgcgctctc | 1320 |
| cgcccatcc  | gggtgtgggt | tcagtgggtt | caacaggggg | acccttcagt | ccaattcaac | 1380 |
| aaatcagctc | cagtcatctt | tcgctaattc | acagaggttt | ccaacatcag | aaagtggagg | 1440 |
| agggtccacg | ttcttattcg | gtgcactgcc | tcgacagaa  | caccaccaca | atcaccagtt | 1500 |
| tcagctttac | tatgaaaatg | gatgcagaaa | ctcatcagac | cataagggta | aaggcagaag | 1560 |
| ctgattgata | taattattgc | atctttgttt | ttgttcaaat | cctcatcttt | tatgtttatc | 1620 |
| ttttggttat | ttcaaaacaa | atgttaattc | cttttgttgt | ctgatgtgtg | ttagggtttt | 1680 |
| ttctcacata | tgtattgagg | gtctttggaa | atctttttgc | attgtgctgt | taattgttga | 1740 |
| tttttgata  | atagcatttt | gttttgtgag | ttataattca | atttttgaat | ggt        |      |

(2) INFORMATION FOR SEQ ID NO:2375:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 1572801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2375:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Gly | Asp | Leu | Met | Lys | Asn | Asn | Asn | Asn | Gly | Asp | Val | Val | Asp |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |     |
| Asn | Glu | Val | Asn | Asn | Arg | Leu | Ser | Arg | Trp | His | His | Asn | Ser | Ser | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Ile | Ile | Arg | Val | Ser | Arg | Ala | Ser | Gly | Gly | Lys | Asp | Arg | His | Ser | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Val | Leu | Thr | Ser | Lys | Gly | Pro | Arg | Asp | Arg | Arg | Val | Arg | Leu | Ser | Val |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Thr | Ala | Leu | Gln | Phe | Tyr | Asp | Leu | Gln | Asp | Arg | Leu | Gly | Tyr | Asp |
|     |     |     | 65  |     | 70  |     | 75  |     |     |     | 80  |     |     |     |     |
| Gln | Pro | Ser | Lys | Ala | Val | Glu | Trp | Leu | Ile | Lys | Ala | Ala | Glu | Asp | Ser |
|     |     |     | 85  |     |     |     | 90  |     |     |     | 95  |     |     |     |     |
| Ile | Xaa | Glu | Leu | Pro | Ser | Leu | Asn | Asn | Thr | His | Phe | Pro | Thr | Asp | Asp |
|     |     |     | 100 |     |     |     | 105 |     |     |     | 110 |     |     |     |     |
| Glu | Asn | His | Gln | Asn | Gln | Thr | Leu | Thr | Thr | Val | Ala | Ala | Asn | Ser | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Ser | Lys | Ser | Ala | Cys | Ser | Ser | Asn | Ser | Asp | Thr | Ser | Lys | Asn | Ser | Leu |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Xaa | Xaa | Xaa | Gln | Asp | Arg | Ser | Leu | Glu | Ile | Lys | Leu | Glu | Arg | Glu |
|     |     |     | 145 |     | 150 |     |     |     | 155 |     | 160 |     |     |     |     |
| Leu | Glu | Arg | Glu | Gln | Leu | Lys | Arg | Pro | Arg | Arg | Glu | Ile | Ile | Thr | Thr |
|     |     |     | 165 |     |     |     | 170 |     |     |     | 175 |     |     |     |     |
| Leu | Arg | Leu | Pro | Ile | Cys |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..177

(D) OTHER INFORMATION: / Ceres Seq. ID 1572802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2376:

```
Met Lys Asn Asn Asn Asn Gly Asp Val Val Asp Asn Glu Val Asn Asn
1 5 10 15
Arg Leu Ser Arg Trp His His Asn Ser Ser Arg Ile Ile Arg Val Ser
 20 25 30
Arg Ala Ser Gly Gly Lys Asp Arg His Ser Lys Val Leu Thr Ser Lys
 35 40 45
Gly Pro Arg Asp Arg Arg Val Arg Leu Ser Val Ser Thr Ala Leu Gln
 50 55 60
Phe Tyr Asp Leu Gln Asp Arg Leu Gly Tyr Asp Gln Pro Ser Lys Ala
 65 70 75 80
Val Glu Trp Leu Ile Lys Ala Ala Glu Asp Ser Ile Xaa Glu Leu Pro
 85 90 95
Ser Leu Asn Asn Thr His Phe Pro Thr Asp Asp Glu Asn His Gln Asn
 100 105 110
Gln Thr Leu Thr Thr Val Ala Ala Asn Ser Leu Ser Lys Ser Ala Cys
 115 120 125
Ser Ser Asn Ser Asp Thr Ser Lys Asn Ser Leu Val Xaa Xaa Xaa Gln
 130 135 140
Asp Arg Ser Leu Glu Ile Lys Leu Glu Arg Glu Leu Glu Arg Glu Gln
 145 150 155 160
Leu Lys Arg Pro Arg Glu Ile Ile Thr Thr Leu Arg Leu Pro Ile
 165 170 175
Cys
```

(2) INFORMATION FOR SEQ ID NO:2377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1572803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2377:

```
Met Ala Ser Ala Pro Ser Ser Ser Pro Met Glu Tyr Phe Ser Ser Gly
1 5 10 15
Leu Ile Leu Gly Ser Gly Gln Gln Thr His Phe Pro Ile Ser Thr Asn
 20 25 30
Ser His Pro Phe Ser Ser Ile Ser Asp His His His Pro His His Gln
 35 40 45
His Gln Glu Phe Ser Phe Val Pro Asp His Leu Ile Ser Pro Ala Glu
 50 55 60
Ser Asn Gly Gly Ala Phe Asn Leu Asp Phe Asn Met Ser Thr Pro Ser
 65 70 75 80
Gly Ala Gly Ala Ala Val Ser Ala Ala Ser Gly Gly Gly Phe Ser Gly
 85 90 95
Phe Asn Arg Gly Thr Leu Gln Ser Asn Ser Thr Asn Gln His Gln Ser
 100 105 110
Phe Leu Ala Asn Leu Gln Arg Phe Pro Thr Ser Glu Ser Gly Gly Gly
 115 120 125
Pro Gln Phe Leu Phe Gly Ala Leu Pro Ala Glu Asn His His His Asn
 130 135 140
His Gln Phe Gln Leu Tyr Tyr Glu Asn Gly Cys Arg Asn Ser Ser Asp
 145 150 155 160
```

His Lys Gly Lys Gly Lys Asn  
165

(2) INFORMATION FOR SEQ ID NO:2378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..493
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2378:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| aagttacact | ataaactcaa  | acacatctat | cggaagtc   | taacacacga | agatttccaa | 60  |
| aatggctaag | gccgaagGtc  | ttttcttct  | tgttttagta | gttatttcaa | gtttatgtat | 120 |
| gttaaccgag | agccgactcg  | caagaaaaga | ctgggggatt | gacctaggtg | ggattggaat | 180 |
| cggtttgggc | gttggtattgg | ggatttgtct | tggcggcggg | tcgggctccg | gtgctgggtc | 240 |
| aggttctgga | tcagggttcag | gttcagatc  | atcatctagc | tccagctcat | catcaagtc  | 300 |
| gagttctagt | gggtcgggtg  | gttcagctgg | tcatctgcc  | ggttcatttg | ctggctctag | 360 |
| agctggatca | ggatctggga  | actaaattat | ataaattact | tttcgaacta | aagtgtagaa | 420 |
| caataagtat | gttttatgtt  | tttggttcgt | cgtagttaat | atcgtatgta | cggaatggaa | 480 |
| tgataaattt | ggt         |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2379:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Ala | Glu | Gly | Leu | Phe | Leu | Leu | Gly | Leu | Val | Val | Ile | Ser |
| 1   |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |     |     |
| Ser | Leu | Val | Met | Leu | Thr | Glu | Ser | Arg | Leu | Ala | Arg | Lys | Asp | Leu | Gly |
|     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |     |
| Ile | Asp | Leu | Gly | Gly | Ile | Gly | Ile | Gly | Leu | Gly | Val | Gly | Leu | Gly | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |     |
| Gly | Leu | Gly | Gly | Gly | Ser | Gly | Ser | Gly | Ala | Gly | Ala | Gly | Ser | Gly | Ser |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly | Ser | Gly | Ser | Arg | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ser |
|     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     |
| Ser | Ser | Ser | Gly | Ser | Gly | Gly | Ser | Ala | Gly | Ser | Ser | Ala | Gly | Ser | Phe |
|     |     |     | 85  |     |     | 90  |     |     |     | 95  |     |     |     |     |     |
| Ala | Gly | Ser | Arg | Ala | Gly | Ser | Gly | Ser | Gly | Asn |     |     |     |     |     |
|     |     |     | 100 |     |     | 105 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2380:



Met Leu Thr Glu Ser Arg Leu Ala Arg Lys Asp Leu Gly Ile Asp Leu  
1 5 10 15  
Gly Gly Ile Gly Ile Gly Leu Gly Val Gly Leu Gly Ile Gly Leu Gly  
20 25 30  
Gly Gly Ser Gly Ser Gly Ala Gly Ala Gly Ser Gly Ser Gly Ser Gly  
35 40 45  
Ser Arg Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser  
50 55 60  
Gly Ser Gly Gly Ser Ala Gly Ser Ser Ala Gly Ser Phe Ala Gly Ser  
65 70 75 80  
Arg Ala Gly Ser Gly Ser Gly Asn  
85

(2) INFORMATION FOR SEQ ID NO:2381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1491
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2381:

aattgtcaaa aactcacaag gcattatcat gtggacatgc aaaccttttt ttctatacgc 60  
attacagaaa tgaaaaacaat gattaggatc gcatgcacgt caagaaaaaa acctatagta 120  
gtactttgat atactaactc aatcattgtc ttggctcaag cacacaagct tctagctaga 180  
tacaactgca aacatatatg atggctttgt ctaataaaga gacgacgact tgggcaccgc 240  
tttgaccagt caatacacca aatctgtatg tatcatttat ataatattta tctttccaca 300  
gttggtgaag aatcacatatg acagcacaca cggattccat ggagactaaa cagagtatcc 360  
ctctctcatc gccctataag atgggacccct toaatcttct tccacagggtt gttttggcgc 420  
cattgacag atcagagatcg tatggttaaca ttctcagcc taatgccaaa ttatattaca 480  
ctcagagaa acacactgggt ggtcttctta ttctcgaatc ctgtgtatgc tccgagacat 540  
cattgggcta tcgggattta ctctggattt ggaacagaga ccaagtggag gcattggaagc 600  
ccatcgtgga tcgcggttcat tcgaaaaggcg gtatcttctt ctgccagatt tggcattggtg 660  
gcagagtttt tcatcaagac cagccaaatg ggggaagcacc cgtctctctt acagacaagc 720  
cattgatgtg caagaacatg tatggaggtc agtttaagcc tccacggcgg ttaaggagcg 780  
acgagcttcc cgccattgtc aacgacttta gaatcgtcgc acgaaacgct atcgaagctg 840  
gcttcgatgg agtgagggtt caccggcgac atggttacct agatgatcac tctcctgaaag 900  
acaaagtga tgcagaagt gaccaatatg gtggGtcatt agagaaaccg ttagatattg 960  
ctcttgaagt aatcagaagca gtggtaaacg agatcgggtt agatogtgtt ggaatcacag 1020  
tctcgcattt tcagagattac atggagtcag gagactcgaa tccagaagca ttagggctct 1080  
acctgtgcca agctatgaac aagcatggca tggagtcgtc tacggctaca tggttgaacc 1140  
tagaatgaaa acccttgaag gaattcttga atgcacggaa tcgcttaacg ccatcgcaaa 1200  
agccttcaaa ggtacgttca tagtagcagg aggatattct agagaagacg ggaacaagcg 1260  
gggtgaagag ggaagaaccg atcttctggc ttattggacg cgttctctgg ggaatccggg 1320  
tctcagagag agattagcaac tcaatgagcc gttgaatagg tacgatagat caactgttca 1380  
caactcagat cctgtagtgg gctatacaga ctacccttct ctcgagacca cagatacaac 1440  
aacctgctaa ggggtttatt catagtcatt attagcaaaa catatttttc c

(2) INFORMATION FOR SEQ ID NO:2382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..269
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2382:

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```

Met Glu Thr Lys Gln Ser Ile Pro Leu Leu Met Pro Tyr Lys Met Gly
1 5 10 15
Pro Phe Asn Leu Ser His Arg Val Val Leu Ala Pro Leu Thr Arg Ser
20 25 30
Arg Ser Tyr Gly Asn Ile Pro Gln Pro Asn Ala Lys Leu Tyr Tyr Thr
35 40 45
Gln Arg Thr Thr Pro Gly Gly Leu Leu Ile Ser Glu Ser Cys Val Val
50 55 60
Ser Glu Thr Ser Leu Gly Tyr Pro Asp Leu Pro Gly Leu Trp Asn Arg
65 70 75 80
Asp Gln Val Glu Ala Trp Lys Pro Ile Val Asp Ala Val His Ser Lys
85 90 95
Gly Gly Ile Phe Phe Cys Gln Ile Trp His Gly Gly Arg Val Phe His
100 105 110
Gln Asp Gln Pro Asn Gly Glu Ala Pro Val Ser Ser Thr Asp Lys Pro
115 120 125
Leu Met Cys Lys Asn Met Tyr Gly Gly Gln Phe Lys Pro Pro Arg Arg
130 135 140
Leu Arg Ser Asp Glu Leu Pro Ala Ile Val Asn Asp Phe Arg Ile Ala
145 150 155 160
Ala Arg Asn Ala Ile Glu Ala Gly Phe Asp Gly Val Glu Val His Gly
165 170 175
Ala His Gly Tyr Leu Ile Asp Gln Phe Leu Lys Asp Lys Val Asn Asp
180 185 190
Arg Ser Asp Gln Tyr Gly Gly Ser Leu Glu Asn Arg Cys Arg Phe Ala
195 200 205
Leu Glu Val Ile Glu Ala Val Val Asn Glu Ile Gly Ser Asp Arg Val
210 215 220
Gly Ile Arg Leu Ser Pro Phe Ala Asp Tyr Met Glu Ser Gly Asp Ser
225 230 235 240
Asn Pro Glu Ala Leu Gly Leu Tyr Leu Val Gln Ala Met Asn Lys His
245 250 255
Gly Met Glu Ser Ser Thr Val Thr Trp Leu Asn Leu Glu
260 265

```

(2) INFORMATION FOR SEQ ID NO:2383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..259

(D) OTHER INFORMATION: / Ceres Seq. ID 1572809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2383:

```

Met Pro Tyr Lys Met Gly Pro Phe Asn Leu Ser His Arg Val Val Leu
1 5 10 15
Ala Pro Leu Thr Arg Ser Arg Ser Tyr Gly Asn Ile Pro Gln Pro Asn
20 25 30
Ala Lys Leu Tyr Tyr Thr Gln Arg Thr Thr Pro Gly Gly Leu Leu Ile
35 40 45
Ser Glu Ser Cys Val Val Ser Glu Thr Ser Leu Gly Tyr Pro Asp Leu
50 55 60
Pro Gly Leu Trp Asn Arg Asp Gln Val Glu Ala Trp Lys Pro Ile Val
65 70 75 80
Asp Ala Val His Ser Lys Gly Gly Ile Phe Phe Cys Gln Ile Trp His
85 90 95
Gly Gly Arg Val Phe His Gln Asp Gln Pro Asn Gly Glu Ala Pro Val
100 105 110
Ser Ser Thr Asp Lys Pro Leu Met Cys Lys Asn Met Tyr Gly Gly Gln

```

(2) INFORMATION FOR SEQ ID NO:2384:

(A) LENGTH: 255 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

$\langle \underline{1}x \rangle$  FEATURE:

(B) LOCATION: 1..255

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:2384:

Gly Pro Phe Asn Leu Ser His Arg Val Val Le

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Arg | Ser | 5   | Tyr | Gly | Asn | Ile | Pro | Gln | Pro | Asn | Ala | Lys | 15  | Leu | Tyr |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Tyr | Thr | Gln | Arg | Thr | Thr | Pro | Gly | Gly | Leu | Leu | Ile | Ser | Glu | Ser | Cys |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
| Val | Val | Ser | Glu | Thr | Ser | Leu | Gly | Tyr | Pro | Asp | Leu | Pro | Gly | Leu | Trp |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |     |
| Asn | Arg | Asp | Gln | Val | Glu | Ala | Trp | Lys | Pro | Ile | Val | Asp | Ala | Val | His |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |     |
| Ser | Lys | Gly | Gly | Ile | Phe | Phe | Cys | Gln | Ile | Trp | His | Gly | Gly | Arg | Val |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |
| Phe | His | Gln | Asp | Gln | Pro | Asn | Gly | Glu | Ala | Pro | Val | Ser | Ser | Thr | Asp |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |     |
| Lys | Pro | Leu | Met | Cys | Lys | Asn | Met | Tyr | Gly | Gly | Gln | Phe | Lys | Pro | Pro |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |     |
| Arg | Arg | Leu | Arg | Ser | Asp | Glu | Leu | Pro | Ala | Ile | Val | Asn | Asp | Phe | Arg |     |     |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |     |
| Ile | Ala | Ala | Arg | Asn | Ala | Ile | Glu | Ala | Gly | Phe | Asp | Gly | Val | Glu | Val |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |     |     |
| His | Gly | Ala | His | Gly | Tyr | Leu | Ile | Asp | Gln | Phe | Leu | Lys | Asp | Lys | Val |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |
| Asn | Asp | Arg | Ser | Asp | Gln | Tyr | Gly | Gly | Ser | Leu | Glu | Asn | Arg | Cys | Arg |     |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     |
| Phe | Ala | Leu | Glu | Val | Ile | Glu | Ala | Val | Val | Asn | Glu | Ile | Gly | Ser | Asp |     |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |     |
| Arg | Val | Gly | Ile | Arg | Leu | Ser | Pro | Phe | Ala | Asp | Tyr | Met | Glu | Ser | Gly |     |     |
|     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |     |     |
| Asp | Ser | Asn | Pro | Glu | Ala | Leu | Gly | Leu | Tyr | Leu | Val | Gln | Ala | Met | Asn |     |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |     |     |

Lys His Gly Met Glu Ser Ser Thr Val Thr Trp Leu Asn Leu Glu  
245 250 255

(2) INFORMATION FOR SEQ ID NO:2385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..342
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2385:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aatgctattg | ttgggttcca | tggacgggta | ggttcttg   | ttgatagat  | cgggtcatat | 60  |
| tacgtccgt  | tttctccttc | tctccacct  | acagagaaac | tagagggaca | aggtggat   | 120 |
| ggaggagatt | cttgggacga | tgggtcttcc | ctaaatgtaa | agaaagtata | tgttggacaa | 180 |
| ggctcgaacg | gtattgtcgc | cgtaaagttt | gagtacgaga | acgacgctag | tgaggttggt | 240 |
| gttggagatg | aacatggaaa | gactacattg | cttggatacg | aaKgTggtga | tgactactcc | 300 |
| ttactttaat | tgtttaaagt | ttcaaaacta | tactatatat | cg         |            |     |

(2) INFORMATION FOR SEQ ID NO:2386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2386:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Ala | Ile | Val | Gly | Phe | His | Gly | Arg | Val | Gly | Ser | Cys | Val | Asp | Ser |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     | 15  |     |     |     |     |  |
| Ile | Gly | Ala | Tyr | Tyr | Ala | Pro | Phe | Ser | Pro | Ser | Pro | Pro | Pro | Thr | Glu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Lys | Leu | Glu | Gly | Gln | Gly | Gly | Asp | Gly | Gly | Asp | Ser | Trp | Asp | Asp | Gly |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Ala | Phe | Leu | Asn | Val | Lys | Lys | Val | Tyr | Val | Gly | Gln | Gly | Ser | Asn | Gly |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Ile | Val | Ala | Val | Lys | Phe | Glu | Tyr | Glu | Asn | Asp | Ala | Ser | Glu | Val | Val |  |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     |     | 80  |     |  |
| Val | Gly | Asp | Glu | His | Gly | Lys | Thr | Thr | Leu | Leu | Gly | Tyr | Glu | Xaa | Gly |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Asp | Asp | Tyr | Ser | Leu | Leu |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..57
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2387:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Leu | Asp | Lys | Ala | Arg | Thr | Val | Leu | Ser | Pro | Leu | Ser | Leu | Ser | Thr |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |     |  |
| Arg | Thr | Thr | Leu | Val | Arg | Leu | Leu | Leu | Glu | Met | Asn | Met | Glu | Arg | Leu |  |

20 25 30  
His Cys Leu Asp Thr Xaa Val Val Met Thr Thr Pro Tyr Phe Asn Cys  
35 40 45  
Leu Lys Phe Gln Asn Tyr Thr Ile Tyr  
50 55

(2) INFORMATION FOR SEQ ID NO:2388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1125

(D) OTHER INFORMATION: / Ceres Seq. ID 1572814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2388:

```
cmcraracca ttmcctagat catcctaaat caaaagtctt tcaaaaatca aaatcccttc 60
ctctctctct ctcaccgagc cggcgagccc gttctctcgg tgtttttaa gatgcttatg 120
atgatgatgg ggagtaatat cagaaatcaa gctttttcac aatctcagaa attgtagtag 180
agtttgggga ttttatcaac ctccggaaca agctctctct tcttcgtttt actcttgtea 240
tccgtaaaKg ggttgtttcc attccacggc tgccagagaa ttcccgatc acgaaaaacc 300
tgtgaagctt gcttctgaga ctgcttttag tgttagtgaa tgtgaagcat tgtatgaatt 360
gttcaagagc ataagcagct cggttgttga cgatggcttg ataaacaagg aagagttttc 420
acttgctttg tcaagaaca gaaagaaga aaatttgttt gccaatagga tatttgattt 480
atttgatgtt aaacgaaaag gcgtaattga ttttgagac tttgtgagat cactcaatgt 540
tttccatcct aatgcttccc tagaggagaa aacagacttt acctttaggc ttacagacat 600
ggaactgcaca ggcctcattg agcgccaaga ggtgaagcag atgttgattg cacttctctg 660
cgaatctgaa atgaaactcg ctgatgatac aatagagatg atacttgatc agacatttga 720
ggagcgcagat gtggatcggg atggaaagat tgataagaca gaatggagca atttcgttat 780
caaaaaccca tctttgttta aaatcatgac tcttcogtat ctcagggata taacagcgac 840
atttccgagt ttctgtattta actcggaggt ggacgagatt gcgacgtgaa agagacaaga 900
caagctggtt tatagagacc aagtctgtag ctggaccaag aataaaaaag aagattgatt 960
ccaacaatgt tatatagcag gatcgagctc tatttccttt ggaattttta gtctatttga 1020
tttcaatttc tatatgtgag attactttt gctctcttct tttaacagtt ttgaatactc 1080
aagttgtagt tctacgaaaa gattaatata aaaccacaat ttctgt
```

(2) INFORMATION FOR SEQ ID NO:2389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1572815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2389:

```
Met Asp Cys Thr Gly Phe Ile Glu Arg Gln Glu Val Lys Gln Met Leu
1 5 10 15
Ile Ala Leu Leu Cys Glu Ser Glu Met Lys Leu Ala Asp Asp Thr Ile
20 25 30
Glu Met Ile Leu Asp Gln Thr Phe Glu Asp Ala Asp Val Asp Arg Asp
35 40 45
Gly Lys Ile Asp Lys Thr Glu Trp Ser Asn Phe Val Ile Lys Asn Pro
50 55 60
Ser Leu Leu Lys Ile Met Thr Leu Pro Tyr Leu Arg Asp Ile Thr Thr
65 70 75 80
Thr Phe Pro Ser Phe Val Phe Asn Ser Glu Val Asp Glu Ile Ala Thr
85 90 95
```

(2) INFORMATION FOR SEQ ID NO:2390:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 82 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1572816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2390:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ile | Ala | Leu | Leu | Cys | Glu | Ser | Glu | Met | Lys | Leu | Ala | Asp | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Ile | Glu | Met | Ile | Leu | Asp | Gln | Thr | Phe | Glu | Asp | Ala | Asp | Val | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Asp | Gly | Lys | Ile | Asp | Lys | Thr | Glu | Trp | Ser | Asn | Phe | Val | Ile | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Pro | Ser | Leu | Leu | Lys | Ile | Met | Thr | Leu | Pro | Tyr | Leu | Arg | Asp | Ile |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Thr | Thr | Phe | Pro | Ser | Phe | Val | Phe | Asn | Ser | Glu | Val | Asp | Glu | Ile |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Thr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2391:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1572817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2391:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Leu | Ala | Asp | Asp | Thr | Ile | Glu | Met | Ile | Leu | Asp | Gln | Thr | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Asp | Ala | Asp | Val | Asp | Arg | Asp | Gly | Lys | Ile | Asp | Lys | Thr | Glu | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Asn | Phe | Val | Ile | Lys | Asn | Pro | Ser | Leu | Leu | Lys | Ile | Met | Thr | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Tyr | Leu | Arg | Asp | Ile | Thr | Thr | Thr | Phe | Pro | Ser | Phe | Val | Phe | Asn |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Glu | Val | Asp | Glu | Ile | Ala | Thr |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2392:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 950 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..950

(D) OTHER INFORMATION: / Ceres Seq. ID 1572826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2392:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| acatcaaaaa | ctaaacaata | aaccatatac | cataaaaaac | atgaaaatcc | tctcactttc | 60  |
| acttctcttg | ctcttgccg  | ctacggtctc | tgcatccatt | ccagagctca | tcgaactcgt | 120 |

```
cgattcgaac accatcttta cgaacgaagc cgaactctta gagaaagaga aactttccat 180
caactacgcc aactcgagaa gctggcacct tgggtgtgag acctctaata tcatagacct 240
cgacacggtg cccgcaaat gcaaaagacta tgttgaagac tacttgatca ctccaacaca 300
gtaccaaatc gactccaaaa ccgtgtgcaa agaggcttat tcttatgcca aaggacttgc 360
ctaaagaac gacaccgtta atgtttggat ctttgaccta gatgataccc tccctcttag 420
tattccctac tacgcaaaat atggatacgg gacagagaag accgacccgg gggcgtagctg 480
gtgttggtta gggacccggag catcaacccc tggactcccg gagGccttgc atctttacca 540
aaacatcata gagctcgagg ttgaacccat catactcagt gacgcttga aattgtggaa 600
gaatgtcact ctogacaatc tcgaagctgc tggcgtggcc tactggaagc atctcatatt 660
gaagcctaatt ggttcgaact tgaggcaagt ggtttacaag tcaaaaggtga ggaagagtct 720
cgtaagaana ggatacaaca tcgttgccaa tatcggagac caatgggctg atttggttga 780
ggataccctt ggaagggttt ttaagctccc aaatccactc tactacgtac ctctctaagc 840
atttatcttc atggcatttt ccccttgtat ccacttcata tctatgtcgt ttctgtttac 900
tttgtagccg tttttggacc gttgcataaa taaaatttct atcctatcgc
```

(2) INFORMATION FOR SEQ ID NO:2393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..278

(D) OTHER INFORMATION: / Ceres Seq. ID 1572827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2393:

```
His Gln Lys Leu Asn Asn Lys Pro Tyr Thr Ile Lys Asn Met Lys Ile
1 5 10 15
Leu Ser Leu Ser Leu Leu Leu Leu Ala Ala Thr Val Ser Ala Ser
20 25 30
Ile Pro Glu Leu Ile Glu Leu Val Asp Ser Asn Thr Ile Phe Thr Asn
35 40 45
Glu Ala Glu Leu Leu Glu Lys Glu Lys Leu Ser Ile Asn Tyr Ala Asn
50 55 60
Cys Arg Ser Trp His Leu Gly Val Glu Thr Ser Asn Ile Ile Asp Phe
65 70 75 80
Asp Thr Val Pro Ala Asn Cys Lys Asp Tyr Val Glu Asp Tyr Leu Ile
85 90 95
Thr Ser Lys Gln Tyr Gln Tyr Asp Ser Lys Thr Val Cys Lys Glu Ala
100 105 110
Tyr Phe Tyr Ala Lys Gly Leu Ala Leu Lys Asn Asp Thr Val Asn Val
115 120 125
Trp Ile Phe Asp Leu Asp Asp Thr Leu Leu Ser Ser Ile Pro Tyr Tyr
130 135 140
Ala Lys Tyr Gly Tyr Gly Thr Glu Lys Thr Asp Pro Gly Ala Tyr Trp
145 150 155 160
Leu Trp Leu Gly Thr Gly Ala Ser Thr Pro Gly Leu Pro Glu Ala Leu
165 170 175
His Leu Tyr Gln Asn Ile Ile Glu Leu Gly Ile Glu Pro Ile Ile Leu
180 185 190
Ser Asp Arg Trp Lys Leu Trp Lys Asn Val Thr Leu Asp Asn Leu Glu
195 200 205
Ala Ala Gly Val Ala Tyr Trp Lys His Leu Ile Leu Lys Pro Asn Gly
210 215 220
Ser Asn Leu Arg Gln Val Val Tyr Lys Ser Lys Val Arg Lys Ser Leu
225 230 235 240
Val Lys Lys Gly Tyr Asn Ile Val Gly Asn Ile Gly Asp Gln Trp Ala
245 250 255
Asp Leu Val Glu Asp Thr Pro Gly Arg Val Phe Lys Leu Pro Asn Pro
260 265 270
Leu Tyr Tyr Val Pro Ser
```

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(2) INFORMATION FOR SEQ ID NO:2394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..265

(D) OTHER INFORMATION: / Ceres Seq. ID 1572828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2394:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ile | Leu | Ser | Leu | Ser | Leu | Leu | Leu | Ala | Ala | Thr | Val |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Ser | Ala | Ser | Ile | Pro | Glu | Leu | Ile | Glu | Leu | Val | Asp | Ser | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  | Thr |
| Phe | Thr | Asn | Glu | Ala | Glu | Leu | Leu | Glu | Lys | Glu | Lys | Leu | Ser |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  | Ile |
| Tyr | Ala | Asn | Cys | Arg | Ser | Trp | His | Leu | Gly | Val | Glu | Thr | Ser |
|     |     |     | 50  |     |     |     |     | 55  |     |     | 60  |     | Asn |
| Ile | Asp | Phe | Asp | Thr | Val | Pro | Ala | Asn | Cys | Lys | Asp | Tyr | Val |
|     |     |     | 65  |     |     |     |     | 70  |     |     | 75  |     | Glu |
| Tyr | Leu | Ile | Thr | Ser | Lys | Gln | Tyr | Gln | Tyr | Asp | Ser | Lys | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  | Val |
| Lys | Glu | Ala | Tyr | Phe | Tyr | Ala | Lys | Gly | Leu | Ala | Leu | Lys | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 | Asp |
| Val | Asn | Val | Trp | Ile | Phe | Asp | Leu | Asp | Asp | Thr | Leu | Leu | Ser |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 | Ile |
| Pro | Tyr | Tyr | Ala | Lys | Tyr | Gly | Tyr | Gly | Thr | Glu | Lys | Thr | Asp |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     | 140 | Pro |
| Ala | Tyr | Trp | Leu | Trp | Leu | Gly | Thr | Gly | Ala | Ser | Thr | Pro | Gly |
|     |     |     | 145 |     |     |     |     | 150 |     |     | 155 |     | Leu |
| Glu | Ala | Leu | His | Leu | Tyr | Gln | Asn | Ile | Ile | Glu | Leu | Gly | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 | Pro |
| Ile | Ile | Leu | Ser | Asp | Arg | Trp | Lys | Leu | Trp | Lys | Asn | Val | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 | Leu |
| Asn | Leu | Glu | Ala | Ala | Gly | Val | Ala | Tyr | Trp | Lys | His | Leu | Ile |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     | 205 | Leu |
| Pro | Asn | Gly | Ser | Asn | Leu | Arg | Gln | Val | Val | Tyr | Lys | Ser | Lys |
|     |     |     | 210 |     |     |     |     | 215 |     |     |     | 220 | Val |
| Lys | Ser | Leu | Val | Lys | Lys | Gly | Tyr | Asn | Ile | Val | Gly | Asn | Ile |
|     |     |     | 225 |     |     |     |     | 230 |     |     |     | 235 | Gly |
| Gln | Trp | Ala | Asp | Leu | Val | Glu | Asp | Thr | Pro | Gly | Arg | Val | Phe |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     | 255 | Lys |
| Pro | Asn | Pro | Leu | Tyr | Tyr | Val | Pro | Ser |     |     |     |     | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1005 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1005

(D) OTHER INFORMATION: / Ceres Seq. ID 1572833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2395:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ctaccactta | agaagcacag | atggacataa | tctcagggca | agctctgtta | ctctcttttt | 60  |
| gctttatctt | atcatgtttt | cttatcttca | ccaccacaag | atctggagca | atctcccgcg | 120 |



```

ggggccacgc gctgcctcca ggacctccac gggtaccgat catcggaat attcacctcg 180
tcggaaaaca tccacatcgc tcattcgccg agctctcaaa aacttatgga ccagtcgatga 240
gtcttaagct tggaaagttta aatacagtggt ttatagcttc accagaagct gcgagagagg 300
ttttacgaac acatgaccag attttgtctg cccgtagctc cactaacgcg gtacgggtcca 360
tcaatcacca agacgcttct cttgtctggc ttctctgtgc gtcgctcgt tggaggctgt 420
tgagaaggct gtcggtgact cagctcttgt caccacagcg tatcgaagcc acgaaagcct 480
tgaggatgaa caagggtgaag gaacttgta gcttcataag tgaagcagc gataggggaag 540
aatctGgttg atatttctcg tgtagccttc atcacaaact ttaatatcat atcgaaacatt 600
ctgttttccg tcgactctcg tagctacaac gcgaaagctt ctattaatgg ggttcaagac 660
acgggtgatta gtgttatgga gtctgcccgg actccagacg ctgctaatta ctttccattt 720
ctgagggtttc ttgacttcga aggtaatgtg aagactttta aggtttgcac ggagaggctg 780
gtaagggtttt tccgtgggtt cattgatgct aagattgocg aaaaatcatc gcagaataac 840
cctaaagatg tttaaaaaaa cgattttcgtt gacaaccttc tcgattacaa aggagatgaa 900
tcagaactct ccattagcga tattgaacac cttctcttgg taagtctgac cttactgcag 960
ataatcatga ttataagat aatggaataa tcaattttgt ggatg

```

(2) INFORMATION FOR SEQ ID NO:2396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1572834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2396:

```

Met Asp Ile Ile Ser Gly Gln Ala Leu Leu Leu Phe Cys Phe Ile
1 5 10 15
Leu Ser Cys Phe Leu Ile Phe Thr Thr Thr Arg Ser Gly Arg Ile Ser
20 25 30
Arg Gly Ala Thr Ala Leu Pro Pro Gly Pro Pro Arg Leu Pro Ile Ile
35 40 45
Gly Asn Ile His Leu Val Gly Lys His Pro His Arg Ser Phe Ala Glu
50 55 60
Leu Ser Lys Thr Tyr Gly Pro Val Met Ser Leu Lys Leu Gly Ser Leu
65 70 75 80
Asn Thr Val Val Ile Ala Ser Pro Glu Ala Ala Arg Glu Val Leu Arg
85 90 95
Thr His Asp Gln Ile Leu Ser Ala Arg Ser Pro Thr Asn Ala Val Arg
100 105 110
Ser Ile Asn His Gln Asp Ala Ser Leu Val Trp Leu Pro Ser Ser Ser
115 120 125
Ala Arg Trp Arg Leu Leu Arg Arg Leu Ser Val Thr Gln Leu Leu Ser
130 135 140
Pro Gln Arg Ile Glu Ala Thr Lys Ala Leu Arg Met Asn Lys Val Lys
145 150 155 160
Glu Leu Val Ser Phe Ile Ser Glu Ser Ser Asp Arg Glu Glu Ser Gly
165 170 175

```

(2) INFORMATION FOR SEQ ID NO:2397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

[illegible][illegible]

|             |            |             |            |             |            |     |
|-------------|------------|-------------|------------|-------------|------------|-----|
| aacacacata  | cataaaagta | gtagaaactaa | aaataggcaa | acctcttggg  | ctctactttc | 160 |
| aatattttccg | acatttttgt | ctactccaac  | gcacacggcg | caacattgcc  | aatctaaac  | 170 |
| caattgtagt  | acacgtgtgt | ggctgccgca  | agccctggag | gtggccgcagc | tctagatgtc | 180 |
| gggcaatcat  | ggaggctaga | tctcgccgct  | ggcactaaaa | tggccagatt  | tgggggtagg | 190 |
| accaatgtga  | actttgactc | gtgcagatgc  | ggcgcgatgc | aaactgtgtg  | ctgcagtggt | 200 |
| ggactccaat  | gacttggctg | ggcacaccca  | ccaaacacgt | tggctgagta  | cgatttgaac | 210 |
| caattccaaca | ctactgaact | ctgcatactc  | ctacttgcgc | atggaattta  | caactctatg | 220 |

|            |             |             |            |            |             |     |
|------------|-------------|-------------|------------|------------|-------------|-----|
| gagtttagcc | caactagttc  | gaactgccat  | cggatactat | gtaccgcaga | cataaacgga  | 480 |
| caatgtccaa | acgtgttgag  | agccccaggt  | ggatgcaaca | accogtgtag | tgatattcag  | 540 |
| acgaaccaat | actgtgtgtac | gaacgggtcag | ggatcatgta | gcgatactga | ctactcaaga  | 600 |
| ttctttaagc | agagatgccc  | tgNacgctta  | cagctatcca | caagatgacc | cgactagcac  | 660 |
| tttcacttgc | accaacacta  | actacagggt  | cgtgttttgt | ccaaggtcta | ggctcgggtgc | 720 |
| tactggatcc | caccagctcc  | cgatcaagat  | ggtaaccgag | gagaattaat | agactcgtat  | 780 |
| ctactgtatg | tgtgtgtgtg  | tgaggggtga  | cgtagatatg | cgtacgtgtg | acgtgatcat  | 840 |
| atatacgtta | ccataaacac  | ttaattggatt | ataataaggc | atgcaataat | aattacgtta  | 900 |
| gtcgacc    |             |             |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1572838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2400:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Asn | Leu | Leu | Val | Ser | Thr | Phe | Ile | Phe | Ser | Ala | Leu | Leu | Leu |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |  |
| Ile | Ser | Thr | Ala | Thr | Ala | Ala | Thr | Phe | Glu | Ile | Leu | Asn | Gln | Cys | Ser |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |
| Tyr | Thr | Val | Trp | Ala | Ala | Ala | Ser | Pro | Gly | Gly | Gly | Arg | Arg | Leu | Asp |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ala | Gly | Gln | Ser | Trp | Arg | Leu | Asp | Val | Ala | Ala | Gly | Thr | Lys | Met | Ala |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Arg | Ile | Trp | Gly | Arg | Thr | Asn | Cys | Asn | Phe | Asp | Ser | Ser | Gly | Arg | Gly |  |
|     |     |     | 65  |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |  |
| Arg | Cys | Gln | Thr | Gly | Asp | Cys | Ser | Gly | Gly | Leu | Gln | Cys | Thr | Gly | Trp |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |     |  |
| Gly | His | Pro | Pro | Asn | Thr | Leu | Ala | Glu | Tyr | Ala | Leu | Asn | Gln | Phe | Asn |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |  |
| Asn | Leu | Asp | Phe | Tyr | Asp | Ile | Ser | Leu | Val | Asp | Gly | Phe | Asn | Ile | Pro |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |     |  |
| Met | Glu | Phe | Ser | Pro | Thr | Ser | Ser | Asn | Cys | His | Arg | Ile | Leu | Cys | Thr |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |  |
| Ala | Asp | Ile | Asn | Gly | Gln | Cys | Pro | Asn | Val | Leu | Arg | Ala | Pro | Gly | Gly |  |
|     |     |     | 145 |     | 150 |     |     |     | 155 |     |     |     | 160 |     |     |  |
| Cys | Asn | Asn | Pro | Cys | Thr | Val | Phe | Gln | Thr | Asn | Gln | Tyr | Cys | Cys | Thr |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |     |     |     |  |
| Asn | Gly | Gln | Gly | Ser | Cys | Ser | Asp | Thr | Asp | Tyr | Ser | Arg | Phe | Phe | Lys |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |     |  |
| Gln | Arg | Cys | Pro | Xaa | Arg | Leu | Gln | Leu | Ser | Thr | Arg |     |     |     |     |  |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1572839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2401:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Arg | Ile | Trp | Gly | Arg | Thr | Asn | Cys | Asn | Phe | Asp | Ser | Ser | Gly |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |     |  |

```

Arg Gly Arg Cys Gln Thr Gly Asp Cys Ser Gly Gly Leu Gln Cys Thr
 20 25 30
Gly Trp Gly His Pro Pro Asn Thr Leu Ala Glu Tyr Ala Leu Asn Gln
 35 40 45
Phe Asn Asn Leu Asp Phe Tyr Asp Ile Ser Leu Val Asp Gly Phe Asn
 50 55 60
Ile Pro Met Glu Phe Ser Pro Thr Ser Ser Asn Cys His Arg Ile Leu
 65 70 75 80
Cys Thr Ala Asp Ile Asn Gly Gln Cys Pro Asn Val Leu Arg Ala Pro
 85 90 95
Gly Gly Cys Asn Asn Pro Cys Thr Val Phe Gln Thr Asn Gln Tyr Cys
 100 105 110
Cys Thr Asn Gly Gln Gly Ser Cys Ser Asp Thr Asp Tyr Ser Arg Phe
 115 120 125
Phe Lys Gln Arg Cys Pro Xaa Arg Leu Gln Leu Ser Thr Arg
 130 135 140

```

(2) INFORMATION FOR SEQ ID NO:2402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 703 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..703
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2402:

```

aaaaagagat ggtctctgcta gagaagcctt gggatgatgt tgtggctgga cctcagcctg 60
accgtggcct tggccgcctc cgtaagatca ccaccaacc cattaatatc cgagatatag 120
gagaaggagag cagcagtaag tgggtgatgc ataggtcgtt gaccatgccg gcggcagtgga 180
gccctgggaac tccaacgact ccaaccactc cgacgacgcc acgtaaggat aacgtgttga 240
ggagcgtcttt taatccggga agcaaccctcg ccaactagagc catcggtctcc aacatctttg 300
ataaacccac ccatacaaat tctccctcgc tctacgactg gtgttacagc ggtgactcaa 360
ggagtcagca coggtaGgga tgggtccgatg gagtgtgaca tcggggtgatc gtaaaatagg 420
tgacctgatc ttccgccacc ttacttttgt ttttttatat tgttttttgt tactttatca 480
gagtgagataa agtgacgggg aatgtttttc ttttgtacaa aaaactgtct tcccacctaa 540
gcaatgtgtg ttatgtttct ttttggtgtg tgttttgcaa gtttttgtat ttcagagtggt 600
tagtgtagtt gcaagtggcg gttggatctt tcaatatctt gttggatttt gatgatgggt 660
gatgcttttg cttaaagtgt aaataataaa gcatactttt gct

```

(2) INFORMATION FOR SEQ ID NO:2403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2403:

```

Lys Glu Met Val Leu Leu Glu Lys Leu Trp Asp Asp Val Val Ala Gly
1 5 10 15
Pro Gln Pro Asp Arg Gly Leu Gly Arg Leu Arg Lys Ile Thr Thr Gln
 20 25 30
Pro Ile Asn Ile Arg Asp Ile Gly Glu Gly Ser Ser Ser Lys Val Val
 35 40 45
Met His Arg Ser Leu Thr Met Pro Ala Ala Val Ser Pro Gly Thr Pro
 50 55 60
Thr Thr Pro Thr Thr Pro Thr Thr Pro Arg Lys Asp Asn Val Trp Arg

```

65 70 75 80  
Ser Val Phe Asn Pro Gly Ser Asn Leu Ala Thr Arg Ala Ile Gly Ser  
85 90 95  
Asn Ile Phe Asp Lys Pro Thr His Pro Asn Ser Pro Ser Val Tyr Asp  
100 105 110  
Trp Leu Tyr Ser Gly Asp Ser Arg Ser Gln His Arg  
115 120

(2) INFORMATION FOR SEQ ID NO:2404:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1572842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2404:

Met Val Leu Leu Glu Lys Leu Trp Asp Asp Val Val Ala Gly Pro Gln  
1 5 10 15  
Pro Asp Arg Gly Leu Gly Arg Leu Arg Lys Ile Thr Thr Gln Pro Ile  
20 25 30  
Asn Ile Arg Asp Ile Gly Glu Gly Ser Ser Ser Lys Val Val Met His  
35 40 45  
Arg Ser Leu Thr Met Pro Ala Ala Val Ser Pro Gly Thr Pro Thr Thr  
50 55 60  
Pro Thr Thr Pro Thr Thr Pro Arg Lys Asp Asn Val Trp Arg Ser Val  
65 70 75 80  
Phe Asn Pro Gly Ser Asn Leu Ala Thr Arg Ala Ile Gly Ser Asn Ile  
85 90 95  
Phe Asp Lys Pro Thr His Pro Asn Ser Pro Ser Val Tyr Asp Trp Leu  
100 105 110  
Tyr Ser Gly Asp Ser Arg Ser Gln His Arg  
115 120

(2) INFORMATION FOR SEQ ID NO:2405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1572843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2405:

Met His Arg Ser Leu Thr Met Pro Ala Ala Val Ser Pro Gly Thr Pro  
1 5 10 15  
Thr Thr Pro Thr Thr Pro Thr Thr Pro Arg Lys Asp Asn Val Trp Arg  
20 25 30  
Ser Val Phe Asn Pro Gly Ser Asn Leu Ala Thr Arg Ala Ile Gly Ser  
35 40 45  
Asn Ile Phe Asp Lys Pro Thr His Pro Asn Ser Pro Ser Val Tyr Asp  
50 55 60  
Trp Leu Tyr Ser Gly Asp Ser Arg Ser Gln His Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 597 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1.597  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572844  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2406:  
tccttatata attaatgttc accctctctc ttaatagctc ttcaaaacac ttttgttcaa 60  
actctctctt aNttaaaatga aggtctctcc tegtgtgaag tcagcccttc tcctattgtt 120  
catgatcctt gccacagtga tgggtccggt cagggtagag gcacggagct gtgaaacgag 180  
tagcaacttg ttcaatggac catgtctgag tccaagcaat tgcgctaag tttgccacaa 240  
tgaaggtttt tcaatgtgtg actgccgtgg attccgtctg cgtctgtttg gcaccagacc 300  
ctgttgatag atgatctatt tatataaat gaatatatat tatcaaaaac taaatgatct 360  
ttctatgtt ttctatctct ttgatcattt tctgactttt atcctatcgt ttgaccttga 420  
aacaacgata aggagatcta aaatctttta gtctcttttg cttagagctt ctattatcta 480  
ccaaggttaa acaataatac cttttatagt taccatttcc aaatcttatg accttttatg 540  
tatcaaaata gattggactt acacatccaa tctaaataaa acatgattat ccaatct  
(2) INFORMATION FOR SEQ ID NO:2407:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 76 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1.76  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572845  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2407:  
Met Lys Val Ser Pro Arg Leu Lys Ser Ala Leu Leu Leu Leu Phe Met  
1 5 10 15  
Ile Leu Ala Thr Val Met Gly Pro Val Arg Val Glu Ala Arg Thr Cys  
20 25 30  
Glu Thr Ser Ser Asn Leu Phe Asn Gly Pro Cys Leu Ser Ser Ser Asn  
35 40 45  
Cys Ala Asn Val Cys His Asn Glu Gly Phe Ser Asp Gly Asp Cys Arg  
50 55 60  
Gly Phe Arg Arg Arg Cys Leu Cys Thr Arg Pro Cys  
65 70 75  
(2) INFORMATION FOR SEQ ID NO:2408:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 61 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1.61  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572846  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2408:  
Met Ile Leu Ala Thr Val Met Gly Pro Val Arg Val Glu Ala Arg Thr  
1 5 10 15  
Cys Glu Thr Ser Ser Asn Leu Phe Asn Gly Pro Cys Leu Ser Ser Ser  
20 25 30  
Asn Cys Ala Asn Val Cys His Asn Glu Gly Phe Ser Asp Gly Asp Cys  
35 40 45  
Arg Gly Phe Arg Arg Arg Cys Leu Cys Thr Arg Pro Cys  
50 55 60  
(2) INFORMATION FOR SEQ ID NO:2409:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 59 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..59  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572847  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2409:  
Met Ile Tyr Leu Tyr Ile Met Asn Ile Tyr Tyr Gln Lys Leu Asn Asp  
1                  5                  10                  15  
Leu Phe Tyr Val Phe Tyr Leu Phe Asp His Phe Leu Thr Phe Ile Leu  
                  20                  25                  30  
Ser Phe Ala Phe Glu Thr Thr Ile Arg Arg Ser Lys Ile Phe Lys Ser  
                  35                  40                  45  
Phe Trp Leu Glu Leu Ser Ile Ile Tyr Gln Gly  
                  50                  55

(2) INFORMATION FOR SEQ ID NO:2410:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 1145 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..1145  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1572852  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2410:  
aaattttccc cattaaacaa aaaaaaatca aatctctctc ttctctctc taatggcgcc 60  
gacatttaggc agagaccagt atgtgtacat ggccaagCtc gccgagcagg cggaagcgcta 120  
cgaagagatg gttcaattca tggaacagct cgttacagcc gctactccag cggaagagct 180  
cacogttgaa gagaggaatc tctctctctg tgcttacaaa aacgtgatcg gatctctacg 240  
cgccgcctgg aggatcttgt ctctgatgta gcagaaggaa gagagtagga agaagcgacga 300  
gcacgtgtcg ctgtccaagg attacatata taaagttagg tctgagcttt ctctgtgttg 360  
ctctggaatc cttaagctcc ttgactcgca tctgatccca tctgctggag cgagtgaagt 420  
taaggtcttt tacttgaaga tgaagggtga ttatcatcgg tacatggctg agtttaagtc 480  
tggtgatgag aggaaaactg ctgctgaaga taccatgctc gcttacaaaag cagctcaagg 540  
tatcgacgct gcgatatagg cacctactca tccgataaagg ctggtctgg cctgaattt 600  
ctcagtggtc tactatgaga ttctcaatc ttacagacaa gcttgtaaca tggccaaaca 660  
ggcttttgag gaggccatag ctgagcttga cactctggga gaggaatcct acaagacag 720  
cactctcata atgcagttgc tgagggacaa ttttaacctt tggacctccg atatgcagga 780  
gcagatggag gaggcctgag gatctagatg aaggggggga ggggtgttac gcgatgtttc 840  
tgccaccaaa tgcatactcaa aatccccata accttctgct aaaaactgtg aaaaagatt 900  
gaagtgttta tgatgattat gattgtgcac agcttgatga ttatctact ctactaaaac 960  
tctgtgtctt taatatattat tgtctcagct ctgctcaagc cttaaaaaaca tctttctcct 1020  
taaggtcctc ctggttaaat tatgatcctt ctactgtatc gtcaaaatca agttgggaac 1080  
caaaattgtg ggattttttg tcggtgtgaa actgtgaata ataaaaaccg tcaattgtgt 1140  
tactg

(2) INFORMATION FOR SEQ ID NO:2411:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 248 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..248

(D) OTHER INFORMATION: / Ceres Seq. ID 1572853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2411:

```
Met Ala Ala Thr Leu Gly Arg Asp Gln Tyr Val Tyr Met Ala Lys Leu
1 5 10 15
Ala Glu Gln Ala Glu Arg Tyr Glu Glu Met Val Gln Phe Met Glu Gln
20 25 30
Leu Val Thr Gly Ala Thr Pro Ala Glu Glu Leu Thr Val Glu Glu Arg
35 40 45
Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly Ser Leu Arg Ala
50 55 60
Ala Trp Arg Ile Leu Ser Ser Ile Glu Gln Lys Glu Glu Ser Arg Lys
65 70 75 80
Asn Asp Glu His Val Ser Leu Val Lys Asp Tyr Ile Ser Lys Val Glu
85 90 95
Ser Glu Leu Ser Ser Val Cys Ser Gly Ile Leu Lys Leu Leu Asp Ser
100 105 110
His Leu Ile Pro Ser Ala Gly Ala Ser Glu Ser Lys Val Phe Tyr Leu
115 120 125
Lys Met Lys Gly Asp Tyr His Arg Tyr Met Ala Glu Phe Lys Ser Gly
130 135 140
Asp Glu Arg Lys Thr Ala Ala Glu Asp Thr Met Leu Ala Tyr Lys Ala
145 150 155 160
Ala Gln Asp Ile Ala Ala Ala Asp Met Ala Pro Thr His Pro Ile Arg
165 170 175
Leu Gly Leu Ala Leu Asn Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn
180 185 190
Ser Ser Asp Lys Ala Cys Asn Met Ala Lys Gln Ala Phe Glu Glu Ala
195 200 205
Ile Ala Glu Leu Asp Thr Leu Gly Glu Glu Ser Tyr Lys Asp Ser Thr
210 215 220
Leu Ile Met Gln Leu Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp
225 230 235 240
Met Gln Glu Gln Met Asp Glu Ala
245
```

(2) INFORMATION FOR SEQ ID NO:2412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1572854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2412:

```
Met Ala Lys Leu Ala Glu Gln Ala Glu Arg Tyr Glu Glu Met Val Gln
1 5 10 15
Phe Met Glu Gln Leu Val Thr Gly Ala Thr Pro Ala Glu Glu Leu Thr
20 25 30
Val Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly
35 40 45
Ser Leu Arg Ala Ala Trp Arg Ile Leu Ser Ser Ile Glu Gln Lys Glu
50 55 60
Glu Ser Arg Lys Asn Asp Glu His Val Ser Leu Val Lys Asp Tyr Ile
65 70 75 80
Ser Lys Val Glu Ser Glu Leu Ser Ser Val Cys Ser Gly Ile Leu Lys
85 90 95
Leu Leu Asp Ser His Leu Ile Pro Ser Ala Gly Ala Ser Glu Ser Lys
100 105 110
Val Phe Tyr Leu Lys Met Lys Gly Asp Tyr His Arg Tyr Met Ala Glu
```



115 120 125  
Phe Lys Ser Gly Asp Glu Arg Lys Thr Ala Ala Glu Asp Thr Met Leu  
130 135 140  
Ala Tyr Lys Ala Ala Gln Asp Ile Ala Ala Asp Met Ala Pro Thr  
145 150 155 160  
His Pro Ile Arg Leu Gly Leu Ala Leu Asn Phe Ser Val Phe Tyr Tyr  
165 170 175  
Glu Ile Leu Asn Ser Ser Asp Lys Ala Cys Asn Met Ala Lys Gln Ala  
180 185 190  
Phe Glu Glu Ala Ile Ala Glu Leu Asp Thr Leu Gly Glu Glu Ser Tyr  
195 200 205  
Lys Asp Ser Thr Leu Ile Met Gln Leu Leu Arg Asp Asn Leu Thr Leu  
210 215 220  
Trp Thr Ser Asp Met Gln Glu Gln Met Asp Glu Ala  
225 230 235

(2) INFORMATION FOR SEQ ID NO:2413:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1572855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2413:

Met Val Gln Phe Met Glu Gln Leu Val Thr Gly Ala Thr Pro Ala Glu  
1 5 10 15  
Glu Leu Thr Val Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn  
20 25 30  
Val Ile Gly Ser Leu Arg Ala Ala Trp Arg Ile Leu Ser Ser Ile Glu  
35 40 45  
Gln Lys Glu Glu Ser Arg Lys Asn Asp Glu His Val Ser Leu Val Lys  
50 55 60  
Asp Tyr Ile Ser Lys Val Glu Ser Glu Leu Ser Ser Val Cys Ser Gly  
65 70 75 80  
Ile Leu Lys Leu Leu Asp Ser His Leu Ile Pro Ser Ala Gly Ala Ser  
85 90 95  
Glu Ser Lys Val Phe Tyr Leu Lys Met Lys Gly Asp Tyr His Arg Tyr  
100 105 110  
Met Ala Glu Phe Lys Ser Gly Asp Glu Arg Lys Thr Ala Ala Glu Asp  
115 120 125  
Thr Met Leu Ala Tyr Lys Ala Ala Gln Asp Ile Ala Ala Ala Asp Met  
130 135 140  
Ala Pro Thr His Pro Ile Arg Leu Gly Leu Ala Leu Asn Phe Ser Val  
145 150 155 160  
Phe Tyr Tyr Glu Ile Leu Asn Ser Ser Asp Lys Ala Cys Asn Met Ala  
165 170 175  
Lys Gln Ala Phe Glu Glu Ala Ile Ala Glu Leu Asp Thr Leu Gly Glu  
180 185 190  
Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met Gln Leu Leu Arg Asp Asn  
195 200 205  
Leu Thr Leu Trp Thr Ser Asp Met Gln Glu Gln Met Asp Glu Ala  
210 215 220

(2) INFORMATION FOR SEQ ID NO:2414:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1208 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1208

(D) OTHER INFORMATION: / Ceres Seq. ID 1572858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2414:

```

acaagcaaaa aaaattcaact ttttgtttt gttaacactc acgtgaaagc ttcgtttctt 60
ttcaaacctt ttgaacaatt ttcctgatgc cggtaaatac cgggtttacg tttagctacc 120
ggttactctt cctcatcttc ctttttgagt tcgaaacggc acagcggttg gtcaccgggtg 180
accacaacga cgaagcatgc ttgacgaatc tccgtcggag tttagaagat ccgcgcaata 240
atcttcgtta ctggacaaaa tcttttcttc taaatccttg ctcocggctt tctttttatc 300
ttcatggagt catttgcac aaatggcagaa tttaacaaat ctcttaaga aaatctcttc 360
tccgtggctc aatctctcog tttctctcta attgcacaaa tctccaatcc ctagatctat 420
cttccaacca gatctccggc gagatccggc cgcaattaca gtttctcgtt aacctagccg 480
ttcttaactc ctcttctaata cgtctctcgc gtcaaatctc accaacaatc gctctctgcg 540
cttacttaaa cgtcatcgat ctccacgata accaactctc cgggtcaaat ccgtttcagt 600
tcgggtttct cgttagatta acggcggttg atgtctctaa taacaaatta tccggtcaga 660
ttccctcgaa tctggcgcgt cgtaacggaa acttgcgcgag atttaacgcg agctcgttta 720
tagggaacaa gaaattgttc gggatatccg tggaggagat gaagaacaaa ggattgtcga 780
taattggcgt tttgtgggtt ggacttggaa gtggaatcgc gagcttagtg attagcttca 840
ctggagtttg tataagggtt aagattacag agaagaagat ggaggaagaa gaaggaaata 900
taagtcaact catgcctgtt tactaaacac aaacatttgc ttttttttct tcttaagtat 960
aattaacggg ttttttttct acataattag tttttttttt ccatattgat caaaagcata 1020
cagcaaatag gagggttcaa ttaagcgaa ttagggttaa ttaatgcttt gatcataat 1080
acatgtttct ttggttatct ttggatacat attacaacaaa atcacaaagt ttaagcatga 1140
ggactaagt tattgttgta tagtttttgg agttatgaaa gtgtaattta tagtgacatc 1200
atttatgc

```

(2) INFORMATION FOR SEQ ID NO:2415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..279

(D) OTHER INFORMATION: / Ceres Seq. ID 1572859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2415:

```

Met Pro Val Asn His Arg Phe Thr Phe Ser Tyr Arg Leu Leu Phe Leu
1 5 10 15
Ile Phe Leu Leu Ser Phe Glu Thr Ala Gln Arg Leu Val Thr Gly Asp
20 25 30
Pro Asn Asp Glu Ala Cys Leu Thr Asn Leu Arg Arg Ser Leu Glu Asp
35 40 45
Pro Ala Asn Asn Leu Arg Asn Trp Thr Lys Ser Phe Phe Ile Asn Pro
50 55 60
Cys Ser Gly Phe Ser Ser Tyr Leu His Gly Val Ile Cys Asn Asn Gly
65 70 75 80
Arg Ile Tyr Lys Leu Ser Leu Thr Asn Leu Ser Leu Arg Gly Ser Ile
85 90 95
Ser Pro Phe Leu Ser Asn Cys Thr Asn Leu Gln Ser Leu Asp Leu Ser
100 105 110
Ser Asn Gln Ile Ser Gly Glu Ile Pro Pro Gln Leu Gln Phe Leu Val
115 120 125
Asn Leu Ala Val Leu Asn Leu Ser Ser Asn Arg Leu Ser Gly Gln Ile
130 135 140
Ser Pro Gln Ile Ala Leu Cys Ala Tyr Leu Asn Val Ile Asp Leu His
145 150 155 160
Asp Asn Gln Leu Ser Gly Gln Ile Pro Phe Gln Phe Gly Leu Leu Ala
165 170 175

```

20250110 10:00:00

Arg Leu Thr Ala Phe Asp Val Ser Asn Asn Lys Leu Ser Gly Gln Ile  
180 185 190  
Pro Ser Asn Leu Ala Met Arg Asn Gly Asn Leu Pro Arg Phe Asn Ala  
195 200 205  
Ser Ser Phe Ile Gly Asn Lys Lys Leu Phe Gly Tyr Pro Leu Glu Glu  
210 215 220  
Met Lys Asn Lys Gly Leu Ser Ile Met Ala Ile Val Gly Ile Gly Leu  
225 230 235 240  
Gly Ser Gly Ile Ala Ser Leu Val Ile Ser Phe Thr Gly Val Cys Ile  
245 250 255  
Trp Leu Lys Ile Thr Glu Lys Lys Met Glu Glu Glu Glu Gly Lys Ile  
260 265 270  
Ser His Ser Met Pro Val Tyr  
275

(2) INFORMATION FOR SEQ ID NO:2416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 989 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..989
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2416:

|             |            |            |             |            |             |     |
|-------------|------------|------------|-------------|------------|-------------|-----|
| aagttgaatg  | tactgatcaa | gataacaaat | ttatcaaaaa  | taaatacatc | atactggttt  | 60  |
| atgagcaaga  | aacattgtct | agaattatta | ccaaataaga  | tgtttagaaa | ccaagactcg  | 120 |
| aaatacttga  | tcccggtgca | gaaagaagcg | ccaccggtga  | caactttacc | gatgaaagct  | 180 |
| tcaacgggtg  | aatctccaca | caactgtgag | gccattctca  | gagacgcaga | tcctccgatc  | 240 |
| ctctctctct  | ctgttaatct | ctctgaacag | ctacggtctg  | gtgttttctt | gaaacccaag  | 300 |
| aaacagatca  | aatattgggt | ggacgagaga | aacagcaact  | gcttcattgt | ctttgcaaa   | 360 |
| aacctctcta  | taacttgggt | tgatgacgtc | aactattgga  | cttggtttac | cgaaaaagag  | 420 |
| tcaccaaaacg | agaatgtgga | agctgtggga | ttgaaaaacg  | ttgttgggt  | cgacatcacg  | 480 |
| ggaaaaattcg | acacgaggaa | cctcactccg | gggattgttt  | acgagggtgt | cttcaagggt  | 540 |
| aagctagagg  | atccggccta | tggatgggac | acgccggtga  | acctaaaagt | agtccttgCct | 600 |
| aacggtgaag  | agacgccaca | agagcaaaag | ttgagtttga  | gggaacttcc | aagggtataaa | 660 |
| tgggtgcgatg | tcagagtgtg | cgagtgcgtg | cctgagaaaat | ccgctgcgcg | agagatcact  | 720 |
| ttctcaatgt  | atgagcatgt | ggctggtggt | tggaaagaaa  | ggctctccct | caaaagtggt  | 780 |
| gcaattcgct  | ccaaacagta | ataattgtta | tggcatagaa  | aaacataaat | ctccatatgc  | 840 |
| accaatggac  | cttctcaaca | tataattcac | atcatgtcat  | gtgtgtataa | taaggttggt  | 900 |
| ctatcgattt  | tttagtttta | ataataaact | taatgttggt  | gttgaataaa | ctcaaaaacga | 960 |
| gtgttttgaa  | ggtgtgtata | ttcgaatcg  |             |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2417:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Leu | Asn | Val | Leu | Ile | Lys | Ile | Thr | Asn | Leu | Ser | Lys | Ile | Asn | Thr |
| 1   |     |     |     |     | 5   |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Tyr | Trp | Phe | Met | Ser | Lys | Lys | His | Cys | Ser | Glu | Leu | Leu | Pro | Asn |
|     |     |     |     |     | 20  |     |     | 25  |     |     |     |     |     | 30  |     |
| Lys | Met | Phe | Arg | Asn | Gln | Asp | Ser | Lys | Tyr | Leu | Ile | Pro | Val | Gln | Lys |
|     |     |     |     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ala | Pro | Pro | Val | Thr | Thr | Leu | Pro | Met | Lys | Ala | Ser | Thr | Val | Lys |
| 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ser | Pro | His | Asn | Cys | Glu | Ala | Ile | Leu | Arg | Asp | Ala | Asp | Pro | Pro | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Leu | Ser | Ser | Val | Asn | Leu | Ser | Glu | Gln | Leu | Arg | Ser | Gly | Val | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Lys | Pro | Lys | Lys | Gln | Ile | Lys | Tyr | Trp | Val | Asp | Glu | Arg | Asn | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Cys | Phe | Met | Leu | Phe | Ala | Lys | Asn | Leu | Ser | Ile | Thr | Trp | Ser | Asp |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Asp | Val | Asn | Tyr | Trp | Thr | Trp | Phe | Thr | Glu | Lys | Glu | Ser | Pro | Asn | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Val | Glu | Ala | Val | Gly | Leu | Lys | Asn | Val | Cys | Trp | Leu | Asp | Ile | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Lys | Phe | Asp | Thr | Arg | Asn | Leu | Thr | Pro | Gly | Ile | Val | Tyr | Glu | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Phe | Lys | Val | Lys | Leu | Glu | Asp | Pro | Ala | Tyr | Gly | Trp | Asp | Thr | Pro |
|     |     |     |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Asn | Leu | Lys | Leu | Val | Leu | Pro | Asn | Gly | Lys | Glu | Thr | Pro | Gln | Glu |
|     |     |     |     |     |     |     |     | 200 |     |     |     | 205 |     |     |     |
| Gln | Lys | Leu | Ser | Leu | Arg | Glu | Leu | Pro | Arg | Tyr | Lys | Trp | Val | Asp | Val |
|     |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Arg | Val | Gly | Glu | Phe | Val | Pro | Glu | Lys | Ser | Ala | Ala | Gly | Glu | Ile | Thr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Phe | Ser | Met | Tyr | Glu | His | Val | Ala | Gly | Val | Trp | Lys | Lys | Gly | Leu | Ser |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Lys | Gly | Val | Ala | Ile | Arg | Pro | Lys | Gln |     |     |     |     |     |     |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2418:

### (i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 246 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..246

(D) OTHER INFORMATION: / Ceres Seq. ID 1572862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2418:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   | Ser | Lys | Lys | His | Cys | Ser | Glu | Leu | Leu | Pro | Asn | Lys | Met | Phe | Arg |
| 5   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |
| Asn | Gln | Asp | Ser | Lys | Tyr | Leu | Ile | Pro | Val | Gln | Lys | Glu | Ala | Pro | Pro |
| 20  |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Thr | Thr | Leu | Pro | Met | Lys | Ala | Ser | Thr | Val | Lys | Ser | Pro | His | Asn |
| 35  |     |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Glu | Ala | Ile | Leu | Arg | Asp | Ala | Asp | Pro | Pro | Ile | Ser | Leu | Ser | Ser |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Asn | Leu | Ser | Glu | Gln | Lys | Arg | Ser | Gly | Val | Phe | Leu | Lys | Pro | Lys |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Lys | Gln | Ile | Lys | Tyr | Trp | Val | Asp | Glu | Arg | Asn | Ser | Asn | Cys | Phe | Met |
| 85  |     |     |     |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Phe | Ala | Lys | Asn | Leu | Ser | Ile | Thr | Trp | Ser | Asp | Asp | Val | Asn | Tyr |
| 100 |     |     |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Trp | Thr | Trp | Phe | Thr | Glu | Lys | Glu | Ser | Pro | Asn | Glu | Asn | Val | Glu | Ala |
| 115 |     |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Gly | Lys | Lys | Asn | Val | Cys | Trp | Leu | Asp | Ile | Thr | Gly | Lys | Phe | Asp |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Arg | Asn | Leu | Thr | Pro | Gly | Ile | Val | Tyr | Glu | Val | Val | Phe | Lys | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Leu | Glu | Asp | Pro | Ala | Tyr | Gly | Trp | Asp | Thr | Pro | Val | Asn | Leu | Lys |

165 170 175  
Leu Val Leu Pro Asn Gly Lys Glu Thr Pro Gln Glu Gln Lys Leu Ser  
180 185 190  
Leu Arg Glu Leu Pro Arg Tyr Lys Trp Val Asp Val Arg Val Gly Glu  
195 200 205  
Phe Val Pro Glu Lys Ser Ala Ala Gly Glu Ile Thr Phe Ser Met Tyr  
210 215 220  
Glu His Val Ala Gly Val Trp Lys Lys Gly Leu Ser Leu Lys Gly Val  
225 230 235 240  
Ala Ile Arg Pro Lys Gln  
245

(2) INFORMATION FOR SEQ ID NO:2419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..233

(D) OTHER INFORMATION: / Ceres Seq. ID 1572863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2419:

Met Phe Arg Asn Gln Asp Ser Lys Tyr Leu Ile Pro Val Gln Lys Glu  
1 5 10 15  
Ala Pro Pro Val Thr Thr Leu Pro Met Lys Ala Ser Thr Val Lys Ser  
20 25 30  
Pro His Asn Cys Glu Ala Ile Leu Arg Asp Ala Asp Pro Pro Ile Ser  
35 40 45  
Leu Ser Ser Val Asn Leu Ser Glu Gln Leu Arg Ser Gly Val Phe Leu  
50 55 60  
Lys Pro Lys Lys Gln Ile Lys Tyr Trp Val Asp Glu Arg Asn Ser Asn  
65 70 75 80  
Cys Phe Met Leu Phe Ala Lys Asn Leu Ser Ile Thr Trp Ser Asp Asp  
85 90 95  
Val Asn Tyr Trp Thr Trp Phe Thr Glu Lys Glu Ser Pro Asn Glu Asn  
100 105 110  
Val Glu Ala Val Gly Leu Lys Asn Val Cys Trp Leu Asp Ile Thr Gly  
115 120 125  
Lys Phe Asp Thr Arg Asn Leu Thr Pro Gly Ile Val Tyr Glu Val Val  
130 135 140  
Phe Lys Val Lys Leu Glu Asp Pro Ala Tyr Gly Trp Asp Thr Pro Val  
145 150 155 160  
Asn Leu Lys Leu Val Leu Pro Asn Gly Lys Glu Thr Pro Gln Glu Gln  
165 170 175  
Lys Leu Ser Leu Arg Glu Leu Pro Arg Tyr Lys Trp Val Asp Val Arg  
180 185 190  
Val Gly Glu Phe Val Pro Glu Lys Ser Ala Ala Gly Glu Ile Thr Phe  
195 200 205  
Ser Met Tyr Glu His Val Ala Gly Val Trp Lys Lys Gly Leu Ser Leu  
210 215 220  
Lys Gly Val Ala Ile Arg Pro Lys Gln  
225 230

(2) INFORMATION FOR SEQ ID NO:2420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 516 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..516

(D) OTHER INFORMATION: / Ceres Seq. ID 1572868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2420:

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| aaaccctaga | cctaatactt  | tagcgaaatt  | aagcagagca | acattttcgt | aatccgagct | 60  |
| ccgtcgtcgt | cgtcgaatca  | gataaaaaatg | gcgaaGcggt | tgatcccgac | tctcaaccgt | 120 |
| gtattggtgg | agaagattct  | cccaccgtca  | aagaccgtct | ccggcattct | cctaccggag | 180 |
| aaatcatctc | agttgaattc  | cgggagaggtt | atagcagttg | gtcctgggag | tagagacaga | 240 |
| cgagggaatc | taattccggt  | ttcggttaag  | gaaggagaca | atgtttcttt | gcctgaattt | 300 |
| ggtgtgtact | aagtttaagct | tggagagaaa  | gagttcctat | tgtataggga | tgaagataac | 360 |
| atggctaac  | ttcacgagtg  | atgtgttaaa  | gagatagaat | ttagtattcc | tctttgtttt | 420 |
| gttgctctga | attgtctgac  | atttggatca  | attgttatga | ttgttcttca | ctgttgccaa | 480 |
| caagtcttta | taattcaata  | atctcttttg  | tttggc     |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2421:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1572869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2421:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Lys | Arg | Leu | Ile | Pro | Thr | Leu | Asn | Arg | Val | Leu | Val | Glu | Lys |  |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |  |
| Ile | Leu | Pro | Pro | Ser | Lys | Thr | Val | Ser | Gly | Ile | Leu | Leu | Pro | Glu | Lys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Ser | Gln | Leu | Asn | Ser | Gly | Arg | Val | Ile | Ala | Val | Gly | Pro | Gly | Ala |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Asp | Arg | Ala | Gly | Asn | Leu | Ile | Pro | Val | Ser | Val | Lys | Glu | Gly | Asp |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Asn | Val | Leu | Leu | Pro | Glu | Phe | Gly | Gly | Thr | Gln | Val | Lys | Leu | Gly | Glu |  |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |  |
| Lys | Glu | Phe | Leu | Leu | Tyr | Arg | Asp | Glu | Asp | Ile | Met | Ala | Thr | Leu | His |  |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     | 95  |     |  |
| Glu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2422:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 691 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..691

(D) OTHER INFORMATION: / Ceres Seq. ID 1572878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2422:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| atcagaaatc | gaaaaatcaa | agttctcaag | aagatatcaa | caaaaaaaa  | gtaaattctt  | 60  |
| taaaatgtcg | atgatctcaa | gtttcttcaa | caacaacaga | cgaagcaaca | tctttgatcc  | 120 |
| attctctctt | gacgtatggg | atccattcaa | ggaactaaca | tcatcatcac | tttctcgtga  | 180 |
| gaactcagcg | atcgtgaacg | cacgtgtgga | ctggagagag | acgcctgagg | cgcacgtgtt  | 240 |
| taaaagtgc  | tgtcctggat | tgaagaagga | ggaagttaaa | gttgagattg | aggagggatg  | 300 |
| tgttttgaag | atcagtgag  | agagacacgt | ggagaaagaa | gataagaatg | acacgtggca  | 360 |
| ccgtgtggag | agatcagatg | gacagtttac | gaggagggtt | aggttgccgg | agaattgtga  | 420 |
| gatgatcag  | gttaagcgtg | cagtgagaga | tggtgtgttg | actgttacgg | tgccataaggc | 480 |
| tgagRactaa | gaagcgtgat | gttaagtcta | ttcagatctc | tggttgagta | atggggttgc  | 540 |
| gttttatcat | cggagtgtct | tgtgtttttg | tcatggttat | ggttcatggt | ttacttgagt  | 600 |

gtgtgagtcc tctatctctaaa ttataataat ctccgattga gctatgaatt atgatgtatc 660

ggatacatatt gatcctaagt aagtatggaa t  
(2) INFORMATION FOR SEQ ID NO:2423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2423:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Glu | Ile | Glu | Lys | Ser | Lys | Phe | Ser | Arg | Arg | Tyr | Gln | Gln | Lys | Lys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Lys | Phe | Phe | Lys | Met | Ser | Met | Ile | Pro | Ser | Phe | Phe | Asn | Asn | Asn |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Arg | Ser | Asn | Ile | Phe | Asp | Pro | Phe | Ser | Leu | Asp | Val | Trp | Asp | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Lys | Glu | Leu | Thr | Ser | Ser | Ser | Leu | Ser | Arg | Glu | Asn | Ser | Ala | Ile |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Asn | Ala | Arg | Val | Asp | Trp | Arg | Glu | Thr | Pro | Glu | Ala | His | Val | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Ala | Asp | Leu | Pro | Gly | Leu | Lys | Lys | Glu | Glu | Val | Lys | Val | Glu | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Glu | Asp | Ser | Val | Leu | Lys | Ile | Ser | Gly | Glu | Arg | His | Val | Glu | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Asp | Lys | Asn | Asp | Thr | Trp | His | Arg | Val | Glu | Arg | Ser | Ser | Gly | Gln |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Thr | Arg | Arg | Phe | Arg | Leu | Pro | Glu | Asn | Val | Lys | Met | Asp | Gln | Val |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Ala | Ala | Met | Glu | Asn | Gly | Val | Leu | Thr | Val | Thr | Val | Pro | Lys | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Glu | Xaa |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2424:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Met | Ile | Pro | Ser | Phe | Phe | Asn | Asn | Asn | Arg | Arg | Ser | Asn | Ile |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Phe | Asp | Pro | Phe | Ser | Leu | Asp | Val | Trp | Asp | Pro | Phe | Lys | Glu | Leu | Thr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ser | Ser | Leu | Ser | Arg | Glu | Asn | Ser | Ala | Ile | Val | Asn | Ala | Arg | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Trp | Arg | Glu | Thr | Pro | Glu | Ala | His | Val | Phe | Lys | Ala | Asp | Leu | Pro |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Leu | Lys | Lys | Glu | Glu | Val | Lys | Val | Glu | Ile | Glu | Glu | Asp | Ser | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Lys | Ile | Ser | Gly | Glu | Arg | His | Val | Glu | Lys | Glu | Asp | Lys | Asn | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |     |
| Thr | Trp | His | Arg | Val | Glu | Arg | Ser | Ser | Gly | Gln | Phe | Thr | Arg | Arg | Phe |

100 105 110  
Arg Leu Pro Glu Asn Val Lys Met Asp Gln Val Lys Ala Ala Met Glu  
115 120 125  
Asn Gly Val Leu Thr Val Thr Val Pro Lys Ala Glu Xaa  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1572861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2425:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Pro | Ser | Phe | Phe | Asn | Asn | Asn | Arg | Ser | Asn | Ile | Phe | Asp |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     | 15  |     |     |
| Pro | Phe | Ser | Leu | Asp | Val | Trp | Asp | Pro | Phe | Lys | Glu | Leu | Thr | Ser |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Leu | Ser | Arg | Glu | Asn | Ser | Ala | Ile | Val | Asn | Ala | Arg | Val | Asp |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     | Trp |
| Arg | Glu | Thr | Pro | Glu | Ala | His | Val | Phe | Lys | Ala | Asp | Leu | Pro | Gly |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     | Leu |
| Lys | Lys | Glu | Glu | Val | Lys | Val | Glu | Ile | Glu | Glu | Asp | Ser | Val | Leu |
|     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Ser | Gly | Glu | Arg | His | Val | Glu | Lys | Glu | Asp | Lys | Asn | Asp | Thr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  | Trp |
| His | Arg | Val | Glu | Arg | Ser | Ser | Gly | Gln | Phe | Thr | Arg | Arg | Phe | Arg |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 | Leu |
| Pro | Glu | Asn | Val | Lys | Met | Asp | Gln | Val | Lys | Ala | Ala | Met | Glu | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 | Gly |
| Val | Leu | Thr | Val | Thr | Val | Pro | Lys | Ala | Glu | Xaa |     |     |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1524

(D) OTHER INFORMATION: / Ceres Seq. ID 1572886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2426:

|             |             |            |            |             |             |     |
|-------------|-------------|------------|------------|-------------|-------------|-----|
| ttttttctttc | ttttttcttc  | tgggagtttg | ggattttctt | gagggtcttt  | ttcaattttc  | 60  |
| gtctcaatttt | gtacgcatag  | aactgggttt | gtgtttacac | acataaagct  | cttatctttt  | 120 |
| ttctctcttc  | aatcgagaag  | attatagagc | tgagtgaact | attggtggtt  | tcttgaggatt | 180 |
| ttaattgggag | gttggtttcag | caatcggatt | aaaacagata | ttgcttcacg  | tacatggcta  | 240 |
| agttcgaaat  | tcttgagtag  | agatgggagc | aagggtctcg | cgaccgcttc  | ctctcttatt  | 300 |
| atgctctgaa  | cagaaggcga  | gatcttgcaa | aatgctaact | tcaagaactt  | tagtctcagt  | 360 |
| gaactgaaat  | ctgcaactag  | gaatttcagg | ctgatatagt | tggttggtga  | agggtgattt  | 420 |
| ggttggtgtt  | tcaaaagctg  | gatcgatgag | tctctctctg | ctccttctaa  | accggggacc  | 480 |
| Gggattgtca  | ttgctgtgaa  | aagacttaac | caagaagggt | ttcaagggtca | tgcagagtgg  | 540 |
| ctggctgaga  | tcaattattt  | aggccagctg | gatcatccta | acctgtgtaa  | actgattgga  | 600 |
| tactgcttgg  | aagaggagca  | caggctctct | gtttacgagt | ttaatgactg  | tggtagtctt  | 660 |
| gagaaatcag  | tattcagaag  | aggaacattc | tatcagccac | tttcaatgaa  | cacgcggggt  | 720 |
| cgtatggctc  | ttggtgcagc  | tagaggactt | gcttttcttc | acaatgtcta  | accgcaagtt  | 780 |
| atataccgag  | acttcaaagc  | atctaaacat | ttgctagatt | cgaactacaa  | cgcaaaagctt | 840 |



|             |             |             |             |             |            |      |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| tcgggatttcg | gtttggctag  | agatgggtcca | atgggtgaca  | acagccatgt  | ttctaccaga | 900  |
| gtcatgggaa  | ctcagggata  | cgctgtccca  | gaatatctag  | ctacagggtca | tttatcggtg | 960  |
| aagagcgatg  | tatacagttt  | tggggttggt  | ttactggagt  | tgttatcagg  | aagacgagca | 1020 |
| attgacaaga  | atcaaccagt  | aggagaacac  | aatctcgtg   | attgggcaag  | accctactta | 1080 |
| acaaacaaga  | gaagacttct  | gcgagtgatg  | gatcctcgtc  | tccaagggtca | atactacta  | 1140 |
| accggagctt  | tgaaaaattgc | agttcttgca  | ctcgtattgca | tatctataga  | tgccaagagt | 1200 |
| agaccggaca  | tgaacgaat   | cgtaacagaca | atggaagaac  | ttcatatcca  | gaaggaagca | 1260 |
| tcaaaagagc  | agcagaatcc  | tcaaatcagc  | attgacaaca  | tcatacaaca  | atctccacaa | 1320 |
| gctgtgaatt  | atcctagggc  | ttcaattatg  | taacaatcct  | aggcgagcta  | tttaccgagt | 1380 |
| tttagagatg  | tatagactct  | ttaccctctg  | tctgtttaga  | tattatgttg  | tttggtagta | 1440 |
| acaaaagagc  | tgggcaatgta | agggagagaa  | ggaaacctac  | tagttgttaa  | cttaggttct | 1500 |
| cttacaacgt  | tcacatgtta  | tccc        |             |             |            |      |

(2) INFORMATION FOR SEQ ID NO:2427:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 389 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..389

(D) OTHER INFORMATION: / Ceres Seq. ID 1572887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2427:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Gly | Cys | Phe | Ser | Asn | Arg | Ile | Lys | Thr | Asp | Ile | Ala | Ser | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Thr | Trp | Leu | Ser | Ser | Lys | Phe | Leu | Ser | Arg | Asp | Gly | Ser | Lys | Gly | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Thr | Ala | Ser | Phe | Ser | Tyr | Met | Pro | Arg | Thr | Glu | Gly | Glu | Ile | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Asn | Ala | Asn | Leu | Lys | Asn | Phe | Ser | Leu | Ser | Glu | Leu | Lys | Ser | Ala |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Arg | Asn | Phe | Arg | Pro | Asp | Ser | Val | Val | Gly | Glu | Gly | Gly | Phe | Gly |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Cys | Val | Phe | Lys | Gly | Trp | Ile | Asp | Glu | Ser | Ser | Leu | Ala | Pro | Ser | Lys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Gly | Thr | Gly | Ile | Val | Ile | Ala | Val | Lys | Arg | Leu | Asn | Gln | Glu | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Gln | Gly | His | Arg | Glu | Trp | Leu | Ala | Glu | Ile | Asn | Tyr | Leu | Gly | Gln |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Asp | His | Pro | Asn | Leu | Val | Lys | Leu | Ile | Gly | Tyr | Cys | Leu | Glu | Glu |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Glu | His | Arg | Leu | Leu | Val | Tyr | Glu | Phe | Met | Thr | Arg | Gly | Ser | Leu | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Asn | His | Leu | Phe | Arg | Arg | Gly | Thr | Phe | Tyr | Gln | Pro | Leu | Ser | Trp | Asn |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Thr | Arg | Val | Arg | Met | Ala | Leu | Gly | Ala | Ala | Arg | Gly | Leu | Ala | Phe | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| His | Asn | Ala | Gln | Pro | Gln | Val | Ile | Tyr | Arg | Asp | Phe | Lys | Ala | Ser | Asn |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     | 205 |     |     |     |
| Ile | Leu | Leu | Asp | Ser | Asn | Tyr | Asn | Ala | Lys | Leu | Ser | Asp | Phe | Gly | Leu |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Ala | Arg | Asp | Gly | Pro | Met | Gly | Asp | Asn | Ser | His | Val | Ser | Thr | Arg | Val |
| 225 |     |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     |
| Met | Gly | Thr | Gln | Gly | Tyr | Ala | Ala | Pro | Glu | Tyr | Leu | Ala | Thr | Gly | His |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Ser | Val | Lys | Ser | Asp | Val | Tyr | Ser | Phe | Gly | Val | Val | Leu | Leu | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Leu | Ser | Gly | Arg | Arg | Ala | Ile | Asp | Lys | Asn | Gln | Pro | Val | Gly | Glu |
|     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |
| His | Asn | Leu | Val | Asp | Trp | Ala | Arg | Pro | Tyr | Leu | Thr | Asn | Lys | Arg | Arg |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 290                                                             | 295 | 300 |
| Leu Leu Arg Val Met Asp Pro Arg Leu Gln Gly Gln Tyr Ser Leu Thr |     |     |
| 305                                                             | 310 | 315 |
| Arg Ala Leu Lys Ile Ala Val Leu Ala Leu Asp Cys Ile Ser Ile Asp |     | 320 |
|                                                                 | 325 | 330 |
| Ala Lys Ser Arg Pro Thr Met Asn Glu Ile Val Lys Thr Met Glu Glu |     | 335 |
|                                                                 | 340 | 345 |
| Leu His Ile Gln Lys Glu Ala Ser Lys Glu Gln Gln Asn Pro Gln Ile |     | 350 |
|                                                                 | 355 | 360 |
| Ser Ile Asp Asn Ile Ile Asn Lys Ser Pro Gln Ala Val Asn Tyr Pro |     | 365 |
|                                                                 | 370 | 375 |
| Arg Pro Ser Ile Met                                             |     | 380 |
| 385                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:2428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..350
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2428:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Pro Arg Thr Glu Gly Glu Ile Leu Gln Asn Ala Asn Leu Lys Asn |     |
| 1                                                               | 5   |
| Phe Ser Leu Ser Glu Leu Lys Ser Ala Thr Arg Asn Phe Arg Pro Asp | 10  |
|                                                                 | 15  |
|                                                                 | 20  |
| Ser Val Val Gly Glu Gly Gly Phe Gly Cys Val Phe Lys Gly Trp Ile | 25  |
|                                                                 | 30  |
| Asp Glu Ser Ser Leu Ala Pro Ser Lys Pro Gly Thr Gly Ile Val Ile | 35  |
|                                                                 | 40  |
| Ala Val Lys Arg Leu Asn Gln Glu Gly Phe Gln Gly His Arg Glu Trp | 45  |
| 65                                                              | 50  |
| Leu Ala Glu Ile Asn Tyr Leu Gly Gln Leu Asp His Pro Asn Leu Val | 55  |
|                                                                 | 60  |
| Lys Leu Ile Gly Tyr Cys Leu Glu Glu His Arg Leu Leu Val Tyr     | 65  |
|                                                                 | 70  |
| Glu Phe Met Thr Arg Gly Ser Leu Glu Asn His Leu Phe Arg Arg Gly | 75  |
|                                                                 | 80  |
| Thr Phe Tyr Gln Pro Leu Ser Trp Asn Thr Arg Val Arg Met Ala Leu | 85  |
|                                                                 | 90  |
| Gly Ala Ala Arg Gly Leu Ala Phe Leu His Asn Ala Gln Pro Gln Val | 95  |
| 145                                                             | 100 |
| Ile Tyr Arg Asp Phe Lys Ala Ser Asn Ile Leu Leu Asp Ser Asn Tyr | 105 |
|                                                                 | 110 |
| Asn Ala Lys Leu Ser Asp Phe Gly Leu Ala Arg Asp Gly Pro Met Gly | 115 |
|                                                                 | 120 |
| Asp Asn Ser His Val Ser Thr Arg Val Met Gly Thr Gln Gly Tyr Ala | 125 |
|                                                                 | 130 |
| Ala Pro Glu Tyr Leu Ala Thr Gly His Leu Ser Val Lys Ser Asp Val | 135 |
|                                                                 | 140 |
| Tyr Ser Phe Gly Val Val Leu Leu Glu Leu Leu Ser Gly Arg Arg Ala | 145 |
|                                                                 | 150 |
| Ile Asp Lys Asn Gln Pro Val Gly Glu His Asn Leu Val Asp Trp Ala | 155 |
|                                                                 | 160 |
| Arg Pro Tyr Leu Thr Asn Lys Arg Arg Leu Leu Arg Val Met Asp Pro | 165 |
|                                                                 | 170 |
| Arg Leu Gln Gly Gln Tyr Ser Leu Thr Arg Ala Leu Lys Ile Ala Val | 175 |
|                                                                 | 180 |
|                                                                 | 185 |
|                                                                 | 190 |
|                                                                 | 195 |
|                                                                 | 200 |
|                                                                 | 205 |
|                                                                 | 210 |
|                                                                 | 215 |
|                                                                 | 220 |
|                                                                 | 225 |
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|                                                                 | 255 |
|                                                                 | 260 |
|                                                                 | 265 |
|                                                                 | 270 |
|                                                                 | 275 |
|                                                                 | 280 |
|                                                                 | 285 |

Leu Ala Leu Asp Cys Ile Ser Ile Asp Ala Lys Ser Arg Pro Thr Met  
290 295 300  
Asn Glu Ile Val Lys Thr Met Glu Leu His Ile Gln Lys Glu Ala  
305 310 315 320  
Ser Lys Glu Gln Gln Asn Pro Gln Ile Ser Ile Asp Asn Ile Ile Asn  
325 330 335  
Lys Ser Pro Gln Ala Val Asn Tyr Pro Arg Pro Ser Ile Met  
340 345 350

(2) INFORMATION FOR SEQ ID NO:2429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1572889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2429:

Met Thr Arg Gly Ser Leu Glu Asn His Leu Phe Arg Arg Gly Thr Phe  
1 5 10 15  
Tyr Gln Pro Leu Ser Trp Asn Thr Arg Val Arg Met Ala Leu Gly Ala  
20 25 30  
Ala Arg Gly Leu Ala Phe Leu His Asn Ala Gln Pro Gln Val Ile Tyr  
35 40 45  
Arg Asp Phe Lys Ala Ser Asn Ile Leu Leu Asp Ser Asn Tyr Asn Ala  
50 55 60  
Lys Leu Ser Asp Phe Gly Leu Ala Arg Asp Gly Pro Met Gly Asp Asn  
65 70 75 80  
Ser His Val Ser Thr Arg Val Met Gly Thr Gln Gly Tyr Ala Ala Pro  
85 90 95  
Glu Tyr Leu Ala Thr Gly His Leu Ser Val Lys Ser Asp Val Tyr Ser  
100 105 110  
Phe Gly Val Val Leu Leu Glu Leu Leu Ser Gly Arg Arg Ala Ile Asp  
115 120 125  
Lys Asn Gln Pro Val Gly Glu His Asn Leu Val Asp Trp Ala Arg Pro  
130 135 140  
Tyr Leu Thr Asn Lys Arg Arg Leu Leu Arg Val Met Asp Pro Arg Leu  
145 150 155 160  
Gln Gly Gln Tyr Ser Leu Thr Arg Ala Leu Lys Ile Ala Val Leu Ala  
165 170 175  
Leu Asp Cys Ile Ser Ile Asp Ala Lys Ser Arg Pro Thr Met Asn Glu  
180 185 190  
Ile Val Lys Thr Met Glu Glu Leu His Ile Gln Lys Glu Ala Ser Lys  
195 200 205  
Glu Gln Gln Asn Pro Gln Ile Ser Ile Asp Asn Ile Ile Asn Lys Ser  
210 215 220  
Pro Gln Ala Val Asn Tyr Pro Arg Pro Ser Ile Met  
225 230 235

(2) INFORMATION FOR SEQ ID NO:2430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 583 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..583

(D) OTHER INFORMATION: / Ceres Seq. ID 1572890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2430:

|             |             |            |             |             |             |     |
|-------------|-------------|------------|-------------|-------------|-------------|-----|
| aaaaacaaaa  | ataaaaaaaa  | catgcacaaa | gaaaaataaaa | gattttgtaga | atcaactaag  | 60  |
| aaaaatggcta | gcaactatgat | gactacattg | cctcagttca  | atggtctctcg | agccaccaaa  | 120 |
| atctctgcag  | ctcctgtaca  | aggcctggca | agtgttcagc  | ccatgagacg  | caagggaagt  | 180 |
| ggagctttgg  | gtgcaaaagt  | tgacttcctc | gggttcacaa  | caaattctgat | aatggtaacg  | 240 |
| tcgacgaccc  | tgattttggt  | cgcggggaga | ttcggacttg  | cgccatcagc  | caataggaag  | 300 |
| gcgacagctg  | gacttagggt  | ggaggcacgt | gactcaggtc  | tacaaacggg  | tgaccocggc  | 360 |
| gggttcacgc  | ttgcggacac  | tttggtctgt | ggcaccgttg  | gtcatatcat  | cgggtgtagga | 420 |
| gttgctcttg  | gccttaaaaa  | cattggtgct | atttgagtt   | cctaaagctc  | ttttatttgt  | 480 |
| attttgaaaa  | Atttgtagat  | ttttataaca | atattctcat  | gcacctgaac  | gagatcctaat | 540 |
| ggattttaca  | agtttttatg  | tttatcttat | aatgtgtgat  | cgc         |             |     |

(2) INFORMATION FOR SEQ ID NO:2431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2431:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Lys | Asn | Lys | Asn | Lys | Lys | Asn | Ile | Ala | Gln | Glu | Asn | Lys | Arg | Phe | Val |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Glu | Ser | Thr | Lys | Lys | Met | Ala | Ser | Thr | Met | Met | Thr | Thr | Leu | Pro | Gln |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Phe | Asn | Gly | Leu | Arg | Ala | Thr | Lys | Ile | Ser | Ala | Ala | Pro | Val | Gln | Gly |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Leu | Ala | Ser | Val | Gln | Pro | Met | Arg | Arg | Lys | Gly | Asn | Gly | Ala | Leu | Gly |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ala | Lys | Cys | Asp | Phe | Ile | Gly | Ser | Ser | Thr | Asn | Leu | Ile | Met | Val | Thr |  |
|     |     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Ser | Thr | Thr | Leu | Ile | Leu | Phe | Ala | Gly | Arg | Phe | Gly | Leu | Ala | Pro | Ser |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ala | Asn | Arg | Lys | Ala | Thr | Ala | Gly | Leu | Arg | Leu | Glu | Ala | Arg | Asp | Ser |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Gly | Leu | Gln | Thr | Gly | Asp | Pro | Ala | Gly | Phe | Thr | Leu | Ala | Asp | Thr | Leu |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ala | Cys | Gly | Thr | Val | Gly | His | Ile | Ile | Gly | Val | Gly | Val | Val | Leu | Gly |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Leu | Lys | Asn | Ile | Gly | Ala | Ile |     |     |     |     |     |     |     |     |     |  |
|     |     | 145 |     |     | 150 |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2432:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Ser | Thr | Met | Met | Thr | Thr | Leu | Pro | Gln | Phe | Asn | Gly | Leu | Arg |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ala | Thr | Lys | Ile | Ser | Ala | Ala | Pro | Val | Gln | Gly | Leu | Ala | Ser | Val | Gln |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro | Met | Arg | Arg | Lys | Gly | Asn | Gly | Ala | Leu | Gly | Ala | Lys | Cys | Asp | Phe |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |

Ile Gly Ser Ser Thr Asn Leu Ile Met Val Thr Ser Thr Thr Leu Ile  
50 55 60  
Leu Phe Ala Gly Arg Phe Gly Leu Ala Pro Ser Ala Asn Arg Lys Ala  
65 70 75 80  
Thr Ala Gly Leu Arg Leu Glu Ala Arg Asp Ser Gly Leu Gln Thr Gly  
85 90 95  
Asp Pro Ala Gly Phe Thr Leu Ala Asp Thr Leu Ala Cys Gly Thr Val  
100 105 110  
Gly His Ile Ile Gly Val Gly Val Leu Gly Leu Lys Asn Ile Gly  
115 120 125  
Ala Ile  
130

(2) INFORMATION FOR SEQ ID NO:2433:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 126 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..126  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2433:

Met Met Thr Thr Leu Pro Gln Phe Asn Gly Leu Arg Ala Thr Lys Ile  
1 5 10 15  
Ser Ala Ala Pro Val Gln Gly Leu Ala Ser Val Gln Pro Met Arg Arg  
20 25 30  
Lys Gly Asn Gly Ala Leu Gly Ala Lys Cys Asp Phe Ile Gly Ser Ser  
35 40 45  
Thr Asn Leu Ile Met Val Thr Ser Thr Thr Leu Ile Leu Phe Ala Gly  
50 55 60  
Arg Phe Gly Leu Ala Pro Ser Ala Asn Arg Lys Ala Thr Ala Gly Leu  
65 70 75 80  
Arg Leu Glu Ala Arg Asp Ser Gly Leu Gln Thr Gly Asp Pro Ala Gly  
85 90 95  
Phe Thr Leu Ala Asp Thr Leu Ala Cys Gly Thr Val Gly His Ile Ile  
100 105 110  
Gly Val Gly Val Val Leu Gly Leu Lys Asn Ile Gly Ala Ile  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2434:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 661 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..661  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2434:

attttccag tgagaaatgg cgacgaagga accagaatct gtttacgagt taagcatcga 60  
ggatgcaaaa gggaacaact tagcactcag tcaatacaaa gacaaagttc ttittaattgt 120  
caatgttgct tccaaatgtg ggatgacaaa ctcaaaactac actgaattga atgagcttta 180  
caacaggatg aaagataaag gctctggagat tctagcattt ccttgtaacc agtttgggtga 240  
cgaggaaccc ggaactaatg accaaattac tgactttgtt tgtactcgct tcaaaactga 300  
attccccatt ttcaacaaga ttgaagttaa cggagagaat gctctctcct tgtataaagt 360  
cctgaagaaa ggcaaatggg gaactctcgg cgtatgacatt caatggaaat ttgctaagtt 420  
tcttgttgac aaaaacggct aagctgtaca acgttattat ccaactactt cccctcttac 480  
acttgagcat gacataaaga atctctctga tatctctga atgatgaagc ttittgtgctg 540

(2) INFORMATION FOR SEO ID NO:2435:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1572895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2435:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2436:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1572896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2436:

|     |     |     |     |    |     |     |     |     |     |     |    |     |     |     |     |     |     |     |
|-----|-----|-----|-----|----|-----|-----|-----|-----|-----|-----|----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Asn | Ser | 5  | Asn | Tyr | Thr | Glu | Leu | Asn | 10 | Glu | Leu | Tyr | Asn | 15  | Arg | Tyr |
| Lys | Asp | Lys | Gly | 20 | Leu | Glu | Ile | Leu | Ala | Phe | 25 | Pro | Cys | Asn | Gln | 30  | Phe | Gly |
| Asp | Glu | Glu | Pro | 35 | Gly | Thr | Asn | Asp | Gln | Ile | 40 | Thr | Asp | Phe | 45  | Val | Cys | Thr |
| Arg | Phe | Lys | Ser | 50 | Glu | Phe | Pro | Ile | Phe | Asn | 55 | Lys | Ile | 60  | Glu | Val | Asn | Gly |
| Glu | Asn | Ala | Ser | 65 | Pro | Leu | Tyr | Lys | Phe | Leu | 70 | Lys | Lys | 75  | Gly | Lys | Trp | Gly |
| Ile | Phe | Gly | Asp | 85 | Asp | Ile | Gln | Trp | Asn | Phe | 90 | Ala | Lys | 95  | Phe | Leu | Val | Asp |

Lys Asn Gly Gln Ala Val Gln Arg Tyr Tyr Pro Thr Thr Ser Pro Leu  
100 105 110  
Thr Leu Glu His Asp Ile Lys Asn Leu Leu Asn Ile Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..879
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2437:

```
gcaaacgcta gttaccggaa gacacgtctt gagtttcgca gcatctctct cctctcctct 60
gttcatactt ctcttttagaa atttctcaat gaacatactc aacagattgg gtttgggagc 120
aagtggggcaa accaatatgg atcctctctc gatcgctcag ggaaatgacg atgacacacc 180
ggcgccgggg aatcagtttg cccaattogg agctggatgt ttctgggggtg tcgagctggc 240
gtttcacaga gtcccagggg tgactcagac cgaggctgga tacacccaag ggaccgtaca 300
caatccttca tacggagatg ttgttcttgg taccacagcg cattcggagg ttgttagggt 360
tcaatatgat cttaacgatt gcacctatga gtctctgctt gatttgttct ggtctaggca 420
tgatcccacc acdtttgaat gccaggggaa tgacgtggga aCccaataca gatctggaat 480
atacttctac acacccgagc aggagaaact agcccgtgag tcacttgaac gtcaccagca 540
acaaatggag agaaagatga gactgaaat ctgtccagct aagaaattct acagagctga 600
agagcatcat caacagatgc tgtcaaaagg tgggcggttt ggccaaggcg aatccaactgc 660
caaggctgc aacgaccocaa tccgctgtta cggttaataa cgtgttttcc tctgtccctc 720
tcgaaaaaca gaggacttag catcaaaagg cttgtgtgtc aaatagattg tgtaaaactt 780
tgactaagtt gtccacacgc tatgtacta ctctcttggg atttcattcg caatgttgta 840
atattgatgt tatactctat aaacataaac caaataatc
```

(2) INFORMATION FOR SEQ ID NO:2438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..231
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2438:

```
Gln Thr Leu Val Thr Gly Arg His Val Leu Ser Phe Ala Ala Ser Leu
1 5 10 15
Ser Ser Pro Leu Phe Ile Ser Leu Phe Arg Asn Phe Ser Met Asn Ile
20 25 30
Leu Asn Arg Leu Gly Leu Gly Ser Ser Gly Gln Thr Asn Met Asp Pro
35 40 45
Ser Pro Ile Ala Gln Gly Asn Asp Asp Asp Thr Pro Ala Pro Gly Asn
50 55 60
Gln Phe Ala Gln Phe Gly Ala Gly Cys Phe Trp Gly Val Glu Leu Ala
65 70 75 80
Phe Gln Arg Val Pro Gly Val Thr Gln Thr Glu Ala Gly Tyr Thr Gln
85 90 95
Gly Thr Val His Asn Pro Ser Tyr Gly Asp Val Cys Ser Gly Thr Thr
100 105 110
Gly His Ser Glu Val Val Arg Val Gln Tyr Asp Leu Asn Asp Cys Thr
115 120 125
Tyr Glu Ser Leu Leu Asp Leu Phe Trp Ser Arg His Asp Pro Thr Thr
130 135 140
```

Leu Asn Arg Gln Gly Asn Asp Val Gly Thr Gln Tyr Arg Ser Gly Ile  
145 150 155 160  
Tyr Phe Tyr Thr Pro Glu Gln Glu Lys Leu Ala Arg Glu Ser Leu Glu  
165 170 175  
Arg His Gln Gln Gln Met Glu Arg Lys Ile Met Thr Glu Ile Leu Pro  
180 185 190  
Ala Lys Lys Phe Tyr Arg Ala Glu His His Gln Gln Tyr Leu Ser  
195 200 205  
Lys Gly Gly Arg Phe Gly Gln Gly Gln Ser Thr Ala Lys Gly Cys Asn  
210 215 220  
Asp Pro Ile Arg Cys Tyr Gly  
225 230

(2) INFORMATION FOR SEQ ID NO:2439:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 202 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..202

(D) OTHER INFORMATION: / Ceres Seq. ID 1572899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2439:

Met Asn Ile Leu Asn Arg Leu Gly Leu Gly Ser Ser Gly Gln Thr Asn  
1 5 10  
Met Asp Pro Ser Pro Ile Ala Gln Gly Asn Asp Asp Asp Thr Pro Ala  
20 25 30  
Pro Gly Asn Gln Phe Ala Gln Phe Gly Ala Gly Cys Phe Trp Gly Val  
35 40 45  
Glu Leu Ala Phe Gln Arg Val Pro Gly Val Thr Gln Thr Glu Ala Gly  
50 55 60  
Tyr Thr Gln Gly Thr Val His Asn Pro Ser Tyr Gly Asp Val Cys Ser  
65 70 75 80  
Gly Thr Thr Gly His Ser Glu Val Val Arg Val Gln Tyr Asp Leu Asn  
85 90 95  
Asp Cys Thr Tyr Glu Ser Leu Leu Asp Leu Phe Trp Ser Arg His Asp  
100 105 110  
Pro Thr Thr Leu Asn Arg Gln Gly Asn Asp Val Gly Thr Gln Tyr Arg  
115 120 125  
Ser Gly Ile Tyr Phe Tyr Thr Pro Glu Gln Glu Lys Leu Ala Arg Glu  
130 135 140  
Ser Leu Glu Arg His Gln Gln Gln Met Glu Arg Lys Ile Met Thr Glu  
145 150 155 160  
Ile Leu Pro Ala Lys Lys Phe Tyr Arg Ala Glu Glu His His Gln Gln  
165 170 175  
Tyr Leu Ser Lys Gly Gly Arg Phe Gly Gln Gly Gln Ser Thr Ala Lys  
180 185 190  
Gly Cys Asn Asp Pro Ile Arg Cys Tyr Gly  
195 200

(2) INFORMATION FOR SEQ ID NO:2440:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 186 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..186

(D) OTHER INFORMATION: / Ceres Seq. ID 1572900



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2440:

Met Asp Pro Ser Pro Ile Ala Gln Gly Asn Asp Asp Asp Thr Pro Ala  
1 5 10 15  
Pro Gly Asn Gln Phe Ala Gln Phe Gly Ala Gly Cys Phe Trp Gly Val  
20 25 30  
Glu Leu Ala Phe Gln Arg Val Pro Gly Val Thr Gln Thr Glu Ala Gly  
35 40 45  
Tyr Thr Gln Gly Thr Val His Asn Pro Ser Tyr Gly Asp Val Cys Ser  
50 55 60  
Gly Thr Thr Gly His Ser Glu Val Val Arg Val Gln Tyr Asp Leu Asn  
65 70 75 80  
Asp Cys Thr Tyr Glu Ser Leu Leu Asp Leu Phe Trp Ser Arg His Asp  
85 90 95  
Pro Thr Thr Leu Asn Arg Gln Gly Asn Asp Val Gly Thr Gln Tyr Arg  
100 105 110  
Ser Gly Ile Tyr Phe Tyr Thr Pro Glu Gln Glu Lys Leu Ala Arg Glu  
115 120 125  
Ser Leu Glu Arg His Gln Gln Gln Met Glu Arg Lys Ile Met Thr Glu  
130 135 140  
Ile Leu Pro Ala Lys Lys Phe Tyr Arg Ala Glu His His Gln Gln  
145 150 155 160  
Tyr Leu Ser Lys Gly Gly Arg Phe Gly Gln Gly Gln Ser Thr Ala Lys  
165 170 175  
Gly Cys Asn Asp Pro Ile Arg Cys Tyr Gly  
180 185

(2) INFORMATION FOR SEQ ID NO:2441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1443
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2441:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| acatgtttttg | ctctgtcttct | ctctttatct  | tctttcttcac | cttttgtcac  | tctttttctc  | 60   |
| tgctctaaac  | tttttctttt  | cgctgcaaaa  | aatttttccca | ggaatatttc  | ttaaaagaaa  | 120  |
| tttctacctc  | aaataagaaa  | aaagcatctc  | cttcttttagt | gtcctctcttc | accctaaactc | 180  |
| tgattccata  | agcatatatt  | aaaaaagctc  | ctgtctttct  | tcaacttttc  | cgggaaaaatc | 240  |
| ttcttggtac  | aaagcatcaa  | tctctgtttt  | taccagtttt  | ctctctttat  | tctcttttttg | 300  |
| ccctttactt  | ttcttaactt  | tggtctttat  | atataaacac  | acgacacaaa  | gaagaacaca  | 360  |
| cataagttaa  | aactattaca  | acagttttta  | agagagagat  | ttaaaaaatg  | gagacagaga  | 420  |
| agaaagtgtt  | tctcccaaga  | atcttacgaa  | tctctgttac  | tgatctctac  | gcaacagatt  | 480  |
| cgctcaagca  | cgaagaagaa  | gaagttgatt  | ttgatgcatt  | atctacaaaa  | cgacgtcgtg  | 540  |
| ttaaagaagta | cgtgaaggaa  | gtggtgcttg  | attcggtggt  | ttctgataaa  | gagaagccga  | 600  |
| tgaagaagaa  | gagaaagaag  | cgcgttggtta | ctgttccagt  | ggttggttac  | acagcgacga  | 660  |
| ggaagtgttc  | tggaagtggg  | caaagaccgt  | ggggaaaatg  | ggcggcgagg  | attagagatc  | 720  |
| cgagtagaac  | tggttagggt  | tggttaggta  | cttttgacac  | ggcgaggagg  | gctgccattc  | 780  |
| tttaacgata  | cgcagctatt  | cagctacgtg  | gtctaacacg  | agagcttaac  | ttccctctct  | 840  |
| ctccggtgac  | ggagaatgtg  | gaagaagcct  | cgacggaggt  | gaaaggagtt  | tcggttttta  | 900  |
| tcattggcgg  | tggaagaatat | cttcgttcgc  | cggtttctgt  | tctcgaatct  | ccgttctccg  | 960  |
| cgagctctac  | tgccgtwaaa  | gaggagtttg  | tcggtgtatc  | gacggcgagg  | attgtggtta  | 1020 |
| aaaaagagcc  | gtcttttaac  | gggttcagatt | tctcgccgac  | gtgtgtctcg  | gacgacgacg  | 1080 |
| tttttggttt  | ctcgaagctg  | atgagtgaag  | gtttcggcgg  | cgattatttt  | ggagataatt  | 1140 |
| tttttgcgga  | tatgagtttt  | ggatccgggt  | ttggtattcg  | gtctggtgct  | ggattctcca  | 1200 |
| gctgcagcgt  | tgaggaccat  | tcttcaaatg  | attggggatt  | tattcgaatc  | ggatcctgtc  | 1260 |
| ttaactgttt  | aagaaaatga  | tgccggttta  | acggcgattt  | gtgaagtttt  | gttacccggc  | 1320 |
| acggcgagga  | ttaaaaaaaa  | acggcgattt  | attttttgaa  | tgaagatttg  | ttaaatatat  | 1380 |
| ttaaactttt  | tgtaacttaa  | ttaatggtga  | ttttattttt  | aaataaaact  | aatggttaaa  | 1440 |

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(2) INFORMATION FOR SEQ ID NO:2442:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..297

(D) OTHER INFORMATION: / Ceres Seq. ID 1572906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2442:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Thr | Glu | Lys | Val | Ser | Leu | Pro | Arg | Ile | Leu | Arg | Ile | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Thr | Asp | Pro | Tyr | Ala | Thr | Asp | Ser | Ser | Asp | Glu | Glu | Glu |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Asp | Phe | Asp | Ala | Leu | Ser | Thr | Lys | Arg | Arg | Arg | Val | Lys | Tyr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Val | Lys | Glu | Val | Val | Leu | Asp | Ser | Val | Val | Ser | Asp | Lys | Glu | Pro |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Met | Lys | Lys | Lys | Arg | Lys | Lys | Arg | Val | Val | Thr | Val | Pro | Val | Val |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Thr | Ala | Thr | Arg | Lys | Phe | Arg | Gly | Val | Arg | Gln | Arg | Pro | Trp |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Trp | Ala | Ala | Glu | Ile | Arg | Asp | Pro | Ser | Arg | Arg | Val | Arg | Val |
|     |     |     |     | 100 |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Gly | Thr | Phe | Asp | Thr | Ala | Glu | Glu | Ala | Ala | Ile | Val | Tyr | Asp |
|     |     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |
| Ala | Ala | Ile | Gln | Leu | Arg | Gly | Pro | Asn | Ala | Glu | Leu | Asn | Phe | Pro |
|     |     |     |     | 130 |     | 135 |     |     |     | 140 |     |     |     |     |
| Ala | Pro | Val | Thr | Glu | Asn | Val | Glu | Glu | Ala | Ser | Thr | Glu | Val | Lys |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Val | Ser | Asp | Phe | Ile | Gly | Gly | Gly | Glu | Tyr | Leu | Arg | Ser | Pro | Val |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Val | Leu | Glu | Ser | Pro | Phe | Ser | Gly | Glu | Ser | Thr | Ala | Xaa | Lys |
|     |     |     |     | 180 |     |     | 185 |     |     |     |     |     | 190 |     |
| Glu | Phe | Val | Gly | Val | Ser | Thr | Ala | Glu | Ile | Val | Val | Lys | Lys | Glu |
|     |     |     |     | 195 |     |     | 200 |     |     |     |     | 205 |     |     |
| Ser | Phe | Asn | Gly | Ser | Asp | Phe | Ser | Ala | Pro | Leu | Phe | Ser | Asp | Asp |
|     |     |     |     | 210 |     | 215 |     |     |     |     | 220 |     |     |     |
| Val | Phe | Gly | Phe | Ser | Thr | Ser | Met | Ser | Glu | Ser | Phe | Gly | Gly | Asp |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | Leu |
| Phe | Gly | Asp | Asn | Leu | Phe | Ala | Asp | Met | Ser | Phe | Gly | Ser | Gly | Phe |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     | 255 |     |
| Phe | Gly | Ser | Gly | Ser | Gly | Phe | Ser | Ser | Trp | His | Val | Glu | Asp | His |
|     |     |     |     | 260 |     |     | 265 |     |     |     |     | 270 |     | Xaa |
| Ser | Arg | Tyr | Trp | Gly | Phe | Ile | Arg | Val | Gly | Ser | Cys | Leu | Asn | Cys |
|     |     |     |     | 275 |     |     | 280 |     |     |     |     | 285 |     |     |
| Arg | Asn | Asn | Trp | Pro | Phe | Asn | Gly | Val |     |     |     |     |     |     |
|     |     |     |     | 290 |     | 295 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..233

(D) OTHER INFORMATION: / Ceres Seq. ID 1572907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2443:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Lys | Arg | Lys | Lys | Arg | Val | Val | Thr | Val | Pro | Val | Val | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Thr | Thr | Ala | Thr | Arg | Lys | Phe | Arg | Gly | Val | Arg | Gln | Arg | Pro | Trp | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Trp | Ala | Ala | Glu | Ile | Arg | Asp | Pro | Ser | Arg | Arg | Val | Arg | Val | Trp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Gly | Thr | Phe | Asp | Thr | Ala | Glu | Glu | Ala | Ala | Ile | Val | Tyr | Asp | Asn |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Ala | Ala | Ile | Gln | Leu | Arg | Gly | Pro | Asn | Ala | Glu | Leu | Asn | Phe | Pro | Pro |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Pro | Val | Thr | Glu | Asn | Val | Glu | Glu | Ala | Ser | Thr | Glu | Val | Lys | Gly |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Val | Ser | Asp | Phe | Ile | Ile | Gly | Gly | Gly | Glu | Tyr | Leu | Arg | Ser | Pro | Val |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ser | Val | Leu | Glu | Ser | Pro | Phe | Ser | Gly | Glu | Ser | Thr | Ala | Xaa | Lys | Glu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Phe | Val | Gly | Val | Ser | Thr | Ala | Glu | Ile | Val | Val | Lys | Lys | Glu | Pro |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Ser | Phe | Asn | Gly | Ser | Asp | Phe | Ser | Ala | Pro | Leu | Phe | Ser | Asp | Asp | Asp |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Val | Phe | Gly | Phe | Ser | Thr | Ser | Met | Ser | Glu | Ser | Phe | Gly | Gly | Asp | Leu |
|     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |     |
| Phe | Gly | Asp | Asn | Leu | Phe | Ala | Asp | Met | Ser | Phe | Gly | Ser | Gly | Phe | Gly |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Phe | Gly | Ser | Gly | Ser | Gly | Phe | Ser | Ser | Trp | His | Val | Glu | Asp | His | Xaa |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Arg | Tyr | Trp | Gly | Phe | Ile | Arg | Val | Gly | Ser | Cys | Leu | Asn | Cys | Leu |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Arg | Asn | Asn | Trp | Pro | Phe | Asn | Gly | Val |     |     |     |     |     |     |     |
|     |     |     | 225 |     |     | 230 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1284 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1284

(D) OTHER INFORMATION: / Ceres Seq. ID 1572912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2444:

|            |             |            |            |             |             |      |
|------------|-------------|------------|------------|-------------|-------------|------|
| caagatgac  | aaagattctgt | tagattattg | gcggttgagg | gttggtgctgc | tcttgaggaaa | 60   |
| ttgttgaggc | ctcaggattg  | tgtccaacac | attcttcccg | tgattgttaa  | ttcttcgacg  | 120  |
| gataagctct | ggcgtgtgag  | ctatatgggt | gcaaatcaac | tctacgagct  | ttgtgaagcc  | 180  |
| gtgggacctg | agcctactag  | gacggagctg | gtgcctgcac | atgtgcgcct  | acttcgtgat  | 240  |
| aatgaagctg | aagtacgcat  | agcagctgcc | ggaaaaagta | caaaagtttg  | tcggattcta  | 300  |
| aacctgaaa  | tgtctatcca  | gcacattctc | ccctgtgtga | aggagctatc  | atcagactct  | 360  |
| tctcagcatg | tcagatctgc  | attggcctca | gttataatgg | gaatggctcc  | agctctgggt  | 420  |
| aaggatgcaa | caattgagca  | tctccttoca | atctttcttt | ctctattgaa  | agatgagttc  | 480  |
| cCgagtgatc | gcttgaacat  | tatcagcaaa | cttgaccaag | tgaatcaggt  | tattgggatt  | 540  |
| gatctactat | cacaatcctt  | gttgccagct | attgtagaAc | ttgctgaaga  | tagacactgg  | 600  |
| agagtgaagc | ttgtcataat  | caggtatatc | cctttgttgg | caagtcagtt  | aggtgttgGc  | 660  |
| ttctttGagc | ataagcttgg  | tgcctttTgc | atgcaatgg  | Tacaagacaa  | ggttcactca  | 720  |
| atcCgcgatg | ctgctgctaa  | caatctcaag | cggcttgctg | aggaatttgg  | tcttgaatgg  | 780  |
| gcaatgcaac | atatagtttc  | tcaggttctt | gagatgggta | acaaccctca  | ctatctctac  | 840  |
| cgaatgacca | ttttgctgtc  | gggtgtctct | cttgcaacct | taatggggct  | agagattaca  | 900  |
| tgctctaaag | tcttacctgt  | agtaatgact | gcactctaa  | acagagttcc  | aaacatcaaa  | 960  |
| ttcaacgtcg | ctaaagtagt  | tcaatccctc | attccaatag | ttgatcaatc  | ggttgtggag  | 1020 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| aagacgattc gtccctgggct tgtggagcta agcgaggatc cagatgttga tgcagggttt | 1080 |
| ttcgaaaacc aagctctaca atctattgac aatgtgatga tgtctagcta aaaacattag  | 1140 |
| atctgtctc tctgtgtata atcgttttct atttgattga aaaaaaaaaa aaatctcaag   | 1200 |
| acttttgtaa cgttagtagtg gattctcgtc ttgtgttttt tattacacgc aaactactag | 1260 |
| agtgccctgg tacgggtttt gtcc                                         |      |

(2) INFORMATION FOR SEQ ID NO:2445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..376
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2445:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Asp | Asp | Gln | Asp | Ser | Val | Arg | Leu | Leu | Ala | Val | Glu | Gly | Cys | Ala | 1   | 5   | 10  | 15  |
| Ala | Leu | Gly | Lys | Leu | Leu | Glu | Pro | Gln | Asp | Cys | Val | Gln | His | Ile | Leu | 20  | 25  | 30  | 35  |
| Pro | Val | Ile | Val | Asn | Phe | Ser | Gln | Asp | Lys | Ser | Trp | Arg | Val | Arg | Tyr | 40  | 45  | 50  | 55  |
| Met | Val | Ala | Asn | Gln | Leu | Tyr | Glu | Leu | Cys | Glu | Ala | Val | Gly | Pro | Glu | 60  | 65  | 70  | 75  |
| Pro | Thr | Arg | Thr | Glu | Leu | Val | Pro | Ala | Tyr | Val | Arg | Leu | Leu | Arg | Asp | 80  | 85  | 90  | 95  |
| Asn | Glu | Ala | Glu | Val | Arg | Ile | Ala | Ala | Ala | Gly | Lys | Val | Thr | Lys | Phe | 100 | 105 | 110 | 115 |
| Cys | Arg | Ile | Leu | Asn | Pro | Glu | Ile | Ala | Ile | Gln | His | Ile | Leu | Pro | Cys | 120 | 125 | 130 | 135 |
| Val | Lys | Glu | Leu | Ser | Ser | Asp | Ser | Ser | Gln | His | Val | Arg | Ser | Ala | Leu | 140 | 145 | 150 | 155 |
| Ala | Ser | Val | Ile | Met | Gly | Met | Ala | Pro | Val | Leu | Gly | Lys | Asp | Ala | Thr | 160 | 165 | 170 | 175 |
| Ile | Glu | His | Leu | Leu | Pro | Ile | Phe | Leu | Ser | Leu | Lys | Asp | Glu | Phe |     | 180 | 185 | 190 | 195 |
| Pro | Asp | Val | Arg | Leu | Asn | Ile | Ile | Ser | Lys | Leu | Asp | Gln | Val | Asn | Gln | 200 | 205 | 210 | 215 |
| Val | Ile | Gly | Ile | Asp | Leu | Leu | Ser | Gln | Ser | Leu | Leu | Pro | Ala | Ile | Val | 220 | 225 | 230 | 235 |
| Glu | Leu | Ala | Glu | Asp | Arg | His | Trp | Arg | Val | Arg | Leu | Ala | Ile | Ile | Glu | 240 | 245 | 250 | 255 |
| Tyr | Ile | Pro | Leu | Leu | Ala | Ser | Gln | Leu | Gly | Val | Gly | Phe | Phe | Asp | Asp | 260 | 265 | 270 | 275 |
| Lys | Leu | Gly | Ala | Leu | Cys | Met | Gln | Trp | Leu | Gln | Asp | Lys | Val | His | Ser | 280 | 285 | 290 | 295 |
| Ile | Arg | Asp | Ala | Ala | Ala | Asn | Asn | Leu | Lys | Arg | Leu | Ala | Glu | Glu | Phe | 300 | 305 | 310 | 315 |
| Gly | Pro | Glu | Trp | Ala | Met | Gln | His | Ile | Val | Pro | Gln | Val | Leu | Glu | Met | 320 | 325 | 330 | 335 |
| Val | Asn | Asn | Pro | His | Tyr | Leu | Tyr | Arg | Met | Thr | Ile | Leu | Arg | Ala | Val | 340 | 345 | 350 |     |
| Ser | Leu | Leu | Ala | Pro | Val | Met | Gly | Ser | Glu | Ile | Thr | Cys | Ser | Lys | Leu |     |     |     |     |
| Leu | Pro | Val | Val | Met | Thr | Ala | Ser | Lys | Asp | Arg | Val | Pro | Asn | Ile | Lys |     |     |     |     |
| Phe | Asn | Val | Ala | Lys | Val | Leu | Gln | Ser | Leu | Ile | Pro | Ile | Val | Asp | Gln |     |     |     |     |
| Ser | Val | Val | Glu | Lys | Thr | Ile | Arg | Pro | Gly | Leu | Val | Glu | Leu | Ser | Glu |     |     |     |     |

Asp Pro Asp Val Asp Val Arg Phe Phe Ala Asn Gln Ala Leu Gln Ser  
355 360 365  
Ile Asp Asn Val Met Met Ser Ser  
370 375

(2) INFORMATION FOR SEQ ID NO:2446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..328

(D) OTHER INFORMATION: / Ceres Seq. ID 1572914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2446:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ala | Asn | Gln | Leu | Tyr | Glu | Leu | Cys | Glu | Ala | Val | Gly | Pro | Glu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Thr | Arg | Thr | Glu | Leu | Val | Pro | Ala | Tyr | Val | Arg | Leu | Leu | Arg | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Glu | Ala | Glu | Val | Arg | Ile | Ala | Ala | Ala | Gly | Lys | Val | Thr | Lys | Phe |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Cys | Arg | Ile | Leu | Asn | Pro | Glu | Ile | Ala | Ile | Gln | His | Ile | Leu | Pro | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Lys | Glu | Leu | Ser | Ser | Asp | Ser | Ser | Gln | His | Val | Arg | Ser | Ala | Leu |
|     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Ser | Val | Ile | Met | Gly | Met | Ala | Pro | Val | Leu | Gly | Lys | Asp | Ala | Thr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Glu | His | Leu | Leu | Pro | Ile | Phe | Leu | Ser | Leu | Leu | Lys | Asp | Glu | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Asp | Val | Arg | Leu | Asn | Ile | Ile | Ser | Lys | Leu | Asp | Gln | Val | Asn | Gln |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Val | Ile | Gly | Ile | Asp | Leu | Leu | Ser | Gln | Ser | Leu | Leu | Pro | Ala | Ile | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Glu | Leu | Ala | Glu | Asp | Arg | His | Trp | Arg | Val | Arg | Leu | Ala | Ile | Ile | Glu |
|     | 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Tyr | Ile | Pro | Leu | Leu | Ala | Ser | Gln | Leu | Gly | Val | Gly | Phe | Phe | Asp | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Leu | Gly | Ala | Leu | Cys | Met | Gln | Trp | Leu | Gln | Asp | Lys | Val | His | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Arg | Asp | Ala | Ala | Ala | Asn | Asn | Leu | Lys | Arg | Leu | Ala | Glu | Glu | Phe |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Pro | Glu | Trp | Ala | Met | Gln | His | Ile | Val | Pro | Gln | Val | Leu | Glu | Met |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Val | Asn | Asn | Pro | His | Tyr | Leu | Tyr | Arg | Met | Thr | Ile | Leu | Arg | Ala | Val |
|     |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Ser | Leu | Leu | Ala | Pro | Val | Met | Gly | Ser | Glu | Ile | Thr | Cys | Ser | Lys | Leu |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Pro | Val | Val | Met | Thr | Ala | Ser | Lys | Asp | Arg | Val | Pro | Asn | Ile | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Phe | Asn | Val | Ala | Lys | Val | Leu | Gln | Ser | Leu | Ile | Pro | Ile | Val | Asp | Gln |
|     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |
| Ser | Val | Val | Glu | Lys | Thr | Ile | Arg | Pro | Gly | Leu | Val | Glu | Leu | Ser | Glu |
|     |     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |
| Asp | Pro | Asp | Val | Asp | Val | Arg | Phe | Phe | Ala | Asn | Gln | Ala | Leu | Gln | Ser |
|     |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |     |
| Ile | Asp | Asn | Val | Met | Met | Ser | Ser |     |     |     |     |     |     |     |     |
|     |     |     |     |     | 325 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 amino acids

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(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..244
(D) OTHER INFORMATION: / Ceres Seq. ID 1572915
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2447:
Met Gly Met Ala Pro Val Leu Gly Lys Asp Ala Thr Ile Glu His Leu
1 5 10 15
Leu Pro Ile Phe Leu Ser Leu Leu Lys Asp Glu Phe Pro Asp Val Arg
20 25
Leu Asn Ile Ile Ser Lys Leu Asp Gln Val Asn Gln Val Ile Gly Ile
35 40 45
Asp Leu Leu Ser Gln Ser Leu Leu Pro Ala Ile Val Glu Leu Ala Glu
50 55 60
Asp Arg His Trp Arg Val Arg Leu Ala Ile Ile Glu Tyr Ile Pro Leu
65 70 75 80
Leu Ala Ser Gln Leu Gly Val Gly Phe Phe Asp Asp Lys Leu Gly Ala
85 90 95
Leu Cys Met Gln Trp Leu Gln Asp Lys Val His Ser Ile Arg Asp Ala
100 105 110
Ala Ala Asn Asn Leu Lys Arg Leu Ala Glu Glu Phe Gly Pro Glu Trp
115 120 125
Ala Met Gln His Ile Val Pro Gln Val Leu Glu Met Val Asn Asn Pro
130 135 140
His Tyr Leu Tyr Arg Met Thr Ile Leu Arg Ala Val Ser Leu Leu Ala
145 150 155 160
Pro Val Met Gly Ser Glu Ile Thr Cys Ser Lys Leu Leu Pro Val Val
165 170 175
Met Thr Ala Ser Lys Asp Arg Val Pro Asn Ile Lys Phe Asn Val Ala
180 185 190
Lys Val Leu Gln Ser Leu Ile Pro Ile Val Asp Gln Ser Val Val Glu
195 200 205
Lys Thr Ile Arg Pro Gly Leu Val Glu Leu Ser Glu Asp Pro Asp Val
210 215 220
Asp Val Arg Phe Phe Ala Asn Gln Ala Leu Gln Ser Ile Asp Asn Val
225 230 235 240
Met Met Ser Ser

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(2) INFORMATION FOR SEO ID NO:2448:

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 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 578 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..578
 (D) OTHER INFORMATION: / Ceres Seq. ID 1572916
 (x1) SEQUENCE DESCRIPTION: SEQ ID NO:2448:

aaaaagaaaa aggttctcttt ttttgactgt gtatccgtgat atcatctttct Atcttcttct 60
tcocagatttt tatctcttate cgttctcatc aattctctctc ctaagcaaaa atgaataaag 120
gaagcatcttt taagatggac acagctatttc aaagaagaaa aggaagaaga agaaggagaa 180
gaagaagccca actactgaag ttgaggtaaa ggaggaagag aagaaaaggtt ttatggagaa 240
gttgaagaag aaagcttctctg cagcaagaag acctgaagac ggctcagccg tcgctcgccg 300
accggttggtt gttctctctc gtctgagaga agcgcctcca gtggagaaga aagggattct 360
tgagaataat aaggagaagc tctocaggaa cacacctaat accaccagat agggagagaa 420
qaaagataaa qaataaqaag attatcatta aagatattaa qaataatgat qttgattttc 480

```

ctttgtttttt atttttttta ttgtgatgat tgatcatcct ttgcttttgt gatgtgtaag 540

tttgttggtt tttttgttga ttacaatttc ttattttc

(2) INFORMATION FOR SEQ ID NO:2449:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..37

(D) OTHER INFORMATION: / Ceres Seq. ID 1572917

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2449:

Lys Lys Lys Lys Val Pro Phe Phe Asp Phe Val Ser Val Asp His Leu

1 5 10 15

Leu Ser Ser Ser Ser Arg Val Leu Ser Leu Ser Val Pro Ser Asn Ser

20 25 30

Leu Ser Lys Gln Arg

35

(2) INFORMATION FOR SEQ ID NO:2450:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1572918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2450:

Met Glu Lys Leu Lys Glu Lys Leu Pro Gly His Lys Lys Pro Glu Asp

1 5 10 15

Gly Ser Ala Val Ala Ala Ala Pro Val Val Val Pro Pro Pro Val Arg

20 25 30

Glu Ala His Pro Val Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Glu

35 40 45

Lys Leu Pro Gly Tyr His Pro Lys Thr Thr Val Glu Glu Glu Lys Lys

50 55 60

Asp Lys Glu

65

(2) INFORMATION FOR SEQ ID NO:2451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 406 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..406

(D) OTHER INFORMATION: / Ceres Seq. ID 1572927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2451:

avaGWacaac aacaacaaac aagaactcaa acacttcata actaaaaacat cctttaaaagc 60

cttttcaaaa actcaatcat gtcaagcaac tgcggaagct ggcactgtgc tgacaagacc 120

cagtgcgtaa agaagggaac cagctacacac ttcgacatcg tgcagactca ggagagctac 180

aaggaggcca tgatcatgga cgttggtgcc gaggagaaca acgcaaatgt caagtgcagg 240

tgcggtctct cttgcagctg cgtcaactgc acttgctgac ccaactaatg aagctctcttt 300

aatcaaaatg taatatgaat aaaagttgat gtttgtattg ttgtttgttt ctgtatgatt 360

agttgcttgg taacaaaata atccaatcta aatgtgtttc ttgagc

(2) INFORMATION FOR SEQ ID NO:2452:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..42  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2452:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Asn | Asn | Asn | Lys | Gln | Glu | Leu | Lys | His | Phe | Ile | Thr | Lys | Thr |
| 1   |     | 5   |     |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Phe | Lys | Ala | Phe | Ser | Lys | Thr | Gln | Ser | Cys | Gln | Ala | Thr | Ala | Glu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ala | Ala | Thr | Val | Leu | Thr | Arg | Pro | Ser | Ala |     |     |     |     |     |     |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2453:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..69  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2453:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ser | Asn | Cys | Gly | Ser | Cys | Asp | Cys | Ala | Asp | Lys | Thr | Gln | Cys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Lys | Lys | Gly | Thr | Ser | Tyr | Thr | Phe | Asp | Ile | Val | Glu | Thr | Gln | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ser | Tyr | Lys | Glu | Ala | Met | Ile | Met | Asp | Val | Gly | Ala | Glu | Glu | Asn | Asn |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Ala | Asn | Cys | Lys | Cys | Lys | Cys | Gly | Ser | Ser | Cys | Ser | Cys | Val | Asn | Cys |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |
| Thr | Cys | Cys | Pro | Asn |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2454:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 615 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..615  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2454:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| aacgaaagct | agggtttttt | ctctgtgaaa | tcgctgcgcg | gcataaaaga  | gagtcagaag | 60  |
| aggaagaaga | gagttacaag | gattgaaaat | gaagggacgt | caaggagaga  | gagttagatt | 120 |
| gtatgttcgt | ggaacagtc  | tcggttacaa | gaggtccaag | tcgaaccaat  | accctaacc  | 180 |
| ttctctcgtc | cagattgaag | gtgtgaacac | tcaagaggag | gttaattggt  | acaagggtaa | 240 |
| gcgtttggct | tacatctaca | aggcaaaagc | aaagaagaac | ggttctcact  | accgttgcat | 300 |
| ttggggcaaa | gtcactaggg | ctcatggtaa | cagtggtgtt | gtccgtttcta | agttcacttc | 360 |
| aaacctacca | cccaagtcaa | tgggagctag | agtcagagtc | ttcatgtacc  | ctagacaact | 420 |
| atgaggaggc | tgattttcaa | caagtatcgg | aaggaatcgc | cattatcatt  | tctcaggagc | 480 |
| tgtagtttta | tctattcact | tttattctag | actctctggt | gggttttgatt | ttatcttgag | 540 |



acgaagTaaa acatTTTTTT tcttgagatc atatactatc gagtattaat ggaacttgag 600  
aaaagctatg atccc

(2) INFORMATION FOR SEQ ID NO:2455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2455:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Gly | Arg | Gln | Gly | Glu | Arg | Val | Arg | Leu | Tyr | Val | Arg | Gly | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Leu | Gly | Tyr | Lys | Arg | Ser | Lys | Ser | Asn | Gln | Tyr | Pro | Asn | Thr | Ser |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Val | Gln | Ile | Glu | Gly | Val | Asn | Thr | Gln | Glu | Glu | Val | Asn | Trp | Tyr |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Gly | Lys | Arg | Leu | Ala | Tyr | Ile | Tyr | Lys | Ala | Lys | Thr | Lys | Lys | Asn |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Gly | Ser | His | Tyr | Arg | Cys | Ile | Trp | Gly | Lys | Val | Thr | Arg | Pro | His | Gly |
|     |     |     |     | 65  |     | 70  |     |     | 75  |     |     |     |     | 80  |     |
| Asn | Ser | Gly | Val | Val | Arg | Ser | Lys | Phe | Thr | Ser | Asn | Leu | Pro | Pro | Lys |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | Met | Gly | Ala | Arg | Val | Arg | Val | Phe | Met | Tyr | Pro | Ser | Asn | Ile |     |
|     |     |     |     | 100 |     |     | 105 |     |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:2456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1803 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1803
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2456:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| acacacatt   | ttcacacat   | cgtacttate  | gccttctctc  | ctctctcaat  | acctctctca  | 60   |
| atttttggt   | ccaccatgca  | agctcttcaa  | tcttcatctc  | tccgtgcttc  | tctctccaaa  | 120  |
| ccaactcgct  | taccatcaaa  | ctcgtcaatca | catcagctaa  | ttaccaatgc  | gagacotttg  | 180  |
| cgaaagacaac | aacgttctct  | catctccgca  | tcagcatcca  | ctgtctccgc  | tcttaaacgc  | 240  |
| gaaaacagatc | cgaaagaaacg | agttgtcatt  | actggtatgg  | gtctgtcttc  | tgtgtttggt  | 300  |
| aacgatgttg  | atgcttacta  | cgagaaaattg | ttgtctggtg  | agagtggaa   | cagtttgatt  | 360  |
| gatcgtttcg  | atgcttccaa  | gttccctact  | cgattcgggt  | gtcagatccg  | tggtgtttagc | 420  |
| tctgaaggtt  | atattgatgg  | caagaatagag | cgtaggcttg  | atgattgttt  | gaactattgc  | 480  |
| attgttgctg  | gtaaaaaagc  | tcttgaaaag  | gccaatcttg  | gtggtgataa  | gccttaaacg  | 540  |
| attgataaga  | ggaaagctgg  | agtaactagt  | gggaactggaa | tgggaggttt  | aactgtgttt  | 600  |
| tcagaaggtg  | ttcagaattt  | gattgagaag  | ggctcatagga | ggattatgcc  | attttttata  | 660  |
| ctttatgcta  | taacaaatat  | gggttctgct  | ttgttggcga  | ttgatcttgg  | tcttatgggt  | 720  |
| cttaactatt  | cgatttcaac  | gtctgtgctc  | acttogaatt  | actgotttta  | cgctgctgcg  | 780  |
| aatcacattc  | gtcgtgggtga | agctgatgat  | atgattgctg  | gtgggactga  | ggctgctatt  | 840  |
| attcctattg  | ggttgggagg  | ttttgttgct  | tgtagggaat  | tgtcccagag  | aaatgatgac  | 900  |
| ctccaaaactg | cttcaggggc  | gtgggataaa  | gcaagagatg  | ggtttgttat  | gggtgaaggga | 960  |
| gctggtgttc  | tggtgatgga  | aagcttggaa  | catgcAaatg  | aaactgtggt  | ctccaatgtg  | 1020 |
| agcagaatat  | cttggagggtg | ctgttaattg  | tgatgctcac  | catatgactg  | atccaaagagc | 1080 |
| tgatgtgtct  | gggtgttctt  | catgcattga  | aagatgtctc  | gaagatgactg | gtgataccac  | 1140 |
| tgaggaggtg  | aattacatca  | atgcacatgc  | aacttccact  | cttgctggtg  | atcttgctga  | 1200 |
| gattaatgac  | atttaaaagg  | tattcaagag  | cacttcaggg  | atcaaaaatca | acgccaccaca | 1260 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| gtctatgata | ggtcactgcc | tgggtgcagc | tggaggtcta | gaagccatcg | ccaccgtgaa | 1320 |
| ggctatcaac | actgcatggc | tgcatccttc | catcaaccaa | ttaaacccag | aacaagctgt | 1380 |
| ggactttgac | acggtcccaa | acgagaagaa | gcaacacgag | gttgatgttg | ccatatcaaa | 1440 |
| ctcgctcggg | ttcggtagac | acaactcggt | agtcgccttc | tctgccttca | aacctcgatt | 1500 |
| tottcatacc | ttttagattc | tctgccttat | cggttactat | catcatccat | catccatcac | 1560 |
| caccacttgc | agctctcttg | ttcacaaagt | ggagctcttc | ctctggcctt | ttgcagttct | 1620 |
| ttcattcccc | gtttcttacg | gttgctgaga | tttcagattt | tgttgtgtct | ctctctgtgc | 1680 |
| tgcggaatgt | tgtgtatctt | agttcgttcc | atatttcggt | aatttataaa | aacagaaact | 1740 |
| gagagaatct | tgtagttaac | gtgttattgt | cagaataatc | caattagggg | attctcatct | 1800 |
| ttt        |            |            |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:2457:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1572937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2457:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | His | His | Phe | His | Asn | Ile | Val | Leu | Ile | Ala | Phe | Leu | Ser | Leu | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Pro | Leu | Ser | Ile | Ser | Gly | Ser | Thr | Met | Gln | Ala | Leu | Gln | Ser | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ser | Leu | Arg | Ala | Ser | Pro | Pro | Asn | Pro | Leu | Arg | Leu | Pro | Ser | Asn | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Ser | His | Gln | Leu | Ile | Thr | Asn | Ala | Arg | Pro | Leu | Arg | Arg | Gln | Gln |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Arg | Ser | Phe | Ile | Ser | Ala | Ser | Ala | Ser | Thr | Val | Ser | Ala | Pro | Lys | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Thr | Asp | Pro | Lys | Lys | Arg | Val | Val | Ile | Thr | Gly | Met | Gly | Leu | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Ser | Val | Phe | Gly | Asn | Asp | Val | Asp | Ala | Tyr | Tyr | Glu | Lys | Leu | Leu | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Glu | Ser | Gly | Ile | Ser | Leu | Ile | Asp | Arg | Phe | Asp | Ala | Ser | Lys | Phe |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Thr | Arg | Phe | Gly | Gly | Gln | Ile | Arg | Gly | Phe | Ser | Ser | Glu | Gly | Tyr |
|     |     |     | 130 |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Ile | Asp | Gly | Lys | Asn | Glu | Arg | Arg | Leu | Asp | Asp | Cys | Leu | Lys | Tyr | Cys |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Ile | Val | Ala | Gly | Lys | Lys | Ala | Leu | Glu | Ser | Ala | Asn | Leu | Gly | Gly | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Lys | Leu | Asn | Thr | Ile | Asp | Lys | Arg | Lys | Ala | Gly | Val | Leu | Val | Gly | Thr |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Gly | Met | Gly | Gly | Leu | Thr | Val | Phe | Ser | Glu | Gly | Val | Gln | Asn | Leu | Ile |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Lys | Gly | His | Arg | Arg | Ile | Ser | Pro | Phe | Phe | Ile | Pro | Tyr | Ala | Ile |
|     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Thr | Asn | Met | Gly | Ser | Ala | Leu | Leu | Ala | Ile | Asp | Leu | Gly | Leu | Met | Gly |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Pro | Asn | Tyr | Ser | Ile | Ser | Thr | Ala | Cys | Ala | Thr | Ser | Asn | Tyr | Cys | Phe |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Tyr | Ala | Ala | Ala | Asn | His | Ile | Arg | Arg | Gly | Glu | Ala | Asp | Met | Met | Ile |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Ala | Gly | Gly | Thr | Glu | Ala | Ala | Ile | Ile | Pro | Ile | Gly | Leu | Gly | Gly | Phe |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Val | Ala | Cys | Arg | Ala | Leu | Ser | Gln | Arg | Asn | Asp | Asp | Pro | Gln | Thr | Ala |
|     |     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |
| Ser | Arg | Pro | Trp | Asp | Lys | Ala | Arg | Asp | Gly | Phe | Val | Met | Gly | Glu | Gly |

305 310 315 320  
Ala Gly Val Leu Val Met Glu Ser Leu Glu His Ala Asn Glu Thr Trp  
325 330 335  
Cys Ser Asn Cys Ser Arg Ile Ser Trp Arg Cys Cys  
340 345

(2) INFORMATION FOR SEQ ID NO:2458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..323

- (D) OTHER INFORMATION: / Ceres Seq. ID 1572938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2458:

Met Gln Ala Leu Gln Ser Ser Ser Leu Arg Ala Ser Pro Pro Asn Pro  
1 5 10 15  
Leu Arg Leu Pro Ser Asn Arg Gln Ser His Gln Leu Ile Thr Asn Ala  
20 25 30  
Arg Pro Leu Arg Arg Gln Gln Arg Ser Phe Ile Ser Ala Ser Ala Ser  
35 40 45  
Thr Val Ser Ala Pro Lys Arg Glu Thr Asp Pro Lys Lys Arg Val Val  
50 55 60  
Ile Thr Gly Met Gly Leu Val Ser Val Phe Gly Asn Asp Val Asp Ala  
65 70 75 80  
Tyr Tyr Glu Lys Leu Leu Ser Gly Glu Ser Gly Ile Ser Leu Ile Asp  
85 90 95  
Arg Phe Asp Ala Ser Lys Phe Pro Thr Arg Phe Gly Gly Gln Ile Arg  
100 105 110  
Gly Phe Ser Ser Glu Gly Tyr Ile Asp Gly Lys Asn Glu Arg Arg Leu  
115 120 125  
Asp Asp Cys Leu Lys Tyr Cys Ile Val Ala Gly Lys Lys Ala Leu Glu  
130 135 140  
Ser Ala Asn Leu Gly Gly Asp Lys Leu Asn Thr Ile Asp Lys Arg Lys  
145 150 155 160  
Ala Gly Val Leu Val Gly Thr Gly Met Gly Gly Leu Thr Val Phe Ser  
165 170 175  
Glu Gly Val Gln Asn Leu Ile Glu Lys Gly His Arg Arg Ile Ser Pro  
180 185 190  
Phe Phe Ile Pro Tyr Ala Ile Thr Asn Met Gly Ser Ala Leu Leu Ala  
195 200 205  
Ile Asp Leu Gly Leu Met Gly Pro Asn Tyr Ser Ile Ser Thr Ala Cys  
210 215 220  
Ala Thr Ser Asn Tyr Cys Phe Tyr Ala Ala Ala Asn His Ile Arg Arg  
225 230 235 240  
Gly Glu Ala Asp Met Met Ile Ala Gly Gly Thr Glu Ala Ala Ile Ile  
245 250 255  
Pro Ile Gly Leu Gly Gly Phe Val Ala Cys Arg Ala Leu Ser Gln Arg  
260 265 270  
Asn Asp Asp Pro Gln Thr Ala Ser Arg Pro Trp Asp Lys Ala Arg Asp  
275 280 285  
Gly Phe Val Met Gly Glu Gly Ala Gly Val Leu Val Met Glu Ser Leu  
290 295 300  
Glu His Ala Asn Glu Thr Trp Cys Ser Asn Cys Ser Arg Ile Ser Trp  
305 310 315 320  
Arg Cys Cys

(2) INFORMATION FOR SEQ ID NO:2459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..256  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572939  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2459:

```

Met Gly Leu Val Ser Val Phe Gly Asn Asp Val Asp Ala Tyr Tyr Glu
1 5 10 15
Lys Leu Leu Ser Gly Glu Ser Gly Ile Ser Leu Ile Asp Arg Phe Asp
20 25 30
Ala Ser Lys Phe Pro Thr Arg Phe Gly Gly Gln Ile Arg Gly Phe Ser
35 40 45
Ser Glu Gly Tyr Ile Asp Gly Lys Asn Glu Arg Arg Leu Asp Asp Cys
50 55 60
Leu Lys Tyr Cys Ile Val Ala Gly Lys Lys Ala Leu Glu Ser Ala Asn
65 70 75 80
Leu Gly Gly Asp Lys Leu Asn Thr Ile Asp Lys Arg Lys Ala Gly Val
85 90 95
Leu Val Gly Thr Gly Met Gly Gly Leu Thr Val Phe Ser Glu Gly Val
100 105 110
Gln Asn Leu Ile Glu Lys Gly His Arg Arg Ile Ser Pro Phe Phe Ile
115 120 125
Pro Tyr Ala Ile Thr Asn Met Gly Ser Ala Leu Leu Ala Ile Asp Leu
130 135 140
Gly Leu Met Gly Pro Asn Tyr Ser Ile Ser Thr Ala Cys Ala Thr Ser
145 150 155 160
Asn Tyr Cys Phe Tyr Ala Ala Ala Asn His Ile Arg Arg Gly Glu Ala
165 170 175
Asp Met Met Ile Ala Gly Gly Thr Glu Ala Ala Ile Ile Pro Ile Gly
180 185 190
Leu Gly Gly Phe Val Ala Cys Arg Ala Leu Ser Gln Arg Asn Asp Asp
195 200 205
Pro Gln Thr Ala Ser Arg Pro Trp Asp Lys Ala Arg Asp Gly Phe Val
210 215 220
Met Gly Glu Gly Ala Gly Val Leu Val Met Glu Ser Leu Glu His Ala
225 230 235 240
Asn Glu Thr Trp Cys Ser Asn Cys Ser Arg Ile Ser Trp Arg Cys Cys
245 250 255

```

(2) INFORMATION FOR SEQ ID NO:2460:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1719 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1719  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2460:

```

attttttctca gccacaacaac actagtctct tctgatttgt accctaacgt ttactcgact 60
tatctaaagc cgtgaacctc gcgcgaattc ttaaaagtgc gatttttccct taacgcgcgtt 120
tgattccctt acggcctttg aggtccaggga gatagcaaat ttgttggtga gtactgaaaa 180
atggaggaaag agaacgaagt agtgaagacg ttgcagagc ttggtgtgcg tgaggaagctt 240
gttaaagcctt gcgagagatt gggatggaag aacccttcca aaattcaagc cgaagaccctt 300

```

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|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| ccttttgcgc  | ttgaagggaa  | agatgtaatt  | ggacttgogc  | aaacccggtc  | tggtaaaacc  | 360  |
| ggagcttttg  | caattctcat  | attgcaagca  | ctacttgagt  | atgtttatga  | tctcgagcct  | 420  |
| aagaaaaggac | gtagaccgga  | tcctgctttc  | ttcgcttggt  | ttttatctcc  | aactcgagaa  | 480  |
| cttgcaattc  | agatttgctg  | acagtttgaa  | gctcttggtg  | ctgatataac  | tcttagggtg  | 540  |
| gctgtgcttt  | ttggagggtat | agacagggatg | caacaaaacta | ttgctcttgg  | gaaacggcct  | 600  |
| catgtttattg | ttgcaaacac  | tggctgctct  | tgggatacata | tgtctgatac  | aaaaggcctt  | 660  |
| tctctgaaat  | catgtgaaata | tcTggtttct  | tgatgaagca  | gatagactgt  | tgaatgaaga  | 720  |
| ttttgagaaa  | tcctcttaacc | agatttttga  | agagatccct  | cgtgagcgga  | aaacattttct | 780  |
| tttttcagcg  | actatgacta  | aaaagggtcg  | aaaacttcaa  | aggggcatgtt | tgagggaatcc | 840  |
| tgtgaagatt  | gaagctgcct  | ccaaatatct  | cactgtcgat  | actcttaagc  | agcagtatcg  | 900  |
| gtttgttgcc  | gctaataata  | aggattgcta  | tctggtatac  | attctgagtg  | aaatgctctga | 960  |
| atcaacatct  | atgattttca  | cocgaacatg  | tgatggtact  | cgctttcttg  | ctttggtgct  | 1020 |
| tcggagcctt  | ggtttttagag | ctattctcat  | cagtggctcaa | atgactcagt  | caaagagact  | 1080 |
| gggagcttta  | aataagttca  | aagcaggggga | atgtaatact  | ttggttttga  | cogatgtggc  | 1140 |
| tagtagaggg  | ctcgatatcc  | catcagttga  | tgtggttatc  | aattatgata  | ttcccaacaa  | 1200 |
| ttcaaaggat  | tacatccata  | gagtaggaag  | aaccgctcgt  | ctgggacggt  | ctgggtgttg  | 1260 |
| gatacaact   | gtaaaccagt  | atgagctcga  | atggtatata  | caaatagaaa  | aactcattgg  | 1320 |
| caagaaaata  | cctgaatatc  | ccgctgagga  | agatgaagtc  | ttgtcattgt  | tgagagagt   | 1380 |
| tgcagaagcg  | aaaaagctat  | ctgcaatgaa  | tatgaagaag  | tcaggaggta  | ggaagagaa   | 1440 |
| gggagaagat  | gatgaagaaa  | gtgagaggtt  | cttggggagt  | aacaaggaca  | gaggcaacaa  | 1500 |
| ggaaagaggt  | ggttaacaaag | acaagaagtc  | ttctaagaag  | ttcaaacgat  | aaaatagctc  | 1560 |
| tgtttttact  | gtttttccgt  | aactcaccaa  | agttttgaat  | tgaagttttc  | catatgaact  | 1620 |
| agggaaaatt  | aatccatttt  | gtactcgtaa  | tttgtatggt  | cttttctttt  | tgctttgttt  | 1680 |
| ctcaatgaca  | gattatacaa  | tttaagttga  | aagatgttt   |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..252
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2461:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Lys | Lys | Val | Arg | Lys | Leu | Gln | Arg | Ala | Cys | Leu | Arg | Asn | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Lys | Ile | Glu | Ala | Ala | Ser | Lys | Tyr | Ser | Thr | Val | Asp | Thr | Lys | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Gln | Tyr | Arg | Phe | Val | Ala | Ala | Lys | Tyr | Lys | Asp | Cys | Tyr | Lys | Val |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Tyr | Ile | Leu | Ser | Glu | Met | Pro | Glu | Ser | Thr | Ser | Met | Ile | Phe | Thr | Arg |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Thr | Cys | Asp | Gly | Thr | Arg | Phe | Leu | Ala | Leu | Val | Leu | Arg | Ser | Leu | Gly |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     | 80  |
| Phe | Arg | Ala | Ile | Pro | Ile | Ser | Gly | Gln | Met | Thr | Gln | Ser | Lys | Arg | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Ala | Leu | Asn | Lys | Phe | Lys | Ala | Gly | Glu | Cys | Asn | Ile | Leu | Val | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Asp | Val | Ala | Ser | Arg | Gly | Leu | Asp | Ile | Pro | Ser | Val | Asp | Val | Val |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Ile | Asn | Tyr | Asp | Ile | Pro | Thr | Asn | Ser | Lys | Asp | Tyr | Ile | His | Arg | Val |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |
| Gly | Arg | Thr | Ala | Arg | Ala | Gly | Arg | Ser | Gly | Val | Gly | Ile | Ser | Leu | Val |
|     |     |     | 145 |     |     |     |     | 150 |     |     |     | 155 |     |     | 160 |
| Asn | Gln | Tyr | Glu | Leu | Glu | Trp | Tyr | Ile | Gln | Ile | Glu | Lys | Leu | Ile | Gly |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Lys | Lys | Leu | Pro | Glu | Tyr | Pro | Ala | Glu | Glu | Asp | Glu | Val | Leu | Ser | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Glu | Arg | Val | Ala | Glu | Ala | Lys | Lys | Leu | Ser | Ala | Met | Asn | Met | Lys |

195 200 205  
Glu Ser Gly Gly Arg Lys Arg Arg Gly Glu Asp Asp Glu Glu Ser Glu  
210 215 220  
Arg Phe Leu Gly Gly Asn Lys Asp Arg Gly Asn Lys Glu Arg Gly Gly  
225 230 235 240  
Asn Lys Asp Lys Lys Ser Ser Lys Lys Phe Lys Arg  
245 250

(2) INFORMATION FOR SEQ ID NO:2462:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..199

(D) OTHER INFORMATION: / Ceres Seq. ID 1572946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2462:

Met Pro Glu Ser Thr Ser Met Ile Phe Thr Arg Thr Cys Asp Gly Thr  
1 5 10 15  
Arg Phe Leu Ala Leu Val Leu Arg Ser Leu Gly Phe Arg Ala Ile Pro  
20 25 30  
Ile Ser Gly Gln Met Thr Gln Ser Lys Arg Leu Gly Ala Leu Asn Lys  
35 40 45  
Phe Lys Ala Gly Glu Cys Asn Ile Leu Val Cys Thr Asp Val Ala Ser  
50 55 60  
Arg Gly Leu Asp Ile Pro Ser Val Asp Val Val Ile Asn Tyr Asp Ile  
65 70 75 80  
Pro Thr Asn Ser Lys Asp Tyr Ile His Arg Val Gly Arg Thr Ala Arg  
85 90 95  
Ala Gly Arg Ser Gly Val Gly Ile Ser Leu Val Asn Gln Tyr Glu Leu  
100 105 110  
Glu Trp Tyr Ile Gln Ile Glu Lys Leu Ile Gly Lys Lys Leu Pro Glu  
115 120 125  
Tyr Pro Ala Glu Glu Asp Glu Val Leu Ser Leu Leu Glu Arg Val Ala  
130 135 140  
Glu Ala Lys Lys Leu Ser Ala Met Asn Met Lys Glu Ser Gly Gly Arg  
145 150 155 160  
Lys Arg Arg Gly Glu Asp Asp Glu Glu Ser Glu Arg Phe Leu Gly Gly  
165 170 175  
Asn Lys Asp Arg Gly Asn Lys Glu Arg Gly Gly Asn Lys Asp Lys Lys  
180 185 190  
Ser Ser Lys Lys Phe Lys Arg  
195

(2) INFORMATION FOR SEQ ID NO:2463:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1572947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2463:

Met Ile Phe Thr Arg Thr Cys Asp Gly Thr Arg Phe Leu Ala Leu Val  
1 5 10 15  
Leu Arg Ser Leu Gly Phe Arg Ala Ile Pro Ile Ser Gly Gln Met Thr  
20 25 30

```

Gln Ser Lys Arg Leu Gly Ala Leu Asn Lys Phe Lys Ala Gly Glu Cys
 35 40 45
Asn Ile Leu Val Cys Thr Asp Val Ala Ser Arg Gly Leu Asp Ile Pro
 50 55 60
Ser Val Asp Val Val Ile Asn Tyr Asp Ile Pro Thr Asn Ser Lys Asp
 65 70 75 80
Tyr Ile His Arg Val Gly Arg Thr Ala Arg Ala Gly Arg Ser Gly Val
 85 90 95
Gly Ile Ser Leu Val Asn Gln Tyr Glu Leu Glu Trp Tyr Ile Gln Ile
 100 105 110
Glu Lys Leu Ile Gly Lys Lys Leu Pro Glu Tyr Pro Ala Glu Glu Asp
 115 120 125
Glu Val Leu Ser Leu Leu Glu Arg Val Ala Glu Ala Lys Lys Leu Ser
 130 135 140
Ala Met Asn Met Lys Glu Ser Gly Gly Arg Lys Arg Arg Gly Glu Asp
 145 150 155 160
Asp Glu Glu Ser Glu Arg Phe Leu Gly Gly Asn Lys Asp Arg Gly Asn
 165 170 175
Lys Glu Arg Gly Gly Asn Lys Asp Lys Lys Ser Ser Lys Lys Lys Lys
 180 185 190
Arg

```

(2) INFORMATION FOR SEQ ID NO:2464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..592
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2464:

```

gaagattaat tgaatcacac aaagtcgaat ccaaagtttt tgatcttaac caagtcgcac 60
aatccagaga ggaatcaaaa gaagatgagt aacgtcagct tcaggcagga tcatgatttc 120
gagaagagga aagctgaggg tttaaggatc agagagaagt attctgacag agtcccggtt 180
atttgggaga agtcagagaa aagtgatatc ccaaaccattg acaagaagaa ataccttgtc 240
ccagctgatac taacggtagg ccagtttggt tatgtgattc gtaagagaa ccaacttagt 300
gcagagaaag ctatcttcac ctgtttgatg aatgtttctc ctcccaccgg agcgatgatg 360
tcaaccattt acgatgagaa taaggagaaga gacggcttct tgtatgttac ctacagtgagg 420
gaaaacattt ttggatcgctc aatgacttaa tttggtgttc ttgcttttaa ttgaatgtaa 480
atatccattt ttcttttctt gtccgtgaac ttgcttagat gcggatatga ttattatggc 540
ttatgtaggg acaaccAatc ggtttgcaaa caaagtgttg gtttttttat cc

```

(2) INFORMATION FOR SEQ ID NO:2465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2465:

```

Met Ser Asn Val Ser Phe Arg Gln Asp His Asp Phe Glu Lys Arg Lys
1 5 10 15
Ala Glu Ala Leu Arg Ile Arg Glu Lys Tyr Ser Asp Arg Val Pro Val
20 25 30
Ile Val Glu Lys Ser Glu Lys Ser Asp Ile Pro Asn Ile Asp Lys Lys

```

|                                             |                             |                     |
|---------------------------------------------|-----------------------------|---------------------|
| 35                                          | 40                          | 45                  |
| Lys Tyr Leu Val Pro Ala Asp                 | Leu Thr Val Gly             | Gln Phe Val Tyr Val |
| 50                                          | 55                          | 60                  |
| Ile Arg Lys Arg Ile Gln Leu Ser Ala Glu Lys | Ala Ile Phe Ile Phe         |                     |
| 65                                          | 70                          | 75                  |
| Val Asp Asn Val Leu Pro Pro Thr Gly Ala Met | Ser Thr Ile Tyr             |                     |
| 85                                          | 90                          | 95                  |
| Asp Glu Asn Lys Glu Glu Asp Gly Phe         | Leu Tyr Val Thr Tyr Ser Gly |                     |
| 100                                         | 105                         | 110                 |
| Glu Asn Thr Phe Gly Ser Ser Met Thr         |                             |                     |
| 115                                         | 120                         |                     |

(2) INFORMATION FOR SEQ ID NO:2466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2466:

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gtttcatctg ttgttccctg tgacctggc tactccactc tcaatctcat caaatctctt    | 60   |
| cacctccgcg cattgttacc gtctccactt atcttctact tcaatcaagg taatctctca   | 120  |
| ttctttctaca aatgtcaatt ttgaatgaat ccataaaaatt ggaatttgaa atgtgtacag | 180  |
| ggaaatgttaa gtgttttggg ggcacaaccca agtcagattc tatctctgaa actcaaccaa | 240  |
| acccttaaaa cgagaaaccca acagcaattt gcgagacccc ttgttgggtg tagccaaacg  | 300  |
| gcggctacgt cgtcggcagt tgtagctccg gagagattcc gtttggataa tcttggacca   | 360  |
| cgccaggtt cgaggaaaga gcagaagaga aaaggtagag gtatctctgc aggacaagga    | 420  |
| gcaagtgtgt gttttggtat gagaggtcag aaatcaagat cgggtctcgg gattatgaga   | 480  |
| ggctttgaag gtggtcaaac tgccttttat cgtcgtcttc ccaaaacttag aggaactcgt  | 540  |
| ggaggtatgc gtctcaggatt acctaaatac ttacoggtta atatcaaaaga catagaacc  | 600  |
| gctgggtttc aagagggaga tgaagtgtca ttggagacat tgaagcaaaa gggtttgatt   | 660  |
| aatccttcag ggagagaaa gaaactccct cttaagattc tgggtacagg agaactaagc    | 720  |
| atgaagctca ccttcaaaag cctgtgccttc tcaacacaag caaaagagaa gcttgaagct  | 780  |
| tcagggttga cactcactgt gttgccggga agaaagaaat ggggttaagcc atctgttgca  | 840  |
| aagaaccaag cagcagcaga tgaatacttt gccagaaga gaagctgcagc agcagaagca   | 900  |
| gcaacttcag agccagcagc cctcgtctaa attacttcag ttccaagctc ttttagtgt    | 960  |
| tgtaaaagctg cagagaagat aattgtctat gacaaatgtt aattacaatt ccttctctt   | 1020 |
| ttgttatggt gaagagattt acattttggt gtttgaagag tcattatcaa aaagatatgt   | 1080 |
| aaacggtaat gaaatattga acattttggt Tc                                 |      |

(2) INFORMATION FOR SEQ ID NO:2467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2467:

|                                                                 |    |
|-----------------------------------------------------------------|----|
| Met Arg Gly Gln Lys Ser Arg Ser Gly Pro Gly Ile Met Arg Gly Phe |    |
| 1                                                               | 15 |
| Glu Gly Gly Gln Thr Ala Leu Tyr Arg Arg Leu Pro Lys Leu Arg Gly |    |
| 20                                                              | 30 |
| Ile Ala Gly Gly Met Arg Ser Gly Leu Pro Lys Tyr Leu Pro Val Asn |    |
| 35                                                              | 45 |
| Ile Lys Asp Ile Glu Thr Ala Gly Phe Gln Glu Gly Asp Glu Val Ser |    |



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 50                                                              | 55  | 60  |
| Leu Glu Thr Leu Lys Gln Lys Gly Leu Ile Asn Pro Ser Gly Arg Glu |     |     |
| 65                                                              | 70  | 75  |
| Arg Lys Leu Pro Leu Lys Ile Leu Gly Thr Gly Glu Leu Ser Met Lys |     | 80  |
|                                                                 | 85  | 90  |
| Leu Thr Phe Lys Ala Arg Ala Phe Ser Thr Gln Ala Lys Glu Lys Leu |     | 95  |
|                                                                 | 100 | 105 |
| Glu Ala Ser Gly Cys Thr Leu Thr Val Leu Pro Gly Arg Lys Lys Trp |     | 110 |
|                                                                 | 115 | 120 |
| Val Lys Pro Ser Val Ala Lys Asn Gln Ala Arg Ala Asp Glu Tyr Phe |     | 125 |
|                                                                 | 130 | 135 |
| Ala Lys Lys Arg Ala Ala Ala Glu Ala Ala Thr Ser Glu Pro Ala     |     | 140 |
|                                                                 | 145 | 150 |
| Ala Ser Ala                                                     |     | 155 |
|                                                                 |     | 160 |

(2) INFORMATION FOR SEQ ID NO:2468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1572964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2468:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Arg Gly Phe Glu Gly Gly Gln Thr Ala Leu Tyr Arg Arg Leu Pro |     |     |
| 1                                                               | 5   | 10  |
| Lys Leu Arg Gly Ile Ala Gly Gly Met Arg Ser Gly Leu Pro Lys Tyr |     | 15  |
|                                                                 | 20  | 25  |
| Leu Pro Val Asn Ile Lys Asp Ile Glu Thr Ala Gly Phe Gln Glu Gly |     | 30  |
|                                                                 | 35  | 40  |
| Asp Glu Val Ser Leu Glu Thr Leu Lys Gln Lys Gly Leu Ile Asn Pro |     | 45  |
|                                                                 | 50  | 55  |
| Ser Gly Arg Glu Arg Lys Leu Pro Leu Lys Ile Leu Gly Thr Gly Glu |     | 60  |
|                                                                 | 65  | 70  |
| Leu Ser Met Lys Leu Thr Phe Lys Ala Arg Ala Phe Ser Thr Gln Ala |     | 75  |
|                                                                 | 85  | 90  |
| Lys Glu Lys Leu Glu Ala Ser Gly Cys Thr Leu Thr Val Leu Pro Gly |     | 95  |
|                                                                 | 100 | 105 |
| Arg Lys Lys Trp Val Lys Pro Ser Val Ala Lys Asn Gln Ala Arg Ala |     | 110 |
|                                                                 | 115 | 120 |
| Asp Glu Tyr Phe Ala Lys Lys Arg Ala Ala Ala Ala Glu Ala Ala Thr |     | 125 |
|                                                                 | 130 | 135 |
| Ser Glu Pro Ala Ala Ser Ala                                     |     | 140 |
|                                                                 | 145 | 150 |

(2) INFORMATION FOR SEQ ID NO:2469:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1572965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2469:

|                                                                 |   |    |
|-----------------------------------------------------------------|---|----|
| Met Arg Ser Gly Leu Pro Lys Tyr Leu Pro Val Asn Ile Lys Asp Ile |   |    |
| 1                                                               | 5 | 10 |
|                                                                 |   | 15 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Glu | Gln | Gln | Gln | His | Phe | Met | Asp | Leu | Gln | Ser | Asp | Ser | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Phe | Xaa | Asp | Asp | Ser | Ser | Trp | Leu | Ala | Gly | Asp | Asp | Asp | Leu | Arg | Leu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Pro | His | Gln | Ser | Ala | Ala | Gly | Thr | Asn | Ser | Gly | Asn | Glu | Asn | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Asp | Arg | Arg | Leu | Leu | Lys | Asp | Leu | Val | Glu | Met | Val | Pro | Leu | Ile | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| His | Tyr | Met | Glu | His | Lys | Glu | Arg | Ser | Ser | Phe | Lys | Arg | Arg | Gly | Ser |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |

Met Ile Tyr Thr Lys Met Pro Ser Lys Glu Ser Leu Ser Arg Arg Gly  
85 90 95  
Arg Asn Ala Ser Gln Thr Val Pro Gly Arg Lys Lys Arg Asp Gln Glu  
100 105 110  
Gly Asn Asp Asp Val Met Asn Asn Ser Arg Glu Asp Asp Glu Asn Ala  
115 120 125  
Lys Ala Leu Ala Gly Ala Glu Lys Glu Glu Met Ser Arg Leu Arg Ala  
130 135 140  
Ser Glu  
145

(2) INFORMATION FOR SEQ ID NO:2472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..138  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2472:

Met Asp Leu Gln Ser Asp Ser Gly Phe Xaa Asp Asp Ser Ser Trp Leu  
1 5 10 15  
Ala Gly Asp Asp Asp Leu Arg Leu Ser Pro His Gln Ser Ala Ala Gly  
20 25 30  
Thr Asn Ser Ser Gly Asn Glu Asn Leu Asp Arg Arg Leu Leu Lys Asp Leu  
35 40 45  
Val Glu Met Val Pro Leu Ile Glu His Tyr Met Glu His Lys Glu Arg  
50 55 60  
Ser Ser Phe Lys Arg Arg Gly Ser Met Ile Tyr Thr Lys Met Pro Ser  
65 70 75 80  
Lys Glu Ser Leu Ser Arg Arg Gly Arg Asn Ala Ser Gln Thr Val Pro  
85 90 95  
Gly Arg Lys Lys Arg Asp Gln Glu Gly Asn Asp Asp Val Met Asn Asn  
100 105 110  
Ser Arg Glu Asp Asp Glu Asn Ala Lys Ala Leu Ala Gly Ala Glu Lys  
115 120 125  
Glu Glu Met Ser Arg Leu Arg Ala Ser Glu  
130 135

(2) INFORMATION FOR SEQ ID NO:2473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..88  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2473:

Met Val Pro Leu Ile Glu His Tyr Met Glu His Lys Glu Arg Ser Ser  
1 5 10 15  
Phe Lys Arg Arg Gly Ser Met Ile Tyr Thr Lys Met Pro Ser Lys Glu  
20 25 30  
Ser Leu Ser Arg Arg Gly Arg Asn Ala Ser Gln Thr Val Pro Gly Arg  
35 40 45  
Lys Lys Arg Asp Gln Glu Gly Asn Asp Asp Val Met Asn Asn Ser Arg  
50 55 60  
Glu Asp Asp Glu Asn Ala Lys Ala Leu Ala Gly Ala Glu Lys Glu Glu

65 70 75 80  
Met Ser Arg Leu Arg Ala Ser Glu  
85

(2) INFORMATION FOR SEQ ID NO:2474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1450
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2474:

```

agggggcctt tgtgttgacg gtgggtggaa caaaggaaca tcgtatccat tctgtccggg 60
aaaRcacagc aatgttcatt tccgacaaat ctgctcctac tgattttctc aaagacgac 120
atcacaaatt ctccaccacc agcaccacac gcgatgatgat gatcgatgta ctccaccact 180
ccaacgaatt agtagatcta caatctcacc accaccacaa tcacaatcac cacaatcat 240
atctccacca atctcagcca caacaacaga ttctcctcgg agaaagcagt ggagaagatc 300
acgaagttaa agcaccaaag aacgagcgg agacatgggt tcaagacgaa actcgtagct 360
taatcatggt ccgtagaggt atggatgggt tattcaatc atccaaatct aataaacatc 420
tctgggaaca gatttcgtct aagatgagag aaaaagggtt tgatcgatct ccgactatgt 480
gtactgataa atggaggaat ctgttgaaag agttaaagaa agctaagcat catgatagag 540
gaaatggatc ggcgagaagt tcgtattaca aagagattga agatattctt agagagagga 600
gcaaaaagt gacaccacca cagtataata agagccctaa tacaccacct acatcagcca 660
aagttgattc ctttatgcaa ttactgata aaggttttga tgatacagac atttcttttt 720
gatccgttga agctaatggc aggccagcct taacccctga aaggcgtctt gatcatgatg 780
gtcatcctct tgcaatcact acagcagttg atgctgttgc agcaaatgga gttactcctt 840
ggaattggag agagaactct gaaacgggt atgatagtc tggtcagcct ttgttggtga 900
gggtcataac agtgaaattt ggtgactata caagaagaat cgggtgtgat ggtagtgcag 960
aagcaatcaa agaggtaatt agatctgctt ttgggttaa aactcgaagg gcttttttgt 1020
tagaagatga agatcagatt attcgtcttc ttgaccgaga catgccctta gggaactact 1080
tactccgtct ggatgatgga ctggccatta gggtttgcc ttatgatgaa tccaaccaat 1140
taccagtcca ttcagaagag aaaattcttc acactgaaga agactaccgc gagtttcttg 1200
ctcgacgggg atggtcactg ctgcaagttg atgggtttag gaacatagaa aacatgggat 1260
attctcaacc tgggtgctgt tatcgaggtg tgagatgagg aaatgagatc acaaaacttc 1320
ttctccaatt ctatcaacag ttatctgata agaaaacagt ccctgtgata tatgatctca 1380
ttctctttat acattttctc tttttttcat gtacttgctc aatatgaaa tatcataact 1440
ggcatttacc

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(2) INFORMATION FOR SEQ ID NO:2475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..431
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2475:

```

Gly Ala Phe Val Leu Thr Val Val Gly Thr Lys Glu His Arg Ile His
1 5 10 15
Ser Val Arg Glu Xaa Thr Ala Met Phe Ile Ser Asp Lys Ser Arg Pro
20 25 30
Thr Asp Phe Tyr Lys Asp Asp His His Asn Ser Ser Thr Thr Ser Thr
35 40 45
Thr Arg Asp Met Met Ile Asp Val Leu Thr Thr Thr Asn Glu Ser Val
50 55 60
Asp Leu Gln Ser Ser His His His Asn His Asn His His Asn His His

```

|                 |                         |                         |     |
|-----------------|-------------------------|-------------------------|-----|
| 65              | 70                      | 75                      | 80  |
| Leu His Gln Ser | Gln Pro Gln Gln Gln Ile | Leu Leu Gly Glu Ser Ser |     |
|                 | 85                      | 90                      | 95  |
| Gly Glu Asp His | Glu Val Lys Ala Pro Lys | Lys Arg Ala Glu Thr Trp |     |
|                 | 100                     | 105                     | 110 |
| Val Gln Asp Glu | Thr Arg Ser Leu Ile Met | Phe Arg Arg Gly Met Asp |     |
|                 | 115                     | 120                     | 125 |
| Gly Leu Phe Asn | Thr Ser Lys Ser Asn Lys | His Leu Trp Glu Gln Ile |     |
|                 | 130                     | 135                     | 140 |
| Ser Ser Lys Met | Arg Glu Lys Gly Phe Asp | Arg Ser Pro Thr Met Cys |     |
|                 | 145                     | 150                     | 155 |
| Thr Asp Lys Trp | Arg Asn Leu Leu Lys Glu | Phe Lys Lys Ala Lys His |     |
|                 | 165                     | 170                     | 175 |
| His Asp Arg Gly | Asn Gly Ser Ala Lys Met | Ser Tyr Tyr Lys Glu Ile |     |
|                 | 180                     | 185                     | 190 |
| Glu Asp Ile Leu | Arg Glu Arg Ser Lys Lys | Val Thr Pro Pro Gln Tyr |     |
|                 | 195                     | 200                     | 205 |
| Asn Lys Ser Pro | Asn Thr Pro Pro Thr Ser | Ala Lys Val Asp Ser Phe |     |
|                 | 210                     | 215                     | 220 |
| Met Gln Phe Thr | Asp Lys Gly Phe Asp Asp | Thr Ser Ile Ser Phe Gly |     |
|                 | 225                     | 230                     | 235 |
| Ser Val Glu Ala | Asn Gly Arg Pro Ala Leu | Asn Leu Glu Arg Arg Leu |     |
|                 | 245                     | 250                     | 255 |
| Asp His Asp Gly | His Pro Leu Ala Ile Thr | Thr Ala Val Asp Ala Val |     |
|                 | 260                     | 265                     | 270 |
| Ala Ala Asn Gly | Val Thr Pro Trp Asn Trp | Arg Glu Thr Pro Gly Asn |     |
|                 | 275                     | 280                     | 285 |
| Gly Asp Asp Ser | His Gly Gln Pro Phe Gly | Gly Arg Val Ile Thr Val |     |
|                 | 290                     | 295                     | 300 |
| Lys Phe Gly Asp | Tyr Thr Arg Arg Ile Gly | Val Asp Gly Ser Ala Glu |     |
|                 | 305                     | 310                     | 315 |
| Ala Ile Lys Glu | Val Ile Arg Ser Ala Phe | Gly Leu Arg Thr Arg Arg |     |
|                 | 325                     | 330                     | 335 |
| Ala Phe Trp Leu | Glu Asp Glu Asp Gln Ile | Ile Arg Cys Leu Asp Arg |     |
|                 | 340                     | 345                     | 350 |
| Asp Met Pro Leu | Gly Asn Tyr Leu Leu Arg | Leu Asp Asp Gly Leu Ala |     |
|                 | 355                     | 360                     | 365 |
| Ile Arg Val Cys | His Tyr Asp Glu Ser Asn | Gln Leu Pro Val His Ser |     |
|                 | 370                     | 375                     | 380 |
| Glu Glu Lys Ile | Phe Tyr Thr Glu Glu Asp | Tyr Arg Glu Phe Leu Ala |     |
|                 | 385                     | 390                     | 395 |
| Arg Arg Gly Trp | Ser Cys Leu Gln Val Asp | Gly Phe Arg Asn Ile Glu |     |
|                 | 405                     | 410                     | 415 |
| Asn Met Asp Asp | Leu Gln Pro Gly Ala Val | Tyr Arg Gly Val Arg     |     |
|                 | 420                     | 425                     | 430 |

(2) INFORMATION FOR SEQ ID NO:2476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..408
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2476:

|                 |                     |                         |         |
|-----------------|---------------------|-------------------------|---------|
| Met Phe Ile Ser | Asp Lys Ser Arg Pro | Thr Asp Phe Tyr Lys Asp | Asp     |
| 1               | 5                   | 10                      | 15      |
| His His Asn Ser | Ser Thr Thr Ser Thr | Thr Arg Asp Met Met     | Ile Asp |
|                 | 20                  | 25                      | 30      |

Val Leu Thr Thr Thr Asn Glu Ser Val Asp Leu Gln Ser His His His  
35 40 45  
His Asn His Asn His His Asn His His Leu His Gln Ser Gln Pro Gln  
50 55 60  
Gln Gln Ile Leu Leu Gly Glu Ser Ser Gly Glu Asp His Glu Val Lys  
65 70 75 80  
Ala Pro Lys Lys Arg Ala Glu Thr Trp Val Gln Asp Glu Thr Arg Ser  
85 90 95  
Leu Ile Met Phe Arg Arg Gly Met Asp Gly Leu Phe Asn Thr Ser Lys  
100 105 110  
Ser Asn Lys His Leu Trp Glu Gln Ile Ser Ser Lys Met Arg Glu Lys  
115 120 125  
Gly Phe Asp Arg Ser Pro Thr Met Cys Thr Asp Lys Trp Arg Asn Leu  
130 135 140  
Leu Lys Glu Phe Lys Lys Ala Lys His His Asp Arg Gly Asn Gly Ser  
145 150 155 160  
Ala Lys Met Ser Tyr Tyr Lys Glu Ile Glu Asp Ile Leu Arg Glu Arg  
165 170 175  
Ser Lys Lys Val Thr Pro Pro Gln Tyr Asn Lys Ser Pro Asn Thr Pro  
180 185 190  
Pro Thr Ser Ala Lys Val Asp Ser Phe Met Gln Phe Thr Asp Lys Gly  
195 200 205  
Phe Asp Asp Thr Ser Ile Ser Phe Gly Ser Val Glu Ala Asn Gly Arg  
210 215 220  
Pro Ala Leu Asn Leu Glu Arg Arg Leu Asp His Asp Gly His Pro Leu  
225 230 235 240  
Ala Ile Thr Thr Ala Val Asp Ala Val Ala Ala Asn Gly Val Thr Pro  
245 250 255  
Trp Asn Trp Arg Glu Thr Pro Gly Asn Gly Asp Asp Ser His Gly Gln  
260 265 270  
Pro Phe Gly Gly Arg Val Ile Thr Val Lys Phe Gly Asp Tyr Thr Arg  
275 280 285  
Arg Ile Gly Val Asp Gly Ser Ala Glu Ala Ile Lys Glu Val Ile Arg  
290 295 300  
Ser Ala Phe Gly Leu Arg Thr Arg Arg Ala Phe Trp Leu Glu Asp Glu  
305 310 315 320  
Asp Gln Ile Ile Arg Cys Leu Asp Arg Asp Met Pro Leu Gly Asn Tyr  
325 330 335  
Leu Leu Arg Leu Asp Asp Gly Leu Ala Ile Arg Val Cys His Tyr Asp  
340 345 350  
Glu Ser Asn Gln Leu Pro Val His Ser Glu Glu Lys Ile Phe Tyr Thr  
355 360 365  
Glu Glu Asp Tyr Arg Glu Phe Leu Ala Arg Arg Gly Trp Ser Cys Leu  
370 375 380  
Gln Val Asp Gly Phe Arg Asn Ile Glu Asn Met Asp Asp Leu Gln Pro  
385 390 395 400  
Gly Ala Val Tyr Arg Gly Val Arg  
405

(2) INFORMATION FOR SEQ ID NO:2477:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..380

(D) OTHER INFORMATION: / Ceres Seq. ID 1572973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2477:

Met Met Ile Asp Val Leu Thr Thr Thr Asn Glu Ser Val Asp Leu Gln

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Ser His His His His Asn His Asn His His His Leu His Gln         | 20  | 25  | 30  |
| Ser Gln Pro Gln Gln Gln Ile Leu Leu Gly Glu Ser Ser Gly Glu Asp | 35  | 40  | 45  |
| His Glu Val Lys Ala Pro Lys Lys Arg Ala Glu Thr Trp Val Gln Asp | 50  | 55  | 60  |
| Glu Thr Arg Ser Leu Ile Met Phe Arg Arg Gly Met Asp Gly Leu Phe | 65  | 70  | 75  |
| Asn Thr Ser Lys Ser Asn Lys His Leu Trp Glu Gln Ile Ser Ser Lys | 85  | 90  | 95  |
| Met Arg Glu Lys Gly Phe Asp Arg Ser Pro Thr Met Cys Thr Asp Lys | 100 | 105 | 110 |
| Trp Arg Asn Leu Leu Lys Glu Phe Lys Lys Ala Lys His Asp Arg     | 115 | 120 | 125 |
| Gly Asn Gly Ser Ala Lys Met Ser Tyr Tyr Lys Glu Ile Glu Asp Ile | 130 | 135 | 140 |
| Leu Arg Glu Arg Ser Lys Lys Val Thr Pro Pro Gln Tyr Asn Lys Ser | 145 | 150 | 155 |
| Pro Asn Thr Pro Pro Thr Ser Ala Lys Val Asp Ser Phe Met Gln Phe | 165 | 170 | 175 |
| Thr Asp Lys Gly Phe Asp Asp Thr Ser Ile Ser Phe Gly Ser Val Glu | 180 | 185 | 190 |
| Ala Asn Gly Arg Pro Ala Leu Asn Leu Glu Arg Arg Leu Asp His Asp | 195 | 200 | 205 |
| Gly His Pro Leu Ala Ile Thr Thr Ala Val Asp Ala Val Ala Ala Asn | 210 | 215 | 220 |
| Gly Val Thr Pro Trp Asn Trp Arg Glu Thr Pro Gly Asn Gly Asp Asp | 225 | 230 | 235 |
| Ser His Gly Gln Pro Phe Gly Gly Arg Val Ile Thr Val Lys Phe Gly | 245 | 250 | 255 |
| Asp Tyr Thr Arg Arg Ile Gly Val Asp Gly Ser Ala Glu Ala Ile Lys | 260 | 265 | 270 |
| Glu Val Ile Arg Ser Ala Phe Gly Leu Arg Thr Arg Arg Ala Phe Trp | 275 | 280 | 285 |
| Leu Glu Asp Glu Asp Gln Ile Ile Arg Cys Leu Asp Arg Asp Met Pro | 290 | 295 | 300 |
| Leu Gly Asn Tyr Leu Leu Arg Leu Asp Asp Gly Leu Ala Ile Arg Val | 305 | 310 | 315 |
| Cys His Tyr Asp Glu Ser Asn Gln Leu Pro Val His Ser Glu Glu Lys | 325 | 330 | 335 |
| Ile Phe Tyr Thr Glu Glu Asp Tyr Arg Glu Phe Leu Ala Arg Arg Gly | 340 | 345 | 350 |
| Trp Ser Cys Leu Gln Val Asp Gly Phe Arg Asn Ile Glu Asn Met Asp | 355 | 360 | 365 |
| Asp Leu Gln Pro Gly Ala Val Tyr Arg Gly Val Arg                 | 370 | 375 | 380 |

(2) INFORMATION FOR SEQ ID NO:2478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2262
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2478:

gtttcttctt caacctcttt gtcagagaag tttaaaacc cccacacac actttacaca  
ctcttcacat tcttctctt cttcatcggt ttgcgattgt tgctccgata atgctggttc

60  
120

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| tataaccgga  | agatcatcaa  | cgaagaaagc  | gaaataaaacc | tcaaaaaatca | cagagattat  | 180  |
| tacaataggc  | ggctactgat  | tttttctctg  | ctttctgtctt | ctctttcact  | cttatctctcg | 240  |
| gcttctcttt  | cgcttggtgat | ctttacgtct  | cttacgattt  | cactctctcc  | tacatcactg  | 300  |
| cttctctctt  | cggtgttctt  | caacaggtca  | tagcagtcac  | tgggaaatct  | ccaggctctg  | 360  |
| tgattaaagc  | tacgacaaac  | tacaatgttc  | atgttaaact  | actcaatcat  | ttggatgagc  | 420  |
| ctcttttact  | tacttggcct  | gggtgttcaga | tgaggcgtaa  | ctcgtggcaa  | gacggtgttc  | 480  |
| ttggaaacaa  | ctgtccaatt  | ccaccgaatt  | ggaacttcac  | ttatgatttt  | cagttgaaag  | 540  |
| atcagatttg  | aagtattttc  | tactctctct  | cacttaactt  | tcagagagcc  | ttcgttggtt  | 600  |
| ttgggtgact  | cataatcaat  | aacagagacc  | ttgttccat   | tcggttcaact | gagcctgatg  | 660  |
| gtgaaattat  | ctttattatt  | gttgatttgg  | atactcagaa  | ccatacagct  | ttagggagga  | 720  |
| tacttgactc  | tggttaaaag  | cttgggatgc  | ccgatggagt  | actcatcaat  | gggaaaggct  | 780  |
| ctttcaagta  | caatagcagt  | gcactgatg   | gaattgaaca  | tgaacccgtt  | aatgttgatc  | 840  |
| cagggaaaac  | atacaggatc  | cgtgttccaa  | atgttggtat  | ctcgacaagc  | ttgaacttca  | 900  |
| ggattcagaa  | ccacaaattg  | ctcttgattg  | agactgaggg  | tcgctacacc  | tcocaaatga  | 960  |
| acttccacga  | ttttgatatt  | catgtgggac  | agtccttatt  | tttctcgtga  | accatggacc  | 1020 |
| aaaacgccac  | aagtgactac  | tacattgttg  | cgagtgtcag  | atttgttaat  | gaacactgtg  | 1080 |
| ggcaaaagag  | tacaggtgtt  | ggcattctcc  | attattccaa  | ttccaaagga  | ctcgtctctg  | 1140 |
| gtcctttggc  | agtttcagca  | actgatgtta  | atcacccctg  | gtctgcaaat  | aaccaaccca  | 1200 |
| gagccataaa  | gcacaaacaca | tctgcaagtg  | gagctcgtcc  | aaatcccgag  | ggatcatttc  | 1260 |
| actacggaca  | gatcaacatt  | acaagaacat  | acatcttgag  | gagtttgctt  | ccaacaaaaa  | 1320 |
| tcaatgggaa  | actctgtgct  | acacttaagt  | gaatttcatt  | tgtcaatcca  | agcaccctcca | 1380 |
| tgaggcttcc  | ggatgaccat  | aaagtgaag   | gagattatat  | gttagatttc  | ccagacagac  | 1440 |
| cacttgatga  | aaaaacttcca | cgtttgtcca  | gctctatcat  | caacccaaca  | tacaagggct  | 1500 |
| ttatacaagt  | tatcttccag  | aacaatgaca  | ccaaaatcca  | gagcttccat  | attgatggat  | 1560 |
| atgcatttta  | cgttggttgcg | atggactttg  | gtatatggtc  | agaagacaga  | aacggttcat  | 1620 |
| atacaacactg | ggatgcagta  | gcacgaagca  | cggtggaggt  | ctatccagga  | gcattggactg | 1680 |
| ctgtacttat  | ttctctcgtc  | Gaatgttga   | gtttggaata  | tcgggttgta  | gaattctgac  | 1740 |
| agatggtatc  | ttggcccaaga | aacatacatg  | cgaattataa  | accctgagga  | aacgggaagt  | 1800 |
| acggaaatgg  | atccgcctga  | aaatgttatg  | tactgtgggt  | ctctcagggc  | catgcaaaag  | 1860 |
| gaacacatc   | acagctcgcc  | cacaaaaatca | atgacaaatg  | gcagcttgat  | actaattttc  | 1920 |
| agcatgatga  | tggttttgct  | ctctctgttt  | togtctcttt  | gctgagctcg  | ttccatcaat  | 1980 |
| tacgaatcta  | ctctgggttg  | gtattctgat  | ctccattag   | ggctgttagat | ggagaatgta  | 2040 |
| taactacaaa  | cagctgttgg  | gttcgttctg  | tttctctcat  | atttcatgta  | ttgttaggta  | 2100 |
| ctcatattct  | ctatctcat   | gattcctaac  | aacgttagtt  | cgtgaggggt  | ttgttttaga  | 2160 |
| gctttgtctt  | togtagttct  | aggtcatttg  | gagttcaaaa  | cttggcacc   | gactgtaact  | 2220 |
| aaagtctcca  | tttgttggtc  | ttctacatta  | atttctacta  | tt          |             |      |

(2) INFORMATION FOR SEQ ID NO:2479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..514
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2479:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Thr | Asp | Phe | Phe | Phe | Ala | Phe | Val | Phe | Ser | Phe | Thr | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Phe | Gly | Phe | Ser | Phe | Ala | Gly | Asp | Pro | Tyr | Val | Ser | Tyr | Asp | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Leu | Ser | Tyr | Ile | Thr | Ala | Ser | Pro | Leu | Gly | Val | Pro | Gln | Gln | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Ile | Ala | Val | Asn | Gly | Lys | Phe | Pro | Gly | Pro | Val | Ile | Asn | Ala | Thr | Thr |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Asn | Tyr | Asn | Val | His | Val | Asn | Val | Leu | Asn | His | Leu | Asp | Glu | Pro | Leu |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Leu | Leu | Thr | Trp | Pro | Gly | Val | Gln | Met | Arg | Arg | Asn | Ser | Trp | Gln | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Val | Leu | Gly | Thr | Asn | Cys | Pro | Ile | Pro | Pro | Asn | Trp | Asn | Phe | Thr |



|     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|
|     | 100 |     | 105 |     | 110 |
| Tyr | Asp | Phe | Gln | Leu | Lys |
|     | 115 |     | 120 |     | 125 |
| Ser | Leu | Asn | Phe | Gln | Arg |
|     | 130 |     | 135 |     | 140 |
| Asn | Asn | Arg | Asp | Leu | Val |
|     | 145 |     | 150 |     | 155 |
| Ile | Ile | Phe | Ile | Ile | Gly |
|     | 165 |     | 170 |     | 175 |
| Arg | Arg | Ile | Leu | Asp | Ser |
|     | 180 |     | 185 |     | 190 |
| Leu | Ile | Asn | Gly | Lys | Pro |
|     | 195 |     | 200 |     | 205 |
| Gly | Ile | Glu | His | Glu | Thr |
|     | 210 |     | 215 |     | 220 |
| Ile | Arg | Val | His | Asn | Val |
|     | 225 |     | 230 |     | 235 |
| Gln | Asn | His | Lys | Leu | Leu |
|     | 245 |     | 250 |     | 255 |
| Gln | Met | Asn | Phe | Thr | Asp |
|     | 260 |     | 265 |     | 270 |
| Phe | Leu | Val | Thr | Met | Asp |
|     | 275 |     | 280 |     | 285 |
| Ala | Ser | Ala | Arg | Phe | Val |
|     | 290 |     | 295 |     | 300 |
| Val | Gly | Ile | Leu | His | Tyr |
|     | 305 |     | 310 |     | 315 |
| Leu | Pro | Val | Ser | Ala | Thr |
|     | 325 |     | 330 |     | 335 |
| Gln | Pro | Arg | Ala | Ile | Lys |
|     | 340 |     | 345 |     | 350 |
| Asn | Pro | Gln | Gly | Ser | Phe |
|     | 355 |     | 360 |     | 365 |
| Tyr | Ile | Leu | Arg | Ser | Leu |
|     | 370 |     | 375 |     | 380 |
| Ala | Thr | Leu | Asn | Gly | Ile |
|     | 385 |     | 390 |     | 395 |
| Leu | Pro | Asp | Asp | His | Lys |
|     | 405 |     | 410 |     | 415 |
| Asp | Arg | Pro | Leu | Asp | Glu |
|     | 420 |     | 425 |     | 430 |
| Asn | Ala | Thr | Tyr | Lys | Gly |
|     | 435 |     | 440 |     | 445 |
| Thr | Lys | Ile | Gln | Ser | Phe |
|     | 450 |     | 455 |     | 460 |
| Ala | Met | Asp | Phe | Gly | Ile |
|     | 465 |     | 470 |     | 475 |
| Asn | Trp | Asp | Ala | Val | Ala |
|     | 485 |     | 490 |     | 495 |
| Trp | Thr | Ala | Val | Leu | Ile |
|     | 500 |     | 505 |     | 510 |
| Pro | Gly |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2480:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..426  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2480:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Arg | Asn | Ser | Trp | Gln | Asp | Gly | Val | Leu | Gly | Thr | Asn | Cys | Pro |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Pro | Pro | Asn | Trp | Asn | Phe | Thr | Tyr | Asp | Phe | Gln | Leu | Lys | Asp | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Gly | Ser | Tyr | Phe | Tyr | Ser | Pro | Ser | Leu | Asn | Phe | Gln | Arg | Ala | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Gly | Phe | Gly | Ala | Leu | Ile | Ile | Asn | Asn | Arg | Asp | Leu | Val | Pro | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Pro | Phe | Thr | Glu | Pro | Asp | Gly | Glu | Ile | Ile | Phe | Ile | Ile | Gly | Asp | Trp |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Tyr | Thr | Gln | Asn | His | Thr | Ala | Leu | Arg | Arg | Ile | Leu | Asp | Ser | Gly | Lys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Leu | Gly | Met | Pro | Asp | Gly | Val | Leu | Ile | Asn | Gly | Lys | Gly | Pro | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Tyr | Asn | Ser | Ser | Val | Pro | Asp | Gly | Ile | Glu | His | Glu | Thr | Val | Asn |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Val | Asp | Pro | Gly | Lys | Thr | Tyr | Arg | Ile | Arg | Val | His | Asn | Val | Gly | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Ser | Thr | Ser | Leu | Asn | Phe | Arg | Ile | Gln | Asn | His | Lys | Leu | Leu | Ile |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Thr | Glu | Gly | Arg | Tyr | Thr | Ser | Gln | Met | Asn | Phe | Thr | Asp | Phe | Asp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | His | Val | Gly | Gln | Ser | Tyr | Ser | Phe | Leu | Val | Thr | Met | Asp | Gln | Asn |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Thr | Ser | Asp | Tyr | Tyr | Ile | Val | Ala | Ser | Ala | Arg | Phe | Val | Asn | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Val | Trp | Gln | Arg | Val | Thr | Gly | Val | Gly | Ile | Leu | His | Tyr | Ser | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Ser | Lys | Gly | Pro | Ala | Ser | Gly | Pro | Leu | Pro | Val | Ser | Ala | Thr | Asp | Val |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Asn | His | Pro | Trp | Ser | Ala | Met | Asn | Gln | Pro | Arg | Ala | Ile | Lys | Gln | Asn |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Ser | Ala | Ser | Gly | Ala | Arg | Pro | Asn | Pro | Gln | Gly | Ser | Phe | His | Tyr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Gln | Ile | Asn | Ile | Thr | Arg | Thr | Tyr | Ile | Leu | Arg | Ser | Leu | Pro | Pro |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Thr | Lys | Ile | Asn | Gly | Lys | Leu | Arg | Ala | Thr | Leu | Asn | Gly | Ile | Ser | Phe |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Val | Asn | Pro | Ser | Thr | Pro | Met | Arg | Leu | Pro | Asp | Asp | His | Lys | Val | Lys |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Gly | Asp | Tyr | Met | Leu | Asp | Phe | Pro | Asp | Arg | Pro | Leu | Asp | Glu | Lys | Leu |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Pro | Arg | Leu | Ser | Ser | Ser | Ile | Ile | Asn | Ala | Thr | Tyr | Lys | Gly | Phe | Ile |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gln | Val | Ile | Phe | Gln | Asn | Asn | Asp | Thr | Lys | Ile | Gln | Ser | Phe | His | Ile |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Asp | Gly | Tyr | Ala | Phe | Tyr | Val | Val | Ala | Met | Asp | Phe | Gly | Ile | Trp | Ser |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Glu | Asp | Arg | Asn | Gly | Ser | Tyr | Asn | Asn | Trp | Asp | Ala | Val | Ala | Arg | Ser |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Thr | Val | Glu | Val | Tyr | Pro | Gly | Ala | Trp | Thr | Ala | Val | Leu | Ile | Ser | Leu |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Asp | Glu | Cys | Trp | Ser | Leu | Glu | Tyr | Pro | Gly |     |     |     |     |     |     |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2481:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 amino acids

SEQUENCE LISTING

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..327  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572977  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2481:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Asp | Gly | Val | Leu | Ile | Asn | Gly | Lys | Gly | Pro | Phe | Lys | Tyr | Asn |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Ser | Val | Pro | Asp | Gly | Ile | Glu | His | Glu | Thr | Val | Asn | Val | Asp | Pro |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gly | Lys | Thr | Tyr | Arg | Ile | Arg | Val | His | Asn | Val | Gly | Ile | Ser | Thr | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Leu | Asn | Phe | Arg | Ile | Gln | Asn | His | Lys | Leu | Leu | Ile | Glu | Thr | Glu |     |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Gly | Arg | Tyr | Thr | Ser | Gln | Met | Asn | Phe | Thr | Asp | Phe | Asp | Ile | His | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Gln | Ser | Tyr | Ser | Phe | Leu | Val | Thr | Met | Asp | Gln | Asn | Ala | Thr | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asp | Tyr | Tyr | Ile | Val | Ala | Ser | Ala | Arg | Phe | Val | Asn | Glu | Thr | Val | Trp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Arg | Val | Thr | Gly | Val | Gly | Ile | Leu | His | Tyr | Ser | Asn | Ser | Lys | Gly |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Pro | Ala | Ser | Gly | Pro | Leu | Pro | Val | Ser | Ala | Thr | Asp | Val | Asn | His | Pro |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Trp | Ser | Ala | Met | Asn | Gln | Pro | Arg | Ala | Ile | Lys | Gln | Asn | Thr | Ser | Ala |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Gly | Ala | Arg | Pro | Asn | Pro | Gln | Gly | Ser | Phe | His | Tyr | Gly | Gln | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Asn | Ile | Thr | Arg | Thr | Tyr | Ile | Leu | Arg | Ser | Leu | Pro | Pro | Thr | Lys | Ile |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asn | Gly | Lys | Leu | Arg | Ala | Thr | Leu | Asn | Gly | Ile | Ser | Phe | Val | Asn | Pro |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Thr | Pro | Met | Arg | Leu | Pro | Asp | Asp | His | Lys | Val | Lys | Gly | Asp | Tyr |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Met | Leu | Asp | Phe | Pro | Asp | Arg | Pro | Leu | Asp | Gly | Lys | Leu | Pro | Arg | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Ser | Ser | Ser | Ile | Ile | Asn | Ala | Thr | Tyr | Lys | Gly | Phe | Ile | Gln | Val | Ile |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Phe | Gln | Asn | Asn | Asp | Thr | Lys | Ile | Gln | Ser | Phe | His | Ile | Asp | Gly | Tyr |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ala | Phe | Tyr | Val | Val | Ala | Met | Asp | Phe | Gly | Ile | Trp | Ser | Glu | Asp | Arg |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asn | Gly | Ser | Tyr | Asn | Asn | Trp | Asp | Ala | Val | Ala | Arg | Ser | Thr | Val | Glu |
|     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| Val | Tyr | Pro | Gly | Ala | Trp | Thr | Ala | Val | Leu | Ile | Ser | Leu | Asp | Glu | Cys |
|     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |     |
| Trp | Ser | Leu | Glu | Tyr | Pro | Gly |     |     |     |     |     |     |     |     |     |
|     |     |     | 325 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2482:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 737 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..737

(D) OTHER INFORMATION: / Ceres Seq. ID 1573108  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2482:

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| agaaaaatcg | caagtgtgaat | gaccttcttg  | atgcgttgga | cttcaatcaa | gttgtcattt | 60  |
| ttgtgaagag | cgtagCagg   | gctgcgggaGc | tgaacaagtt | actggtggaa | tgcaatttcc | 120 |
| cctcaatatg | catacactct  | ggcatgtctc  | aagaagagag | gttgactcga | tacaaaagtt | 180 |
| tcaaggaagg | gcacaagagg  | atccttgtgg  | cgactgactt | ggtaggaaga | gggattgaca | 240 |
| tagagcgtgt | caacatttgt  | atcaactatg  | acatgccaga | ttctgcggat | acctatcttc | 300 |
| atagggttgg | gagagctgg   | agatttgga   | ccaagggctc | tgcaatcaca | tttgttgc   | 360 |
| ctgcttcaga | ttcagaggtc  | cttaaatcagg | ttcaagagag | gtttgaggtc | gatataaagg | 420 |
| agcttccatg | gcagattgat  | acatcgactt  | acatgccgtc | ttaacaagt  | agcatcatct | 480 |
| ctgaggaacg | aaacctcttca | gatttcaacc  | ttttagggtg | tcaaaagggg | catggaggtc | 540 |
| cacaactatc | tctcacacgc  | tttgtgtgctt | cgtattttta | gacttttctc | tgaggacaag | 600 |
| tttttccata | tatttagacc  | gttttgtaac  | tcttgaaaaa | tgagattgag | ctactctcca | 660 |
| aatcgcgcac | agttgagagc  | tctcctgttt  | ttgtactag  | tgatggttat | ctttaaaaa  | 720 |
| taaagatttc | aggatct     |             |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1573109  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2483:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Lys | Asn | Arg | Lys | Leu | Asn | Asp | Leu | Leu | Asp | Ala | Leu | Asp | Phe | Asn | Gln |  |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |  |
| Val | Val | Ile | Phe | Val | Lys | Ser | Val | Ser | Arg | Ala | Ala | Glu | Leu | Asn | Lys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |
| Leu | Leu | Val | Glu | Cys | Asn | Phe | Pro | Ser | Ile | Cys | Ile | His | Ser | Gly | Met |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Ser | Gln | Glu | Glu | Arg | Leu | Thr | Arg | Tyr | Lys | Ser | Phe | Lys | Glu | Gly | His |  |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |
| Lys | Arg | Ile | Leu | Val | Ala | Thr | Asp | Leu | Val | Gly | Arg | Gly | Ile | Asp | Ile |  |
|     | 65  |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Glu | Arg | Val | Asn | Ile | Val | Ile | Asn | Tyr | Asp | Met | Pro | Asp | Ser | Ala | Asp |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Thr | Tyr | Leu | His | Arg | Val | Gly | Arg | Ala | Gly | Arg | Phe | Gly | Thr | Lys | Gly |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| Leu | Ala | Ile | Thr | Phe | Val | Ala | Ser | Ala | Ser | Asp | Ser | Glu | Val | Leu | Asn |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Gln | Val | Gln | Glu | Arg | Phe | Glu | Val | Asp | Ile | Lys | Glu | Leu | Pro | Glu | Gln |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ile | Asp | Thr | Ser | Thr | Tyr | Met | Pro | Ser |     |     |     |     |     |     |     |  |
|     | 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..106  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2484:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Gln | Glu | Glu | Arg | Leu | Thr | Arg | Tyr | Lys | Ser | Phe | Lys | Glu | Gly |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |  |

His Lys Arg Ile Leu Val Ala Thr Asp Leu Val Gly Arg Gly Ile Asp  
20 25 30  
Ile Glu Arg Val Asn Ile Val Ile Asn Tyr Asp Met Pro Asp Ser Ala  
35 40 45  
Asp Thr Tyr Leu His Arg Val Gly Arg Ala Gly Arg Phe Gly Thr Lys  
50 55 60  
Gly Leu Ala Ile Thr Phe Val Ala Ser Ala Ser Asp Ser Glu Val Leu  
65 70 75 80  
Asn Gln Val Gln Glu Arg Phe Glu Val Asp Ile Lys Glu Leu Pro Glu  
85 90 95  
Gln Ile Asp Thr Ser Thr Tyr Met Pro Ser  
100 105

(2) INFORMATION FOR SEQ ID NO:2485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2412
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2485:

|             |             |             |            |            |             |      |
|-------------|-------------|-------------|------------|------------|-------------|------|
| atgcaatatt  | acggagctcc  | acaagtgatg  | cttggtact  | taaaatacca | atggtcactt  | 60   |
| ggagaggaac  | gtaagcgcaa  | agaggcattt  | accaagctgc | agattctaac | gagagagctc  | 120  |
| ccaagtgtgc  | cacattctca  | atctgacata  | ctggctagca | tgttatctag | caagggcgca  | 180  |
| aatgttccac  | ttcttgcaag  | tgtaaatctc  | aaactgggaa | cgctggcagt | ggcactttct  | 240  |
| tcgggtttga  | atgatgggtc  | tattcaagaa  | attcgtgatg | cgcttgacaa | atctactctg  | 300  |
| tatgtctcta  | aatgggctaa  | agcatggcac  | acatgggcac | tattcaatca | acgagtgtat  | 360  |
| tcgcattaca  | tttcaagagg  | tcaaatgtct  | tcccagtagc | ttgtttctgc | agtcactgga  | 420  |
| tatttttatt  | ctatagcatg  | tgccagcaaat | gccaaaggag | ttgatgatag | tttacaggac  | 480  |
| atactgctgc  | ttctgacatt  | gtggttcaac  | catggagcta | cagctgatgt | ccaaaccgca  | 540  |
| ttgaagacag  | gattcagcta  | tgtaacacatt | aacacatggc | ttgttctgct | acctcaaatc  | 600  |
| attgctagga  | tacattctaa  | taatcgtgct  | gtcagggaac | tgattcagtc | tccttctcatc | 660  |
| cgcataaggcg | aaaaccaccc  | acaggctctg  | atgtatcccc | ttctcgttgc | cttgaataatc | 720  |
| ataagcaaatc | ttcggagagc  | tgccggctcaa | gaggtgggtg | ataaaagtgc | ccagcacagt  | 780  |
| gggtcactcg  | tggatcaggc  | gcaacttgta  | tcacatgaac | ttatcagggt | tgccatactt  | 840  |
| tgccatgaaa  | tgtggcatga  | agcactagaa  | gaagctagtc | gcttgatttt | tggtgaacat  | 900  |
| aaacttgaa   | gcattgcgaa  | agtacttgaa  | cccttacatg | acatgctgca | cgaaaggtgta | 960  |
| aaaaaggaca  | gtacgcgatac | acaggaagaa  | gcatttatag | agggcatccg | tacagaaacta | 1020 |
| aaagaggccac | atgaatctgt  | ttgcaattac  | aagataactg | ggaagagatg | tgaacttata  | 1080 |
| cagggttcg   | atcttttacta | tcaactgttc  | aaacggattg | acaaacagct | agccactctc  | 1140 |
| acgacattgg  | atttggaaatc | tggtttctct  | gagttgctgc | tggtgcctga | cttgagagta  | 1200 |
| gcagttccgt  | gaacatattg  | tgccagatgc  | cccgctgtga | ctatatctac | tttttcaagc  | 1260 |
| caacttggtg  | ttataaccttc | taaacaaaga  | ccaaggaat  | tgactattca | cggaatgatc  | 1320 |
| ggtaggagact | acgcctttgtt | gttgaaggga  | catgaagatt | taaggcaaga | tgagcgtggt  | 1380 |
| atgcagcttt  | ttggttttgc  | gaacaacttg  | cttgagaatt | ccagaaaaac | agccgaaaaa  | 1440 |
| gattctttcca | ttcaacgcga  | ttctgttaat  | ccactatctc | ccaatagtgg | actcatcgga  | 1500 |
| tggtttccga  | actgcgatac  | ccctcaccat  | cttattcgag | agcraagaga | tgaagaaag   | 1560 |
| atcattctta  | atcaagaaaa  | taagcatatg  | ttgagtttgc | ctccagacta | tgaacttata  | 1620 |
| ccgctttatg  | caaaggttga  | agttatttgc  | tatgctctag | aaaaacacga | gggaatgatg  | 1680 |
| ctatcccaag  | ttctctggtt  | aaaaagtcgc  | tcgtcagaag | tttgctctga | aagaagaaca  | 1740 |
| aactatacta  | gaagtttagc  | agttatgagt  | atggttgggt | atattctgtg | gttaggtgat  | 1800 |
| cgacacccaa  | gtaaccttat  | gcttcataga  | tacagaatgc | ttgtcaaaag | aatggaagtc  | 1860 |
| agtggtcatt  | aaggaaactt  | ccgctcaacc  | tgcgaaaaag | ttatgcaagt | tctcaagacc  | 1920 |
| aataaagata  | gtgtaatggc  | aatgatggaa  | gcgtttgtac | atgatccttt | aatcaattgg  | 1980 |
| cgctctttcca | atttcaatga  | agtcctccaa  | ttagcactgc | tcggtataac | caactcttct  | 2040 |
| gctcctctgc  | atgttgtagc  | tgacgaagaa  | gatgaagatc | ccgctgatat | agactcttct  | 2100 |
| cagcctcaaa  | ggagtactcg  | agagaaggag  | attcttcagg | ctgtaaatat | gcttgagagt  | 2160 |
| gctaattga   | tttaaatga   | gcgtgcgcga  | gttggtatgc | cagctatgag | tcaataagct  | 2220 |

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acaggcgctg attttttctt gctcgcaatt ccgagcaatc ccattgctga tcataataac 2280  
ttgctcgag gagattctca tgaagtcgaa catggtttgt ctgtgaaagt tcagggttcaa 2340  
aaactaatca atcaagccac ttcccatgag aatctctgtc aaaactatgt tgggtggtgc 2400  
cctttctggt ga

(2) INFORMATION FOR SEQ ID NO:2486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..803
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1573152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2486:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Tyr | His | Gly | Pro | Pro | Gln | Val | Met | Leu | Gly | Tyr | Leu | Lys | Tyr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gln | Trp | Ser | Leu | Gly | Glu | Glu | Arg | Lys | Arg | Lys | Glu | Ala | Phe | Thr | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Gln | Ile | Leu | Thr | Arg | Glu | Leu | Ser | Ser | Val | Pro | His | Ser | Gln | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ile | Leu | Ala | Ser | Met | Val | Ser | Ser | Lys | Gly | Ala | Asn | Val | Pro | Leu |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Leu | Ala | Arg | Val | Asn | Leu | Lys | Leu | Gly | Thr | Trp | Gln | Trp | Ala | Leu | Ser |
|     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Gly | Leu | Asn | Asp | Gly | Ser | Ile | Gln | Glu | Ile | Arg | Asp | Ala | Phe | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Ser | Thr | Cys | Tyr | Ala | Pro | Lys | Trp | Ala | Lys | Ala | Trp | His | Thr | Trp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Leu | Phe | Asn | Thr | Ala | Val | Met | Ser | His | Tyr | Ile | Ser | Arg | Gly | Gln |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ile | Ala | Ser | Gln | Tyr | Val | Val | Ser | Ala | Val | Thr | Gly | Tyr | Phe | Tyr | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Ala | Cys | Ala | Ala | Asn | Ala | Lys | Gly | Val | Asp | Asp | Ser | Leu | Gln | Asp |
|     | 145 |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Ile | Leu | Arg | Leu | Leu | Thr | Leu | Trp | Phe | Asn | His | Gly | Ala | Thr | Ala | Asp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Val | Gln | Thr | Ala | Leu | Lys | Thr | Gly | Phe | Ser | His | Val | Asn | Ile | Asn | Thr |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Trp | Leu | Val | Val | Leu | Pro | Gln | Ile | Ile | Ala | Arg | Ile | His | Ser | Asn | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Ala | Val | Arg | Glu | Leu | Ile | Gln | Ser | Leu | Leu | Ile | Arg | Ile | Gly | Glu |
|     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Asn | His | Pro | Gln | Ala | Leu | Met | Tyr | Pro | Leu | Leu | Val | Ala | Cys | Lys | Ser |
|     | 225 |     |     | 230 |     |     |     |     |     |     | 235 |     |     | 240 |     |
| Ile | Ser | Asn | Leu | Arg | Arg | Ala | Ala | Ala | Gln | Glu | Val | Val | Asp | Lys | Val |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Arg | Gln | His | Ser | Gly | Ala | Leu | Val | Asp | Gln | Ala | Gln | Leu | Val | Ser | His |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Glu | Leu | Ile | Arg | Val | Ala | Ile | Leu | Trp | His | Glu | Met | Trp | His | Glu | Ala |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Glu | Glu | Ala | Ser | Arg | Leu | Tyr | Phe | Gly | Glu | His | Asn | Ile | Glu | Gly |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Met | Leu | Lys | Val | Leu | Glu | Pro | Leu | His | Asp | Met | Leu | Asp | Glu | Gly | Val |
|     | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Lys | Lys | Asp | Ser | Thr | Thr | Ile | Gln | Glu | Arg | Ala | Phe | Ile | Glu | Ala | Tyr |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Arg | His | Glu | Leu | Lys | Glu | Ala | His | Glu | Cys | Cys | Asn | Tyr | Lys | Ile |     |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     | 350 |     |     |     |
| Thr | Gly | Lys | Asp | Ala | Glu | Leu | Thr | Gln | Ala | Trp | Asp | Leu | Tyr | Tyr | His |

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 794 amino acids  
 (B) TYPE: amino acid

| (X1) SEQUENCE DESCRIPTION: SEQ ID: 1 |     |     |     |     |     |     |     |     |     |       |     |     |     |     |     |  |
|--------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-------|-----|-----|-----|-----|-----|--|
| Met                                  | Leu | Gly | Tyr | Leu | Lys | Tyr | Gln | Trp | Ser | Leu   | Gly | Glu | Glu | Arg | Lys |  |
| 1                                    |     |     |     | 5   |     |     |     |     | 10  |       |     |     |     | 15  |     |  |
| Arg                                  | Lys | Glu | Ala | Phe | Thr | Lys | Leu | Gln | Ile | Leu   | Thr | Arg | Glu | Leu | Ser |  |
|                                      |     |     | 20  |     |     |     |     | 25  |     |       |     |     | 30  |     |     |  |
| Ser                                  | Val | Pro | His | Ser | Gln | Ser | Asp | Ile | Leu | Ala   | Ser | Met | Val | Ser | Ser |  |
|                                      |     | 35  |     |     |     |     | 40  |     |     |       |     | 45  |     |     |     |  |
| Lys                                  | Gly | Ala | Asn | Val | Pro | Leu | Leu | Ala | Arg | Val   | Asn | Leu | Lys | Leu | Gly |  |
|                                      | 50  |     |     |     |     | 55  |     |     |     |       | 60  |     |     |     |     |  |
| Thr                                  | Trp | Gln | Trp | Ala | Leu | Ser | Ser | Gly | Leu | Asn   | Asp | Gly | Ser | Ile | Gln |  |
| 65                                   |     |     |     | 70  |     |     |     |     |     | 75    |     |     |     |     | 80  |  |
| Glu                                  | Ile | Arg | Asp | Ala | Phe | Asp | Lys | Ser | Thr | Cys   | Tyr | Ala | Pro | Lys | Trp |  |
|                                      |     |     |     | 85  |     |     |     |     | 90  |       |     |     |     | 95  |     |  |
| Ala                                  | Lys | Ala | Trp | His | Thr | Trp | Ala | Leu | Phe | Asn   | Thr | Ala | Val | Met | Ser |  |
|                                      |     |     |     | 100 |     |     |     | 105 |     |       |     |     | 110 |     |     |  |
| His                                  | Tyr | Ile | Ser | Arg | Gly | Gln | Ile | Ala | Ser | Gln   | Tyr | Val | Val | Ser | Ala |  |
|                                      | 115 |     |     |     |     | 120 |     |     |     |       |     | 125 |     |     |     |  |
| Val                                  | Thr | Gly | Tyr | Phe | Tyr | Ser | Ile | Ala | Cys | Ala   | Ala | Asn | Ala | Lys | Gly |  |
|                                      | 130 |     |     |     |     | 135 |     |     |     |       | 140 |     |     |     |     |  |
| Val                                  | Asp | Asp | Ser | Leu | Gln | Asp | Ile | Leu | Arg | Leu   | Leu | Thr | Leu | Trp | Phe |  |
| 145                                  |     |     |     | 150 |     |     |     |     |     | 155   |     |     |     |     | 160 |  |
| Asn                                  | His | Gly | Ala | Thr | Ala | Asp | Val | Gln | Thr | Ala   | Leu | Lys | Thr | Gly | Phe |  |
|                                      |     |     |     | 165 |     |     |     |     | 170 |       |     |     |     | 175 |     |  |
| Ser                                  | His | Val | Asn | Ile | Asn | Thr | Trp | Leu | Val | Val   | Leu | Pro | Gln | Ile | Ile |  |
|                                      |     |     | 180 |     |     |     |     | 185 |     |       |     |     | 190 |     |     |  |
| Ala                                  | Arg | Ile | His | Ser | Asn | Asn | Arg | Ala | Val | Arg   | Glu | Leu | Ile | Gln | Ser |  |
|                                      | 195 |     |     |     |     | 200 |     |     |     |       | 205 |     |     |     |     |  |
| Leu                                  | Leu | Ile | Arg | Ile | Gly | Glu | Asn | His | Pro | Gln   | Ala | Leu | Met | Tyr | Pro |  |
|                                      | 210 |     |     |     |     | 215 |     |     |     |       | 220 |     |     |     |     |  |
| Leu                                  | Leu | Val | Ala | Cys | Lys | Ser | Ile | Ser | Asn | Leu   | Arg | Arg | Ala | Ala | Ala |  |
| 225                                  |     |     |     | 230 |     |     |     |     |     | 235   |     |     |     | 240 |     |  |
| Gln                                  | Glu | Val | Val | Asp | Lys | Val | Arg | Gln | His | Ser   | Gly | Ala | Leu | Val | Asp |  |
|                                      |     |     |     | 245 |     |     |     |     | 250 |       |     |     |     | 255 |     |  |
| Gln                                  | Ala | Gln | Leu | Val | Ser | His | Glu | Leu | Ile | Arg   | Val | Ala | Ile | Leu | Trp |  |
|                                      |     |     | 260 |     |     |     |     | 265 |     |       |     |     |     | 270 |     |  |
| His                                  | Glu | Met | Trp | His | Glu | Ala | Leu | Glu | Glu | Ala   | Ser | Arg | Leu | Tyr | Phe |  |
|                                      | 275 |     |     |     |     |     | 280 |     |     |       |     | 285 |     |     |     |  |
| Gly                                  | Glu | His | Asn | Ile | Glu | Gly | Met | Leu | Lys | Val   | Leu | Glu | Pro | Leu | His |  |
|                                      | 290 |     |     |     |     | 295 |     |     |     |       | 300 |     |     |     |     |  |
| Asp                                  | Met | Leu | Asp | Glu | Gly | Val | Lys | Lys | Asp | Ser   | Thr | Thr | Ile | Gln | Glu |  |
| 305                                  |     |     |     | 310 |     |     |     |     |     | 315   |     |     |     |     | 320 |  |
| Arg                                  | Ala | Phe | Ile | Glu | Ala | Tyr | Arg | His | Glu | Leu</ |     |     |     |     |     |  |



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420 425 430
Glu Asp Tyr Ala Phe Leu Leu Lys Gly His Glu Asp Leu Arg Gln Asp
435 440 445
Glu Arg Val Met Gln Leu Phe Gly Leu Val Asn Thr Leu Leu Glu Asn
450 455 460
Ser Arg Lys Thr Ala Glu Lys Asp Leu Ser Ile Gln Arg Tyr Ser Val
465 470 475
Ile Pro Leu Ser Pro Asn Ser Gly Leu Ile Gly Trp Val Pro Asn Cys
485 490 495
Asp Thr Leu His His Leu Ile Arg Glu Xaa Arg Asp Ala Arg Lys Ile
500 505 510
Ile Leu Asn Gln Glu Asn Lys His Met Leu Ser Phe Ala Pro Asp Tyr
515 520 525
Asp Asn Leu Pro Leu Ile Ala Lys Val Glu Val Phe Glu Tyr Ala Leu
530 535 540
Glu Asn Thr Glu Gly Asn Asp Leu Ser Arg Val Leu Trp Leu Lys Ser
545 550 555
Arg Ser Ser Glu Val Trp Leu Glu Arg Arg Thr Asn Tyr Thr Arg Ser
565 570 575
Leu Ala Val Met Ser Met Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg
580 585 590
His Pro Ser Asn Leu Met Leu His Arg Tyr Arg Met Leu Val Lys Ala
595 600 605
Met Glu Val Ser Gly Ile Glu Gly Asn Phe Arg Ser Thr Cys Glu Asn
610 615 620
Val Met Gln Val Leu Arg Thr Asn Lys Asp Ser Val Met Ala Met Met
625 630 635
Glu Ala Phe Val His Asp Pro Leu Ile Asn Trp Arg Leu Phe Asn Phe
645 650 655
Asn Glu Val Pro Gln Leu Ala Leu Leu Gly Asn Asn Asn Pro Asn Ala
660 665 670
Pro Ala Asp Val Glu Pro Asp Glu Glu Asp Glu Asp Pro Ala Asp Ile
675 680 685
Asp Leu Pro Gln Pro Gln Arg Ser Thr Arg Glu Lys Glu Ile Leu Gln
690 695 700
Ala Val Asn Met Leu Gly Asp Ala Asn Glu Val Leu Asn Glu Arg Ala
705 710 715
Val Val Val Met Ala Arg Met Ser His Lys Leu Thr Gly Arg Asp Phe
725 730 735
Ser Ser Ser Ala Ile Pro Ser Asn Pro Ile Ala Asp His Asn Asn Leu
740 745 750
Leu Gly Gly Asp Ser His Glu Val Glu His Gly Leu Ser Val Lys Val
755 760 765
Gln Val Gln Lys Leu Ile Asn Gln Ala Thr Ser His Glu Asn Leu Cys
770 775 780
Gln Asn Tyr Val Gly Trp Cys Pro Phe Trp
785 790

```

(2) INFORMATION FOR SEQ ID NO:2488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..837

(D) OTHER INFORMATION: / Ceres Seq. ID 1573308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2488:

```

atggcggaag aagcaaaatc caaaggaaac gcagctttct cttccggcga ttacgccacc 60
gcaataaacc atttcacaga agcaatcaac ctttcatcaa ccaatcacat cctctactca 120

```

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| aacagatccg | cttcttaccg | tctctccac  | cgttacgaag | aagctttatc  | agacgcgaag  | 180 |
| aagactatag | agcttaaac  | tgatttgtct | aaaggatata | gccgattagg  | tgctgcgttt  | 240 |
| attggattgt | ccaagtttga | tgaagcgggt | gattcgtata | agaaaaggatt | agagattgat  | 300 |
| ccgagtaagt | agatgcttaa | atcgggatta | gctgatgctt | cgagatctag  | ggtttcgtca  | 360 |
| aagtcgaatc | cttttgttga | tgcttttcaa | gggaaggaga | tgtggggagaa | gttgacggcg  | 420 |
| gacccgggga | ctaggggtta | tttggagcag | gatgatattg | ttaagacgat  | gaaggagatt  | 480 |
| cagaggaacc | ctaataatct | taatttgtat | atgaaggata | agagagttat  | gaaggcttta  | 540 |
| ggggttttgt | tgaatgtgaa | gtttggtgga | tctagtgtgt | aagatactga  | gatgaaggag  | 600 |
| gctgatgaga | ggaaagagcc | tgaaccggag | atggaacctc | tggagtgtac  | ggagggaggag | 660 |
| aggcagaaga | aggagagaaa | ggagaaggct | ttgaaggaga | aaggggaagg  | aaatgttgct  | 720 |
| tataagaaga | aggattttga | gagagctgtt | gaacattata | ctaaggccat  | ggagctcgat  | 780 |
| gatgcagata | tttcttattt | gacgaatcgt | gtgctgtttt | atcttgagat  | gggggaag    |     |

(2) INFORMATION FOR SEQ ID NO:2489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..279
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2489:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Glu | Ala | Lys | Ser | Lys | Gly | Asn | Ala | Ala | Phe | Ser | Ser | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asp | Tyr | Ala | Thr | Ala | Ile | Thr | His | Phe | Thr | Glu | Ala | Ile | Asn | Leu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Thr | Asn | His | Ile | Leu | Tyr | Ser | Asn | Arg | Ser | Ala | Ser | Tyr | Ala | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | His | Arg | Tyr | Glu | Glu | Ala | Leu | Ser | Asp | Ala | Lys | Lys | Thr | Ile | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Lys | Pro | Asp | Trp | Ser | Lys | Gly | Tyr | Ser | Arg | Leu | Gly | Ala | Ala | Phe |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     |     | 80  |
| Ile | Gly | Leu | Ser | Lys | Phe | Asp | Glu | Ala | Val | Asp | Ser | Tyr | Lys | Lys | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Glu | Ile | Asp | Pro | Ser | Asn | Glu | Met | Leu | Lys | Ser | Gly | Leu | Ala | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Ser | Arg | Ser | Arg | Val | Ser | Ser | Lys | Ser | Asn | Pro | Phe | Val | Asp | Ala |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Phe | Gln | Gly | Lys | Glu | Met | Trp | Glu | Lys | Leu | Thr | Ala | Asp | Pro | Gly | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Val | Tyr | Leu | Glu | Gln | Asp | Asp | Phe | Val | Lys | Thr | Met | Lys | Glu | Ile |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     |     | 160 |
| Gln | Arg | Asn | Pro | Asn | Asn | Leu | Asn | Leu | Tyr | Met | Lys | Asp | Lys | Arg | Val |
|     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Met | Lys | Ala | Leu | Gly | Val | Leu | Leu | Asn | Val | Lys | Phe | Gly | Gly | Ser | Ser |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Glu | Asp | Thr | Glu | Met | Lys | Glu | Ala | Asp | Glu | Arg | Lys | Glu | Pro | Glu |
|     |     | 195 |     |     |     |     |     | 200 |     |     |     | 205 |     |     |     |
| Pro | Glu | Met | Glu | Pro | Met | Glu | Leu | Thr | Glu | Glu | Glu | Arg | Gln | Lys | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Glu | Arg | Lys | Glu | Lys | Ala | Leu | Lys | Glu | Lys | Gly | Glu | Gly | Asn | Val | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |
| Tyr | Lys | Lys | Lys | Asp | Phe | Glu | Arg | Ala | Val | Glu | His | Tyr | Thr | Lys | Ala |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Met | Glu | Leu | Asp | Asp | Glu | Asp | Ile | Ser | Tyr | Leu | Thr | Asn | Arg | Ala | Ala |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Tyr | Leu | Glu | Met | Gly | Lys |     |     |     |     |     |     |     |     |     |
|     |     | 275 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2490:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 175 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..175  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1573311  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2490:  
Met Leu Lys Ser Gly Leu Ala Asp Ala Ser Arg Ser Arg Val Ser Ser  
1                  5                  10                  15  
Lys Ser Asn Pro Phe Val Asp Ala Phe Gln Gly Lys Glu Met Trp Glu  
                  20                  25                  30  
Lys Leu Thr Ala Asp Pro Gly Thr Arg Val Tyr Leu Glu Gln Asp Asp  
                  35                  40                  45  
Phe Val Lys Thr Met Lys Glu Ile Gln Arg Asn Pro Asn Asn Leu Asn  
50                  55                  60  
Leu Tyr Met Lys Asp Lys Arg Val Met Lys Ala Leu Gly Val Leu Leu  
65                  70                  75                  80  
Asn Val Lys Phe Gly Gly Ser Ser Gly Glu Asp Thr Glu Met Lys Glu  
                  85                  90                  95  
Ala Asp Glu Arg Lys Glu Pro Glu Pro Glu Met Glu Pro Met Glu Leu  
                  100                  105                  110  
Thr Glu Glu Glu Arg Gln Lys Lys Glu Arg Lys Glu Lys Ala Leu Lys  
                  115                  120                  125  
Glu Lys Gly Glu Gly Asn Val Ala Tyr Lys Lys Lys Asp Phe Glu Arg  
130                  135                  140  
Ala Val Glu His Tyr Thr Lys Ala Met Glu Leu Asp Asp Glu Asp Ile  
145                  150                  155                  160  
Ser Tyr Leu Thr Asn Arg Ala Ala Val Tyr Leu Glu Met Gly Lys  
                  165                  170                  175  
(2) INFORMATION FOR SEQ ID NO:2491:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 137 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..137  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1573315  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2491:  
acttacacca cgacaaaaag ggaatgtgtt cacgtgtgtc ttgctttttt tgatcgctat          60  
cggattcgct cgagttatcg ttatgtctg ctttgcatca gcacgagaaa cacgtgaaaa          120  
acggcgtgaa gaacaac  
(2) INFORMATION FOR SEQ ID NO:2492:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 38 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..38  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1573316  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2492:  
Thr Tyr Thr Thr Lys Arg Glu Cys Val His Val Cys Leu Arg Phe

1 5 10 15  
Phe Asp Arg Tyr Arg Ile Arg Cys Ser Tyr Arg Leu Cys Leu Leu Cys  
20 25 30  
Ile Ser Thr Arg Asn Thr  
35

(2) INFORMATION FOR SEQ ID NO:2493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2493:

Leu Thr Pro Arg Gln Lys Gly Asn Val Phe Thr Cys Val Phe Val Phe  
1 5 10 15  
Leu Ile Ala Ile Gly Phe Ala Ala Val Ile Val Tyr Val Cys Phe Ala  
20 25 30  
Ser Ala Arg Glu Thr Arg Glu Lys Arg Arg Glu Glu Gln  
35 40 45

(2) INFORMATION FOR SEQ ID NO:2494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2494:

atggaaaaaa acttgaagaa gattcaggct aaggaagagg agctctctat gatgagaagt 60  
gaatttggtg ctgccgtgac gaatgtgtg tcaagcaaga caacgcattct tattcct

(2) INFORMATION FOR SEQ ID NO:2495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2495:

Met Glu Lys Asn Leu Lys Lys Ile Gln Ala Lys Glu Glu Leu Ser  
1 5 10 15  
Met Met Arg Ser Glu Phe Val Ala Ala Val Thr Asn Val Leu Ser Ser  
20 25 30  
Lys Thr Thr His Leu Ile Pro  
35

(2) INFORMATION FOR SEQ ID NO:2496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..114  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1573401  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2496:  
atggatgaag aaggtcacat tatacacatt gatttcggct ttatgctttc aaattctcct 60  
ggtagcgtag actttgagag tgccccattt aagctaactc gggaactctt tgag  
(2) INFORMATION FOR SEQ ID NO:2497:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 38 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..38  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1573402  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2497:  
Met Asp Glu Gly His Ile Ile His Ile Asp Phe Gly Phe Met Leu  
1                  5                  10                  15  
Ser Asn Ser Pro Gly Gly Val Asn Phe Glu Ser Ala Pro Phe Lys Leu  
                  20                  25                  30  
Thr Arg Glu Leu Leu Glu  
                  35  
(2) INFORMATION FOR SEQ ID NO:2498:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 178 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..178  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1573446  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2498:  
atgtatgaaa acaagagtga tgggccaagc tggcgagtac caacggggtcg taaagacggg 60  
agactctcgt tggcaactaa agcatcgaat ctaccttctc cacttgactc tgttgcgtgt 120  
caaaagcaaa agtttcaaga taaaggattg gatactcatg atcttggttac tctactag  
(2) INFORMATION FOR SEQ ID NO:2499:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 59 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..59  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1573447  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2499:  
Met Tyr Glu Asn Lys Ser Asp Gly Pro Ser Trp Arg Val Pro Thr Gly  
1                  5                  10                  15  
Arg Lys Asp Gly Arg Leu Ser Leu Ala Thr Lys Ala Ser Asn Leu Pro  
                  20                  25                  30  
Ser Pro Leu Asp Ser Val Ala Val Gln Lys Gln Lys Phe Gln Asp Lys  
                  35                  40                  45  
Gly Leu Asp Thr His Asp Leu Val Thr Leu Leu  
                  50                  55

(2) INFORMATION FOR SEQ ID NO:2500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1573449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2500:

Cys Met Lys Thr Arg Val Met Gly Gln Ala Gly Glu Tyr Gln Arg Val  
1 5 10 15  
Val Lys Thr Gly Asp Ser Arg Trp Gln Leu Lys His Arg Ile Tyr Leu  
20 25 30  
Leu His Leu Thr Leu Leu Leu Phe Lys Ser Lys Ser Phe Lys Ile Lys  
35 40 45  
Asp Trp Ile Leu Met Ile Leu Leu Tyr  
50 55

(2) INFORMATION FOR SEQ ID NO:2501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..759

(D) OTHER INFORMATION: / Ceres Seq. ID 1573532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2501:

atgcaaaact gatccaaagg ttctgcacac ctactaccat tcagagacgg aatagataga 60  
atagctcgtg agttacaaga aaccaaaagca aaggcaacct gtgatcagca aagaccagct 120  
gctatggatc aacagaacat accagttgat gttcaagacc cacctaagt gtatcaacca 180  
agaaacattg gtgctggtga tgccccaagg aatcatcacc aaagacaagg gatagtgcct 240  
ccaccagttc agaacaacaa ctttgaatc aagagtggtc tcactccat gatagtgcc 300  
aacaagtttc atggtttacc tatggaagt cccctggacc atcttgacag ctttgatagg 360  
ctctgtggcc ttaccaagat caatggtgtc actgaagata tgtttaagct cagactattt 420  
ccctctcttt tgggaaacaa ggcacaccac tgggagaaga ctctgcccc agaactccat 480  
aactcatggg acgattataa gaaagctttt cttgtcaagt ttactctaa cgctcgcaac 540  
gctagattga ggaacagagt cccaggcttc acacagaaaa acaatgaac tttctgtgaa 600  
gcttgggaaa ggtttcaaga aggcttcatt attgagcaca ctctaccaag gagctttacc 660  
aaatatcaga attgctactg acacgcgtc caatggaac ttctggaact aggatgtaga 720  
aagaaggctag gagttagtcg aaaatctagc acaactaa

(2) INFORMATION FOR SEQ ID NO:2502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..252

(D) OTHER INFORMATION: / Ceres Seq. ID 1573533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2502:

Met Gln Thr Arg Ser Lys Gly Ser Ala His Leu Leu Pro Phe Arg Asp  
1 5 10 15  
Gly Ile Asp Arg Ile Ala Arg Glu Leu Gln Glu Thr Lys Ala Lys Ala  
20 25 30

Thr Cys Asp Gln Gln Arg Pro Ala Ala Met Asp Gln Gln Asn Ile Pro  
35 40 45  
Val Asp Val Gln Asp Pro Pro Asn Val Asp Gln Pro Arg Asn Ile Gly  
50 55 60  
Ala Gly Asp Ala Pro Arg Asn His His Gln Arg Gln Gly Ile Val Pro  
65 70 75 80  
Pro Pro Val Gln Asn Asn Asn Phe Glu Ile Lys Ser Gly Leu Ile Ser  
85 90 95  
Met Ile Gln Gly Asn Lys Phe His Gly Leu Pro Met Glu Asp Pro Leu  
100 105 110  
Asp His Leu Asp Ser Phe Asp Arg Leu Cys Gly Leu Thr Lys Ile Asn  
115 120 125  
Gly Val Thr Glu Asp Met Phe Lys Leu Arg Leu Pro Phe Ser Leu  
130 135 140  
Gly Asn Lys Ala His His Trp Glu Lys Thr Leu Pro Pro Asp Ser Ile  
145 150 155 160  
Asn Ser Trp Asp Asp Tyr Lys Lys Ala Phe Leu Val Lys Phe Tyr Ser  
165 170 175  
Asn Ala Arg Thr Ala Arg Leu Arg Asn Glu Ile Pro Gly Phe Thr Gln  
180 185 190  
Lys Asn Asn Glu Thr Phe Cys Glu Ala Trp Glu Arg Phe Gln Glu Gly  
195 200 205  
Phe Ile Glu His Thr Leu Pro Arg Ser Phe Thr Lys Tyr Gln Asn  
210 215 220  
Ala Thr Arg His Arg Val Gln Trp Lys Leu Pro Glu Leu Gly Cys Arg  
225 230 235 240  
Arg Arg Leu Gly Val Ser Arg Lys Ser Ser Thr Ile  
245 250

(2) INFORMATION FOR SEQ ID NO:2503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..211
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2503:

Met Asp Gln Gln Asn Ile Pro Val Asp Val Gln Asp Pro Pro Asn Val  
1 5 10 15  
Asp Gln Pro Arg Asn Ile Gly Ala Gly Asp Ala Pro Arg Asn His His  
20 25 30  
Gln Arg Gln Gly Ile Val Pro Pro Val Gln Asn Asn Asn Phe Glu  
35 40 45  
Ile Lys Ser Gly Leu Ile Ser Met Ile Gln Gly Asn Lys Phe His Gly  
50 55 60  
Leu Pro Met Glu Asp Pro Leu Asp His Leu Asp Ser Phe Asp Arg Leu  
65 70 75 80  
Cys Gly Leu Thr Lys Ile Asn Gly Val Thr Glu Asp Met Phe Lys Leu  
85 90 95  
Arg Leu Phe Pro Phe Ser Leu Gly Asn Lys Ala His His Trp Glu Lys  
100 105 110  
Thr Leu Pro Pro Asp Ser Ile Asn Ser Trp Asp Asp Tyr Lys Lys Ala  
115 120 125  
Phe Leu Val Lys Phe Tyr Ser Asn Ala Arg Thr Ala Arg Leu Arg Asn  
130 135 140  
Glu Ile Pro Gly Phe Thr Gln Lys Asn Asn Glu Thr Phe Cys Glu Ala  
145 150 155 160  
Trp Glu Arg Phe Gln Glu Gly Phe Ile Glu His Thr Leu Pro Arg

(2) INFORMATION FOR SEQ ID NO:2504:

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(D) OTHER INFORMATION: / Ceres Seq. ID 1573558

|             |             |            |             |            |             |     |
|-------------|-------------|------------|-------------|------------|-------------|-----|
| atgctcaaa   | caaccaaaca  | cataaaagag | agattttaata | caaaatagg  | agaaaaaaaa  | 60  |
| aagatataag  | aggactcaac  | acaagaatag | gagagcgact  | ccacattgga | ggaggcagga  | 120 |
| gtgaagcgtga | gcacaaagatt | gttgagagaa | ccaaagaaaca | cgttgcagag | ccacaagaagt | 180 |
| gtgagacacaa | agaaaggtat  | gttgacagaa | tcaaaagacaa | gtatccagct | cagtaagagta | 240 |
| aaagccacga  | cggagaaagg  | aaaagccaac | acggttgagaa | caaaaaggag | aaggcacaaga | 300 |
| aggagaaagca | acatcatgat  | gatgtgtcac | acagacgcag  | cagtgacagc | gacagacatt  | 360 |
| aaggtgagga  | agtgaggagg  | atcgctctga | taaaaacagat | ctgtggtctc | ctattattaa  | 420 |
| taagtgtgtt  | tgtatgtgtt  | tatcatctta | gagagaggtt  | aaagacagga | gacccgtgga  | 480 |
| tctatctgtt  | YYtgttatgt  | tgtgtttttc | ttgtcatgaa  | aattatgctc | atgtatctta  | 540 |
| tctaatacga  | ataataataat | tttatg     |             |            |             |     |

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(D) OTHER INFORMATION

## Val Lys Ala Thr Lys His Ile Lys Glu Arg Ph

(2) INFORMATION FOR SEQ ID NO:2506:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids



(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..98  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573560  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2506:  
Met Ala Gly Leu Ile Asn Lys Ile Gly Asp Ala Leu His Ile Gly Gly  
1 5 10 15  
Gly Asn Lys Glu Gly Glu His Lys Lys Glu Glu Glu His Lys Lys His  
20 25 30  
Val Asp Glu His Lys Ser Gly Glu His Lys Glu Gly Ile Val Asp Lys  
35 40 45  
Ile Lys Asp Lys Ile His Gly Gly Glu Glu Lys Ser His Asp Gly Glu  
50 55 60  
Gly Lys Ser His Asp Gly Glu Lys Lys Lys Lys Lys Asp Lys Lys Glu  
65 70 75 80  
Lys Lys His His Asp Asp Gly His His Ser Ser Ser Asp Ser Asp  
85 90 95  
Ser Ile

(2) INFORMATION FOR SEQ ID NO:2507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1363 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1363  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2507:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| acaatctatc  | gagctaaaa   | actgaagcag  | acattagcgt  | tgagaaaaaW  | aaaaaaaaag  | 60   |
| aagaacgaga  | gagagaaagc  | catgtctcgc  | aaaacaatcc  | tatcatcagt  | agtttttggtg | 120  |
| gttctcgtcg  | cgcgcatcagc | agcggctaata | atcggattcg  | atgagtcaaa  | cccgatccga  | 180  |
| atggtctccg  | atggtctccg  | ggaggtagaa  | gaatctgttt  | cccagatcct  | aggtcaatct  | 240  |
| cgtcacgttc  | tctcttttcg  | tgccttcaact | caccgatatg  | gtaaaaagta  | tcagaaacgtg | 300  |
| gaggagatga  | agcttcgatt  | ctcgcatttcc | aaggagaatc  | ttgatttgat  | cagatccacc  | 360  |
| aacaagaaga  | gcttatctta  | caaaactcggt | gttaatacaat | ttgctgattt  | gacatggcaa  | 420  |
| gagtttcaaa  | ggaccaagct  | tggtgtcgtc  | cagaactgct  | ctgccacttt  | aaaggggcag  | 480  |
| cacaaggcca  | cagaagcagc  | tcttctctgaa | acaaaagact  | ggagagaaga  | tggtatcggt  | 540  |
| agtcgggtca  | aagatcaggg  | agggttggtga | tcttgctgga  | cattcagcac  | aaactggagct | 600  |
| cttgaggcag  | cttaccatca  | ggcatttgga  | aaaggaatat  | ctctctctga  | gcaacagcgt  | 660  |
| gtggttggtg  | ctggagcttt  | caataactat  | gggtgcgaatg | gtggccctcc  | ttctcaagcc  | 720  |
| tttgaataca  | taaaatccaa  | cggtgggcctc | gacacagaga  | aagcttatcc  | ttataccggt  | 780  |
| aagcatagca  | ctgcgaatt   | ttcagctgaa  | aacgttggtg  | tacaagtcct  | caactacgtc  | 840  |
| aatcattact  | tgggtgctga  | agatgaactg  | aagcatgcgg  | ttgBgattgg  | tacggccagt  | 900  |
| aagcatagca  | tttgagttta  | tacactcggt  | cggcttttac  | aagagtgagg  | tttcaactga  | 960  |
| tagtcaactg  | ggaagtactc  | caatggatgt  | gaaccaacgc  | gttttggccg  | ttgggttatgg | 1020 |
| agttgaagac  | ggtgtaccat  | attggcttat  | taagaactca  | tggggagcgg  | attggggcga  | 1080 |
| caaaaggttac | ttcaagatgg  | agatggggaa  | gaacatgtgt  | ggtatttgcta | catgtgcac   | 1140 |
| ataccocggt  | tggtcttgag  | atgatcagcg  | aatctgggtg  | gcgaatttat  | aaattacgaa  | 1200 |
| attgttcacgt | attttatgga  | tttaagacatt | acgttaaaagt | tgggacttgg  | gaatgcata   | 1260 |
| ggtttatgct  | tgttgttaaca | taaaaaggct  | tggttaatatg | tacaaaataa  | agccaaaact  | 1320 |
| atagacgaca  | aatttataat  | attttcatgt  | taaatattatg | aac         |             |      |

(2) INFORMATION FOR SEQ ID NO:2508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..304  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1573562  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2508:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ile | Tyr | Arg | Ala | Lys | Thr | Leu | Lys | Gln | Thr | Leu | Ala | Leu | Arg | Lys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Xaa | Lys | Lys | Ser | Lys | Asn | Glu | Arg | Glu | Lys | Ala | Met | Ser | Ala | Lys | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Leu | Ser | Ser | Val | Val | Leu | Val | Val | Leu | Val | Ala | Ala | Ser | Ala | Ala |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Asn | Ile | Gly | Phe | Asp | Glu | Ser | Asn | Pro | Ile | Arg | Met | Val | Ser | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Leu | Arg | Glu | Val | Glu | Glu | Ser | Val | Ser | Gln | Ile | Leu | Gly | Gln | Ser |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Arg | His | Val | Leu | Ser | Phe | Ala | Arg | Phe | Thr | His | Arg | Tyr | Gly | Lys | Lys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Tyr | Gln | Asn | Val | Glu | Glu | Met | Lys | Leu | Arg | Phe | Ser | Ile | Phe | Lys | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Leu | Asp | Leu | Ile | Arg | Ser | Thr | Asn | Lys | Lys | Gly | Leu | Ser | Tyr | Lys |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Gly | Val | Asn | Gln | Phe | Ala | Asp | Leu | Thr | Trp | Gln | Glu | Phe | Gln | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Lys | Leu | Gly | Ala | Ala | Gln | Asn | Cys | Ser | Ala | Thr | Leu | Lys | Gly | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| His | Lys | Val | Thr | Glu | Ala | Ala | Leu | Pro | Glu | Thr | Lys | Asp | Trp | Arg | Glu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asp | Gly | Ile | Val | Ser | Pro | Val | Lys | Asp | Gln | Gly | Gly | Cys | Gly | Ser | Cys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Trp | Thr | Phe | Ser | Thr | Thr | Gly | Ala | Leu | Glu | Ala | Ala | Tyr | His | Gln | Ala |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Phe | Gly | Lys | Gly | Ile | Ser | Leu | Ser | Glu | Gln | Gln | Leu | Val | Asp | Cys | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Ala | Phe | Asn | Asn | Tyr | Gly | Cys | Asn | Gly | Gly | Leu | Pro | Ser | Gln | Ala |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Phe | Glu | Tyr | Ile | Lys | Ser | Asn | Gly | Gly | Leu | Asp | Thr | Glu | Lys | Ala | Tyr |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Pro | Tyr | Thr | Gly | Lys | Asp | Glu | Thr | Cys | Lys | Phe | Ser | Ala | Glu | Asn | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Val | Gln | Val | Leu | Asn | Ser | Val | Asn | Ile | Thr | Leu | Gly | Ala | Glu | Asp |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Glu | Leu | Lys | His | Ala | Val | Xaa | Ile | Gly | Thr | Ala | Ser | Lys | His | Ser | Ile |
|     | 290 |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:2509:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 277 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..277  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1573563  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2509:  
Met Ser Ala Lys Thr Ile Leu Ser Ser Val Val Leu Val Val Leu Val

1 5 10 15  
Ala Ala Ser Ala Ala Asn Ile Gly Phe Asp Glu Ser Asn Pro Ile  
20 25 30  
Arg Met Val Ser Asp Gly Leu Arg Glu Val Glu Glu Ser Val Ser Gln  
35 40 45  
Ile Leu Gly Gln Ser Arg His Val Leu Ser Phe Ala Arg Phe Thr His  
50 55 60  
Arg Tyr Gly Lys Lys Tyr Gln Asn Val Glu Glu Met Lys Leu Arg Phe  
65 70 75 80  
Ser Ile Phe Lys Glu Asn Leu Asp Leu Ile Arg Ser Thr Asn Lys Lys  
85 90 95  
Gly Leu Ser Tyr Lys Leu Gly Val Asn Gln Phe Ala Asp Leu Thr Trp  
100 105 110  
Gln Glu Phe Gln Arg Thr Lys Leu Gly Ala Ala Gln Asn Cys Ser Ala  
115 120 125  
Thr Leu Lys Gly Ser His Lys Val Thr Glu Ala Ala Leu Pro Glu Thr  
130 135 140  
Lys Asp Trp Arg Glu Asp Gly Ile Val Ser Pro Val Lys Asp Gln Gly  
145 150 155 160  
Gly Cys Gly Ser Cys Trp Thr Phe Ser Thr Thr Gly Ala Leu Glu Ala  
165 170 175  
Ala Tyr His Gln Ala Phe Gly Lys Gly Ile Ser Leu Ser Glu Gln Gln  
180 185 190  
Leu Val Asp Cys Ala Gly Ala Phe Asn Asn Tyr Gly Cys Asn Gly Gly  
195 200 205  
Leu Pro Ser Gln Ala Phe Glu Tyr Ile Lys Ser Asn Gly Gly Leu Asp  
210 215 220  
Thr Glu Lys Ala Tyr Pro Tyr Thr Thr Gly Lys Asp Glu Thr Cys Lys Phe  
225 230 235 240  
Ser Ala Glu Asn Val Gly Val Gln Val Leu Asn Ser Val Asn Ile Thr  
245 250 255  
Leu Gly Ala Glu Asp Glu Leu Lys His Ala Val Xaa Ile Gly Thr Ala  
260 265 270  
Ser Lys His Ser Ile  
275

(2) INFORMATION FOR SEQ ID NO:2510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..244

(D) OTHER INFORMATION: / Ceres Seq. ID 1573564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2510:

Met Val Ser Asp Gly Leu Arg Glu Val Glu Glu Ser Val Ser Gln Ile  
1 5 10 15  
Leu Gly Gln Ser Arg His Val Leu Ser Phe Ala Arg Phe Thr His Arg  
20 25 30  
Tyr Gly Lys Lys Tyr Gln Asn Val Glu Met Lys Leu Arg Phe Ser  
35 40 45  
Ile Phe Lys Glu Asn Leu Asp Leu Ile Arg Ser Thr Asn Lys Lys Gly  
50 55 60  
Leu Ser Tyr Lys Leu Gly Val Asn Gln Phe Ala Asp Leu Thr Trp Gln  
65 70 75 80  
Glu Phe Gln Arg Thr Lys Leu Gly Ala Ala Gln Asn Cys Ser Ala Thr  
85 90 95  
Leu Lys Gly Ser His Lys Val Thr Glu Ala Ala Leu Pro Glu Thr Lys  
100 105 110

Asp Trp Arg Glu Asp Gly Ile Val Ser Pro Val Lys Asp Gln Gly Gly  
115 120 125  
Cys Gly Ser Cys Trp Thr Phe Ser Thr Thr Gly Ala Leu Glu Ala Ala  
130 135 140  
Tyr His Gln Ala Phe Gly Lys Gly Ile Ser Leu Ser Glu Gln Gln Leu  
145 150 155 160  
Val Asp Cys Ala Gly Ala Phe Asn Asn Tyr Gly Cys Asn Gly Gly Leu  
165 170 175  
Pro Ser Gln Ala Phe Glu Tyr Ile Lys Ser Asn Gly Gly Leu Asp Thr  
180 185 190  
Glu Lys Ala Tyr Pro Tyr Thr Gly Lys Asp Glu Thr Cys Lys Phe Ser  
195 200 205  
Ala Glu Asn Val Gly Val Gln Val Leu Asn Ser Val Asn Ile Thr Leu  
210 215 220  
Gly Ala Glu Asp Glu Leu Lys His Ala Val Xaa Ile Gly Thr Ala Ser  
225 230 235 240  
Lys His Ser Ile

(2) INFORMATION FOR SEQ ID NO:2511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..545
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2511:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| ttttttttga | gtcgtttcac | ttcttttgca | tccttcaaac | tcattccacag | gaatggcgac | 60  |
| agCagcagca | ccagcagtg  | tttcatggac | aagatcaggc | attgtgtcca  | aatccggaca | 120 |
| aaaccagaag | aaattctgag | tgaaagtttc | ttacataact | ggacttaact  | catatgggtg | 180 |
| tctcaaggca | cagaacaaca | aggttgtctc | aatgggatca | ccactctgca  | cagaacagt  | 240 |
| ttttgttaac | gttgtgatgt | ctctcaaagg | aagaagaggt | aatggaggag  | ccttatccac | 300 |
| cacgtgtaac | ctgtcggaga | gattttcaag | attgcagcaa | tcattgaacg  | tcttactott | 360 |
| gttggtgttg | cagttggatt | cgttcttctt | cgaatcgaaa | cttctgttga  | agaagctgaa | 420 |
| gcagagtaaa | tagagtaaat | tgctgctctt | ataattatat | atttttggtt  | attgttgttg | 480 |
| tcaagctttg | gtaaaaactg | atggatacat | gttacatttg | tttatgaaga  | agctcttttc | 540 |
| ttggc      |            |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2512:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Thr | Ala | Ala | Ala | Pro | Ala | Val | Ile | Ser | Trp | Thr | Arg | Ser | Gly |
| 1   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ile | Val | Ser | Lys | Ser | Gly | Gln | Thr | Gln | Lys | Lys | Ser | Glu | Met | Lys | Val |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ser | Tyr | Ile | Thr | Gly | Leu | Asn | Ser | Tyr | Gly | Gly | Leu | Lys | Ala | Gln | Asn |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Asn | Lys | Val | Val | Ser | Met | Gly | Ser | Pro | Leu | Cys | Thr | Glu | Gln | Cys | Phe |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ala | Asn | Val | Val | Met | Ser | Leu | Lys | Gly | Arg | Arg | Gly | Asn | Gly | Gly | Ala |

|                                                                 |    |    |    |
|-----------------------------------------------------------------|----|----|----|
| 65                                                              | 70 | 75 | 80 |
| Leu Ser Thr Thr Cys Asn Leu Ser Glu Arg Phe Ser Arg Leu Gln Gln |    |    |    |
|                                                                 | 85 | 90 | 95 |
| Ser                                                             |    |    |    |

(2) INFORMATION FOR SEQ ID NO:2513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2513:

|                                                                 |          |
|-----------------------------------------------------------------|----------|
| Met Lys Val Ser Tyr Ile Thr Gly Leu Asn Ser Tyr Gly Gly Leu Lys |          |
| 1                                                               | 5 10 15  |
| Ala Gln Asn Asn Lys Val Val Ser Met Gly Ser Pro Leu Cys Thr Glu |          |
|                                                                 | 20 25 30 |
| Gln Cys Phe Ala Asn Val Val Met Ser Leu Lys Gly Arg Arg Gly Asn |          |
|                                                                 | 35 40 45 |
| Gly Gly Ala Leu Ser Thr Thr Cys Asn Leu Ser Glu Arg Phe Ser Arg |          |
|                                                                 | 50 55 60 |
| Leu Gln Gln Ser                                                 |          |

(2) INFORMATION FOR SEQ ID NO:2514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1357
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2514:

|            |             |             |            |            |             |      |
|------------|-------------|-------------|------------|------------|-------------|------|
| aaaacctccc | tcaggagcct  | ccgccttatt  | cagagaggag | gatccaaaag | aaaagaggaa  | 60   |
| aaaatggact | atatgtatgk  | gaccagggag  | acaccatctg | tttgtaccag | gaccagtga   | 120  |
| cataccggaa | ccggtaatcc  | ggcgatgaa   | ccggaacaac | gaggattacc | ggtcaccagc  | 180  |
| cattccggcg | cttacgaaaa  | cattgttgga  | ggatgttaag | aagatattca | agaccacatc  | 240  |
| agggacacct | tttctgtttc  | ccacgaccgg  | gactgtgtct | tgggagagtg | ccttgaccaa  | 300  |
| cacgttatct | cctggagaca  | ggattgtttc  | gtttctgatt | ggacaattta | gcttgctctg  | 360  |
| gattgaccag | cagaagaggc  | ttaatttcaa  | tggtgatgtg | gttgagagtg | attggggaca  | 420  |
| aggtgcta   | ctccaagtct  | tggcctcaaa  | gctctcaca  | acacgaagt  | gttgcctcaa  | 480  |
| agccatttgc | attgtccaca  | acgagacgcg  | gaccggagtt | gacgagaatc | ataccaatca  | 540  |
| ccgcacacac | ctcgatcaat  | caaaagcatcc | ggctttgtct | ctagtggagc | gtgttttctg  | 600  |
| catctgcgcg | cttgatttcc  | gaatggatga  | gtggggagtg | gacgtggcct | tgactgggctc | 660  |
| tcagaaagcc | ttatctcttc  | caacaggact  | tggtattgtc | tgccgacgtc | ctaaagcttt  | 720  |
| ggaagctacc | aaaaacttcta | aatctctcaa  | agtattcttt | gactggaatg | actaccttaa  | 780  |
| gttttacaa  | ctaggaaacct | attggccata  | cacacottcc | attcaacttc | tctacaggtc  | 840  |
| tagagctcgt | cttgatcttta | tctttgagga  | aggacttgag | aacatcatcg | cccgccatgc  | 900  |
| tcgtttggga | aaggccaccca | ggcttgcggt  | ggaagcatgg | gggctgaaaa | actgcacaca  | 960  |
| gaaggaggaa | tgataaagta  | acacagtgac  | agcagttatg | gtgcctccgc | atatagacgg  | 1020 |
| ttcggagatt | gtgagaaagg  | catggcagag  | gtacaactta | agtcttggtc | ttgggtctcaa | 1080 |
| caaatggcct | ggaagggttt  | tcagaattgg  | acatctagga | aatgtgaatg | agttgcaact  | 1140 |
| tctcgggttg | cttcggcgag  | ttggagatga  | ctggaagagt | ttgggaacc  | cagttgtaat  | 1200 |
| gggaagtgga | gttgacagtg  | ctctacttta  | tcttcagcac | catactcttc | tcattctctc  | 1260 |
| tagaatctaa | tccatgtggt  | ctttctcttt  | ctttctcttc | ctctcaatgt | aaacaaactc  | 1320 |

tcactgtttttc tctttttcttc atctatatatt ttactgc

(2) INFORMATION FOR SEQ ID NO:2515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 422 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..422

(D) OTHER INFORMATION: / Ceres Seq. ID 1573569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2515:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Pro | Pro | Ser | Gly | Ala | Ser | Ala | Leu | Phe | Arg | Glu | Glu | Asp | Pro | Lys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Lys | Arg | Lys | Lys | Trp | Thr | Ile | Cys | Met | Xaa | Pro | Gly | Arg | His | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Phe | Val | Pro | Gly | Pro | Val | Asn | Ile | Pro | Glu | Pro | Val | Ile | Arg | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Met | Asn | Arg | Asn | Asn | Glu | Asp | Tyr | Arg | Ser | Pro | Ala | Ile | Pro | Ala | Leu |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Thr | Lys | Thr | Leu | Leu | Glu | Asp | Val | Lys | Lys | Ile | Phe | Lys | Thr | Thr | Ser |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Thr | Pro | Phe | Leu | Phe | Pro | Thr | Thr | Gly | Thr | Gly | Ala | Trp | Glu | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Leu | Thr | Asn | Thr | Leu | Ser | Pro | Gly | Asp | Arg | Ile | Val | Ser | Phe | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Gly | Gln | Phe | Ser | Leu | Leu | Trp | Ile | Asp | Gln | Gln | Lys | Arg | Leu | Asn |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Asn | Val | Asp | Val | Val | Glu | Ser | Asp | Trp | Gly | Gln | Gly | Ala | Asn | Leu |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Gln | Val | Leu | Ala | Ser | Lys | Leu | Ser | Gln | Asp | Glu | Asn | His | Thr | Ile | Lys |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Ile | Cys | Ile | Val | His | Asn | Glu | Thr | Ala | Thr | Gly | Val | Thr | Asn | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Ser | Ala | Val | Arg | Thr | Leu | Leu | Asp | His | Tyr | Lys | His | Pro | Ala | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Leu | Val | Asp | Gly | Val | Ser | Ser | Ile | Cys | Ala | Leu | Asp | Phe | Arg | Met |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asp | Glu | Trp | Gly | Val | Asp | Val | Ala | Leu | Thr | Gly | Ser | Gln | Lys | Ala | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Leu | Pro | Thr | Gly | Leu | Gly | Ile | Val | Cys | Ala | Ser | Pro | Lys | Ala | Leu |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Ala | Thr | Lys | Thr | Ser | Lys | Ser | Leu | Lys | Val | Phe | Phe | Asp | Trp | Asn |
|     |     |     | 245 |     |     |     |     |     |     | 250 |     |     |     | 255 |     |
| Asp | Tyr | Leu | Lys | Phe | Tyr | Lys | Leu | Gly | Thr | Tyr | Trp | Pro | Tyr | Thr | Pro |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Ile | Gln | Leu | Leu | Tyr | Gly | Leu | Arg | Ala | Ala | Leu | Asp | Leu | Ile | Phe |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Glu | Glu | Gly | Leu | Glu | Asn | Ile | Ile | Ala | Arg | His | Ala | Arg | Leu | Gly | Lys |
|     |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Ala | Thr | Arg | Leu | Ala | Val | Glu | Ala | Trp | Gly | Leu | Lys | Asn | Cys | Thr | Gln |
|     | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Lys | Glu | Glu | Trp | Ile | Ser | Asn | Thr | Val | Thr | Ala | Val | Met | Val | Pro | Pro |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| His | Ile | Asp | Gly | Ser | Glu | Ile | Val | Arg | Arg | Ala | Trp | Gln | Arg | Tyr | Asn |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Leu | Ser | Leu | Gly | Leu | Gly | Leu | Asn | Lys | Val | Ala | Gly | Lys | Val | Phe | Arg |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ile | Gly | His | Leu | Gly | Asn | Val | Asn | Glu | Leu | Gln | Leu | Leu | Gly | Cys | Leu |
|     | 370 |     |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |

Ala Gly Val Glu Met Ile Leu Lys Asp Val Gly Tyr Pro Val Val Met  
385 390 395 400  
Gly Ser Gly Val Ala Ala Ser Thr Tyr Leu Gln His His Ile Pro  
405 410 415  
Leu Ile Pro Ser Arg Ile  
420

(2) INFORMATION FOR SEQ ID NO:2516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..397

- (D) OTHER INFORMATION: / Ceres Seq. ID 1573570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2516:

Met Xaa Pro Gly Arg His His Leu Phe Val Pro Gly Pro Val Asn Ile  
1 5 10 15  
Pro Glu Pro Val Ile Arg Ala Met Asn Arg Asn Asn Glu Asp Tyr Arg  
20 25 30  
Ser Pro Ala Ile Pro Ala Leu Thr Lys Thr Leu Leu Glu Asp Val Lys  
35 40 45  
Lys Ile Phe Lys Thr Thr Ser Gly Thr Pro Phe Leu Phe Pro Thr Thr  
50 55 60  
Gly Thr Gly Ala Trp Glu Ser Ala Leu Thr Asn Thr Leu Ser Pro Gly  
65 70 75 80  
Asp Arg Ile Val Ser Phe Leu Ile Gly Gln Phe Ser Leu Leu Trp Ile  
85 90 95  
Asp Gln Gln Lys Arg Leu Asn Phe Asn Val Asp Val Val Glu Ser Asp  
100 105 110  
Trp Gly Gln Gly Ala Asn Leu Gln Val Leu Ala Ser Lys Leu Ser Gln  
115 120 125  
Asp Glu Asn His Thr Ile Lys Ala Ile Cys Ile Val His Asn Glu Thr  
130 135 140  
Ala Thr Gly Val Thr Asn Asp Ile Ser Ala Val Arg Thr Leu Leu Asp  
145 150 155 160  
His Tyr Lys His Pro Ala Leu Leu Leu Val Asp Gly Val Ser Ser Ile  
165 170 175  
Cys Ala Leu Asp Phe Arg Met Asp Glu Trp Gly Val Asp Val Ala Leu  
180 185 190  
Thr Gly Ser Gln Lys Ala Leu Ser Leu Pro Thr Gly Leu Gly Ile Val  
195 200 205  
Cys Ala Ser Pro Lys Ala Leu Glu Ala Thr Lys Thr Ser Lys Ser Leu  
210 215 220  
Lys Val Phe Phe Asp Trp Asn Asp Tyr Leu Lys Phe Tyr Lys Leu Gly  
225 230 235 240  
Thr Tyr Trp Pro Tyr Thr Pro Ser Ile Gln Leu Leu Tyr Gly Leu Arg  
245 250 255  
Ala Ala Leu Asp Leu Ile Phe Glu Glu Gly Leu Glu Asn Ile Ile Ala  
260 265 270  
Arg His Ala Arg Leu Gly Lys Ala Thr Arg Leu Ala Val Glu Ala Trp  
275 280 285  
Gly Leu Lys Asn Cys Thr Gln Lys Glu Glu Trp Ile Ser Asn Thr Val  
290 295 300  
Thr Ala Val Met Val Pro Pro His Ile Asp Gly Ser Glu Ile Val Arg  
305 310 315 320  
Arg Ala Trp Gln Arg Tyr Asn Leu Ser Leu Gly Leu Gly Leu Asn Lys  
325 330 335  
Val Ala Gly Lys Val Phe Arg Ile Gly His Leu Gly Asn Val Asn Glu

340 345 350  
Leu Gln Leu Leu Gly Cys Leu Ala Gly Val Glu Met Ile Leu Lys Asp  
355 360 365  
Val Gly Tyr Pro Val Val Met Gly Ser Gly Val Ala Ala Ala Ser Thr  
370 375 380  
Tyr Leu Gln His His Ile Pro Leu Ile Pro Ser Arg Ile  
385 390 395

(2) INFORMATION FOR SEQ ID NO:2517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..374

(D) OTHER INFORMATION: / Ceres Seq. ID 1573571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2517:

Met Asn Arg Asn Asn Glu Asp Tyr Arg Ser Pro Ala Ile Pro Ala Leu  
1 5 10 15  
Thr Lys Thr Leu Leu Glu Asp Val Lys Lys Ile Phe Lys Thr Thr Ser  
20 25 30  
Gly Thr Pro Phe Leu Phe Pro Thr Thr Gly Thr Gly Ala Trp Glu Ser  
35 40 45  
Ala Leu Thr Asn Thr Leu Ser Pro Gly Asp Arg Ile Val Ser Phe Leu  
50 55 60  
Ile Gly Gln Phe Ser Leu Leu Trp Ile Asp Gln Gln Lys Arg Leu Asn  
65 70 75 80  
Phe Asn Val Asp Val Val Glu Ser Asp Trp Gly Gln Gly Ala Asn Leu  
85 90 95  
Gln Val Leu Ala Ser Lys Leu Ser Gln Asp Glu Asn His Thr Ile Lys  
100 105 110  
Ala Ile Cys Ile Val His Asn Glu Thr Ala Thr Gly Val Thr Asn Asp  
115 120 125  
Ile Ser Ala Val Arg Thr Leu Asp His Tyr Lys His Pro Ala Leu  
130 135 140  
Leu Leu Val Asp Gly Val Ser Ser Ile Cys Ala Leu Asp Phe Arg Met  
145 150 155 160  
Asp Glu Trp Gly Val Asp Val Ala Leu Thr Gly Ser Gln Lys Ala Leu  
165 170 175  
Ser Leu Pro Thr Gly Leu Gly Ile Val Cys Ala Ser Pro Lys Ala Leu  
180 185 190  
Glu Ala Thr Lys Thr Ser Lys Ser Leu Lys Val Phe Phe Asp Trp Asn  
195 200 205  
Asp Tyr Leu Lys Phe Tyr Lys Leu Gly Thr Tyr Trp Pro Tyr Thr Pro  
210 215 220  
Ser Ile Gln Leu Leu Tyr Gly Leu Arg Ala Ala Leu Asp Leu Ile Phe  
225 230 235 240  
Glu Glu Gly Leu Glu Asn Ile Ile Ala Arg His Ala Arg Leu Gly Lys  
245 250 255  
Ala Thr Arg Leu Ala Val Glu Ala Trp Gly Leu Lys Asn Cys Thr Gln  
260 265 270  
Lys Glu Glu Trp Ile Ser Asn Thr Val Thr Ala Val Met Val Pro Pro  
275 280 285  
His Ile Asp Gly Ser Glu Ile Val Arg Arg Ala Trp Gln Arg Tyr Asn  
290 295 300  
Leu Ser Leu Gly Leu Gly Leu Asn Lys Val Ala Gly Lys Val Phe Arg  
305 310 315 320  
Ile Gly His Leu Gly Asn Val Asn Glu Leu Gln Leu Leu Gly Cys Leu  
325 330 335

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Ala Gly Val Glu Met Ile Leu Lys Asp Val Gly Tyr Pro Val Val Met  
340 345 350  
Gly Ser Gly Val Ala Ala Ala Ser Thr Tyr Leu Gln His His Ile Pro  
355 360 365  
Leu Ile Pro Ser Arg Ile  
370

(2) INFORMATION FOR SEQ ID NO:2518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1449
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573572

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2518:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| caaaacctcc  | ctcaggagct  | tccgccttat  | tcagagtgtg  | gaggaggatc  | caaaagaaaa  | 60   |
| gaggaaaaaa  | tggactatat  | gtatggacca  | gggagacacc  | atctgtttgt  | accaggacca  | 120  |
| gtgaacatac  | cggaaccggt  | aatccggggc  | atgaaccgga  | acaacggaga  | ttaccgggtc  | 180  |
| cagcgcattc  | cgggcgcttac | gaaaacattg  | ttggaggatg  | ttagaagaat  | attcaagacc  | 240  |
| acatcaaggga | cacctttttc  | gtttccacgc  | accggggactg | gtgcttggga  | gagtgccctt  | 300  |
| accaacacgt  | tatctctctg  | agacaggatt  | gtttcgtttc  | tgattggaca  | atttagcctt  | 360  |
| ctctggattg  | accagcagaa  | gaggcttaat  | ttcaatgttg  | atgtggttga  | gagtgattGg  | 420  |
| gggacaagg   | gctaattctc  | aagtcttggc  | ctcaaagctc  | tcacaagacg  | agaatcatac  | 480  |
| catcaaaagg  | atttgattg   | tcacaaacga  | gaccgcgacc  | ggagttacca  | atgacatctc  | 540  |
| tgctgtccgc  | acactctctg  | atcaactaca  | gcacccggct  | ttgctgctag  | tggacgggtg  | 600  |
| tcgtctccat  | tgccgccttg  | atttcogaat  | ggatgagttg  | ggagtggaag  | tggccttgac  | 660  |
| tgggtctcag  | aaagccttat  | ctcttccaac  | aggacttggg  | attgtctctg  | ccagtcctaa  | 720  |
| agctttggaa  | gctacacaaa  | cttctaaatc  | tctcaaaagta | ttctttgact  | ggaatgacta  | 780  |
| ccttaagtgt  | tacaagctag  | gaacctattg  | gccatacaca  | ccttccattc  | aacttctcta  | 840  |
| cggctcttaga | gctgctcttg  | atcttatctt  | tgaggaaagga | cttgagaaca  | tcacgcgcgc  | 900  |
| ccatgctcgt  | ttgggaaaag  | ccaccaggct  | tgccgttgaa  | gcattggggc  | tgaaaaaactg | 960  |
| cacacagaag  | gaggaaatga  | taagtaaac   | agtgacagca  | gttatgggtc  | ctccgcacat  | 1020 |
| agacgggttg  | gagattgtga  | gaagggcatg  | gcagaggtag  | aacttaagtc  | ttggtcttgg  | 1080 |
| tctcaacaaa  | gtggctggaa  | aggttttcag  | aattggacat  | ctaggaaatg  | tgaatgagtt  | 1140 |
| gcaactcttc  | gggtgtcttg  | cgggagtgga  | gatgatactg  | aaggatgttg  | gataccaggt  | 1200 |
| tgtaattggga | agtggaattg  | cagctgcctc  | tacttatctt  | cagcaccaca  | ttctctctcat | 1260 |
| tcctctctaga | atctaatcca  | tgttggtcctt | ctctttcttt  | ctcttctctt  | caatgtaaac  | 1320 |
| aaactctcat  | gttttctctt  | ttcttcatct  | atatttttacc | tacatttatct | atgttttttat | 1380 |
| ttgctatctc  | caacaaactt  | attgaacaaa  | agatcaaaata | tgttttattac | tcactataaa  | 1440 |
| ctttgtctc   |             |             |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..293
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2519:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Met | Trp | Leu | Arg | Val | Ile | Gly | Gly | Gln | Gly | Ala | Asn | Leu | Gln |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Leu | Ala | Ser | Lys | Leu | Ser | Gln | Asp | Glu | Asn | His | Thr | Ile | Lys | Ala |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ile | Cys | Ile | Val | His | Asn | Glu | Thr | Ala | Thr | Gly | Val | Thr | Asn | Asp | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |

Ser Ala Val Arg Thr Leu Leu Asp His Tyr Lys His Pro Ala Leu Leu  
50 55 60  
Leu Val Asp Gly Val Ser Ser Ile Cys Ala Leu Asp Phe Arg Met Asp  
65 70 75 80  
Glu Trp Gly Val Asp Val Ala Leu Thr Gly Ser Gln Lys Ala Leu Ser  
85 90 95  
Leu Pro Thr Gly Leu Gly Ile Val Cys Ala Ser Pro Lys Ala Leu Glu  
100 105 110  
Ala Thr Lys Thr Ser Lys Ser Leu Lys Val Phe Phe Asp Trp Asn Asp  
115 120 125  
Tyr Leu Lys Phe Tyr Lys Leu Gly Thr Tyr Trp Pro Tyr Thr Pro Ser  
130 135 140  
Ile Gln Leu Leu Tyr Gly Leu Arg Ala Ala Leu Asp Leu Ile Phe Glu  
145 150 155 160  
Glu Gly Leu Glu Asn Ile Ile Ala Arg His Ala Arg Leu Gly Lys Ala  
165 170 175  
Thr Arg Leu Ala Val Glu Ala Trp Gly Leu Lys Asn Cys Thr Gln Lys  
180 185 190  
Glu Glu Trp Ile Ser Asn Thr Val Thr Ala Val Met Val Pro Pro His  
195 200 205  
Ile Asp Gly Ser Glu Ile Val Arg Arg Ala Trp Gln Arg Tyr Asn Leu  
210 215 220  
Ser Leu Gly Leu Gly Leu Asn Lys Val Ala Gly Lys Val Phe Arg Ile  
225 230 235 240  
Gly His Leu Gly Asn Val Asn Glu Leu Gln Leu Leu Gly Cys Leu Ala  
245 250 255  
Gly Val Glu Met Ile Leu Lys Asp Val Gly Tyr Pro Val Val Met Gly  
260 265 270  
Ser Gly Val Ala Ala Ala Ser Thr Tyr Leu Gln His His Ile Pro Leu  
275 280 285  
Ile Pro Ser Arg Ile  
290

(2) INFORMATION FOR SEQ ID NO:2520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..291
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2520:

Met Trp Leu Arg Val Ile Gly Gly Gln Gly Ala Asn Leu Gln Val Leu  
1 5 10 15  
Ala Ser Lys Leu Ser Gln Asp Glu Asn His Thr Ile Lys Ala Ile Cys  
20 25 30  
Ile Val His Asn Glu Thr Ala Thr Gly Val Thr Asn Asp Ile Ser Ala  
35 40 45  
Val Arg Thr Leu Leu Asp His Tyr Lys His Pro Ala Leu Leu Leu Val  
50 55 60  
Asp Gly Val Ser Ser Ile Cys Ala Leu Asp Phe Arg Met Asp Glu Trp  
65 70 75 80  
Gly Val Asp Val Ala Leu Thr Gly Ser Gln Lys Ala Leu Ser Leu Pro  
85 90 95  
Thr Gly Leu Gly Ile Val Cys Ala Ser Pro Lys Ala Leu Glu Ala Thr  
100 105 110  
Lys Thr Ser Lys Ser Leu Lys Val Phe Phe Asp Trp Asn Asp Tyr Leu  
115 120 125  
Lys Phe Tyr Lys Leu Gly Thr Tyr Trp Pro Tyr Thr Pro Ser Ile Gln



(2) INFORMATION FOR SEQ ID NO:2522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..581
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2522:

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| aagaattatt | gtttttggat  | cggaaaagag | atctagaatc | accaaaaggt | tttattttat  | 60  |
| acaatgggtc | gtggaaacag  | ctgtgggtga | ggcacaagct | cattggatta | tctctttggt  | 120 |
| ggtgacgtc  | ctgctctctaa | gccagttcca | gctctcgtc  | ccgctctac  | tgagttctaac | 180 |
| aacggacctg | caccaccagt  | aacagctgtg | actgcaaccg | cactcaagac | tgctactact  | 240 |
| tctgttgagc | ctgcagagct  | taacaagcag | attcctgctg | gtatcaaaac | tcctgttaac  | 300 |
| aactatgcca | gagctgaagg  | acagaacacc | ggcaacttcc | tcactgaccg | tccttcgacc  | 360 |
| aaagttcacg | cagctccggg  | aggaggatca | tccttggtat | atctcttcac | tggtggcgaag | 420 |
| taaaaataat | gcaaaagac   | ttatctatcc | attgtctttg | ctgcgttatc | tcactatgaa  | 480 |
| actgtttgat | gtgagccttt  | aaatgataag | aagtcggttt | cttgtctcaa | ctcttatctg  | 540 |
| taatatattg | ctgaaaaaAt  | gtttgaatca | aaaccttccc | t          |             |     |

(2) INFORMATION FOR SEQ ID NO:2523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2523:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ile | Ile | Val | Phe | Gly | Ser | Glu | Lys | Arg | Ser | Arg | Ile | Thr | Lys | Arg |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Tyr | Phe | Ile | Gln | Trp | Val | Val | Glu | Thr | Ala | Val | Val | Glu | Val | Lys |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Ala | His | Trp | Ile | Ile | Ser | Leu | Val | Val | Thr | Leu | Leu | Leu | Ser | Gln |     |
|     |     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Phe | Gln | Leu | Leu | Val | Pro | Leu | Leu | Ser | Leu | Thr | Thr | Asp | Leu | His |     |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| His | Gln |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2524:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Arg | Gly | Asn | Ser | Cys | Gly | Gly | Gly | Gln | Ser | Ser | Leu | Asp | Tyr |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Leu | Phe | Gly | Gly | Asp | Ala | Pro | Ala | Pro | Lys | Pro | Val | Pro | Ala | Pro | Arg |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Pro | Ala | Pro | Thr | Glu | Ser | Asn | Asn | Gly | Pro | Ala | Pro | Pro | Val | Thr | Ala |

35 40 45  
Val Thr Ala Thr Ala Leu Thr Thr Thr Val Glu Pro Ala  
50 55 60  
Glu Leu Asn Lys Gln Ile Pro Ala Gly Ile Lys Thr Pro Val Asn Asn  
65 70 75  
Tyr Ala Arg Ala Glu Gly Gln Asn Thr Gly Asn Phe Leu Thr Asp Arg  
85 90 95  
Pro Ser Thr Lys Val His Ala Ala Pro Gly Gly Ser Ser Leu Asp  
100 105 110  
Tyr Leu Phe Thr Gly Gly Lys  
115

(2) INFORMATION FOR SEQ ID NO:2525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1573583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2525:

Met Pro Glu Leu Lys Asp Arg Thr Pro Ala Thr Ser Ser Leu Thr Val  
1 5 10 15  
Leu Arg Pro Lys Phe Thr Gln Leu Arg Glu Glu Asp His Pro Trp Ile  
20 25 30  
Ile Ser Ser Leu Val Ala Ser Lys Ile Ile Ala Lys Thr Phe Ile Tyr  
35 40 45  
Pro Leu Ser Leu Leu Arg Tyr Leu Thr Met Lys Leu Phe Asp Val Ser  
50 55 60  
Leu  
65

(2) INFORMATION FOR SEQ ID NO:2526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 982 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..982

(D) OTHER INFORMATION: / Ceres Seq. ID 1573584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2526:

aatttttttt tttgacgac tgcctctctt tctctctctt tctctctctt cttctctctt 60  
aactcgttac catcaacgct caaatcctgt atacaatctt tctcagctg taattcttat 120  
aatctcgtca attatcatct attcagggtt aagctatggg atgtgctct tctctctccag 180  
ataggaaact tggaacttta agtggcttta gcaattcaga gaatgctgtt ccagctgatg 240  
ccaaaaatct acgtgtgaag ttagtcttat taggagaact tgggtgtgtt aaaagtgtga 300  
ttgtcctctg atttgtacct ggtcagtttg acgctacatc taaggtaact gttggagcct 360  
cgttctgttc ccaactata gcaTtgcaag actctaccac agtgaagttt gaaatatggt 420  
atacagcagg acaggagagg tattctgctc ttgcaccact atactaccgt ggagctggag 480  
ttgctgttat tgtttatgat ataacaagcc ctgaatcgtt caagaaagca cagtattggg 540  
ttaaggaact gcaaaagcat ggaagcccaag atattgttat ggctctggtt ggtaacaaag 600  
ctgatctaca tgaaaaaaga gaagtacctt ctgaggatgg aatggagctt gcagagaaga 660  
acggcatgtt cttcattgag acgtcagcca agacagccga taacataaat caactgtttg 720  
aggaaaattg caagaggcta cctcgtcctg ctcctctgtc atgattggag tgttgatcaa 780  
tctcatcttc agccatgtct tcagactact aatctttcca tactttttta tgtaattttt 840  
caaaacaata tttctctatc tgttaagtca agtgtgttgt ataagtga gatttgagtt 900  
tgaaactggg gatattaca acctcaaaag tggaaaccca agttatatca agcaatggat 960

catcagtaca tatttttagtg gg

(2) INFORMATION FOR SEQ ID NO:2527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..202
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2527:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Cys | Ala | Ser | Ser | Leu | Pro | Asp | Arg | Asn | Ser | Gly | Thr | Leu | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gly | Leu | Ser | Asn | Ser | Glu | Asn | Ala | Val | Pro | Ala | Asp | Ala | Lys | Asn | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Val | Lys | Leu | Val | Leu | Leu | Gly | Asp | Ser | Gly | Val | Gly | Lys | Ser | Cys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Val | Leu | Arg | Phe | Val | Arg | Gly | Gln | Phe | Asp | Ala | Thr | Ser | Lys | Val |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Thr | Val | Gly | Ala | Ser | Phe | Leu | Ser | Gln | Thr | Ile | Ala | Leu | Gln | Asp | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Thr | Val | Lys | Phe | Glu | Ile | Trp | Asp | Thr | Ala | Gly | Gln | Glu | Arg | Tyr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Ala | Leu | Ala | Pro | Leu | Tyr | Tyr | Arg | Gly | Ala | Gly | Val | Ala | Val | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Tyr | Asp | Ile | Thr | Ser | Pro | Glu | Ser | Phe | Lys | Lys | Ala | Gln | Tyr | Trp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Lys | Glu | Leu | Gln | Lys | His | Gly | Ser | Pro | Asp | Ile | Val | Met | Ala | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Gly | Asn | Lys | Ala | Asp | Leu | His | Glu | Lys | Arg | Glu | Val | Pro | Thr | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Asp | Gly | Met | Glu | Leu | Ala | Glu | Lys | Asn | Gly | Met | Phe | Phe | Ile | Glu | Thr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Ala | Lys | Thr | Ala | Asp | Asn | Ile | Asn | Gln | Leu | Phe | Glu | Glu | Ile | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Arg | Leu | Pro | Arg | Pro | Ala | Pro | Ser | Ser |     |     |     |     |     |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..619
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2528:

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| ctctctgtgt  | cgctcgtcta | caTttacact | cggagottag | accttccaat  | ctaccggcgg  | 60  |
| cgaaaatggg  | tttcaagagg | tacgttgaga | tccggagagt | agcaacttgtg | aactaccggag | 120 |
| aaagtcatgg  | aaagctcgtc | gttatcgtcg | acgttgttga | ccagaacaga  | gctttgggtgg | 180 |
| atgccctcga  | tatggagagg | atccagatga | acttoaagag | gttgtctctt  | accgatattg  | 240 |
| tcaattgacat | caacogtgtg | ccaaagaaga | aggctttgat | cgaggcaatg  | gaaaaggctg  | 300 |
| atgtgaagaa  | caagtggagg | aaaagctcat | ggggtaggaa | gcttatcgtg  | cagaaacgta  | 360 |
| gggctaaact  | taacgacttt | gataggttca | agatcatgtt | ggccaagatc  | aagaaagctg  | 420 |
| gtgtgtgcag  | gcaagagctt | gcaaaactca | agaaggagat | cactgcctca  | tcaaatatta  | 480 |
| tctacaattc  | tgttgtcttt | cttttttgat | tttgatttcg | gaaattagtg  | tttttggaac  | 540 |
| tatcaaatatc | agtatgtgtc | caattatcag | acattattca | agtttgaaac  | cttgtttgca  | 600 |

aaactcaaaag tttttgtgc

(2) INFORMATION FOR SEQ ID NO:2529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
  - (B) LOCATION: 1..155
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1573587
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2529:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Ala | Val | Ala | Arg | Leu | His | Leu | His | Ser | Glu | Leu | Arg | Pro | Ser | Asn |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Leu | Pro | Ala | Ala | Lys | Met | Gly | Phe | Lys | Arg | Tyr | Val | Glu | Ile | Arg | Arg |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Val | Ala | Leu | Val | Asn | Tyr | Gly | Glu | Asp | His | Gly | Lys | Leu | Val | Val | Ile |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Asp | Val | Val | Asp | Gln | Asn | Arg | Ala | Leu | Val | Asp | Ala | Pro | Asp | Met |  |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Glu | Arg | Ile | Gln | Met | Asn | Phe | Lys | Arg | Leu | Ser | Leu | Thr | Asp | Ile | Val |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Ile | Asp | Ile | Asn | Arg | Val | Pro | Lys | Lys | Lys | Ala | Leu | Ile | Glu | Ala | Met |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Glu | Lys | Ala | Asp | Val | Lys | Asn | Lys | Trp | Glu | Lys | Ser | Ser | Trp | Gly | Arg |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Lys | Leu | Ile | Val | Gln | Lys | Arg | Arg | Ala | Asn | Leu | Asn | Asp | Phe | Asp | Arg |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Phe | Lys | Ile | Met | Leu | Ala | Lys | Ile | Lys | Lys | Ala | Gly | Val | Val | Arg | Gln |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Glu | Leu | Ala | Lys | Leu | Lys | Lys | Glu | Ile | Thr | Ala |     |     |     |     |     |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
  - (B) LOCATION: 1..134
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1573588
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2530:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Phe | Lys | Arg | Tyr | Val | Glu | Ile | Arg | Arg | Val | Ala | Leu | Val | Asn |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Tyr | Gly | Glu | Asp | His | Gly | Lys | Leu | Val | Val | Ile | Val | Asp | Val | Val | Asp |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Gln | Asn | Arg | Ala | Leu | Val | Asp | Ala | Pro | Asp | Met | Glu | Arg | Ile | Gln | Met |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asn | Phe | Lys | Arg | Leu | Ser | Leu | Thr | Asp | Ile | Val | Ile | Asp | Ile | Asn | Arg |  |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Val | Pro | Lys | Lys | Lys | Ala | Leu | Ile | Glu | Ala | Met | Glu | Lys | Ala | Asp | Val |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Lys | Asn | Lys | Trp | Glu | Lys | Ser | Ser | Trp | Gly | Arg | Lys | Leu | Ile | Val | Gln |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |  |
| Lys | Arg | Arg | Ala | Asn | Leu | Asn | Asp | Phe | Asp | Arg | Phe | Lys | Ile | Met | Leu |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| Ala | Lys | Ile | Lys | Lys | Ala | Gly | Val | Val | Arg | Gln | Glu | Leu | Ala | Lys | Leu |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |

Lys Lys Glu Ile Thr Ala  
130

(2) INFORMATION FOR SEQ ID NO:2531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2531:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Arg | Ile | Gln | Met | Asn | Phe | Lys | Arg | Leu | Ser | Leu | Thr | Asp | Ile |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ile | Asp | Ile | Asn | Arg | Val | Pro | Lys | Lys | Lys | Ala | Leu | Ile | Glu | Ala |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Met | Glu | Lys | Ala | Asp | Val | Lys | Asn | Lys | Trp | Glu | Lys | Ser | Ser | Trp | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Lys | Leu | Ile | Val | Gln | Lys | Arg | Arg | Ala | Asn | Leu | Asn | Asp | Phe | Asp |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Arg | Phe | Lys | Ile | Met | Leu | Ala | Lys | Ile | Lys | Lys | Ala | Gly | Val | Val | Arg |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Gln | Glu | Leu | Ala | Lys | Leu | Lys | Lys | Glu | Ile | Thr | Ala |     |     |     |     |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..748
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2532:

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| ccttctcact  | tcaaattcat  | aatctctcta | cttctctctc | tctctaaaat | caaaaatggc  | 60  |
| gaaactcgtg  | atgtgtgttg  | ttctttgtat | cttaccggcg | ataGccatgg | cggaacaggag | 120 |
| gagtaataat  | ggaaagaata  | caatggtggt | tcaaggtagc | acttaactgt | acatttgcga  | 180 |
| attcggcttc  | gagactcctg  | aatcctccta | cttcatcccc | ggtgcaacgg | tgaagctatc  | 240 |
| atgcaaaagc  | aggaagacaa  | tggaagaggt | ttacacagac | aaagctgtat | cggacaaaaga | 300 |
| aggaagatat  | aagttcattg  | tccacgacga | tcacagagac | cagatgtgcg | atgttttgtt  | 360 |
| tgtgaaaagc  | tccgataaaa  | cctgctctaa | aatctccgtt | ggacgtgaga | agctcttgtt  | 420 |
| gatcttgaac  | cattacagtg  | gcattgcctc | gcagatcaga | catgctaaca | acatggggatt | 480 |
| cgagaaagaa  | gtgagtgatg  | tgtttctgct | tgctttgttt | cagaagtata | tggttgatga  | 540 |
| agatgaggat  | gatatttaaaa | accatctcta | atctctctgt | ttaattttat | gatctgtgtg  | 600 |
| ttcttctcatt | aatgagtttc  | gagttatgga | agagatatat | ttgtattttg | ttgattactt  | 660 |
| atttgtgtgc  | tttagagatg  | ttgactctgg | tgactcgata | actatctgtt | tgtgtaaagt  | 720 |
| tcttatatat  | tgatgtgtca  | ttctcttg   |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171



(D) OTHER INFORMATION: / Ceres Seq. ID 1573607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2533:

```
Met Ala Lys Leu Val Met Leu Leu Val Leu Cys Ile Leu Pro Ala Ile
1 5 10 15
Ala Met Ala Ala Arg Arg Ser Asn Ile Gly Lys Asn Thr Met Val Val
20 25 30
Gln Gly Ser Thr Tyr Cys Asp Ile Cys Lys Phe Gly Phe Glu Thr Pro
35 40 45
Glu Ser Ser Tyr Phe Ile Pro Gly Ala Thr Val Lys Leu Ser Cys Lys
50 55 60
Asp Arg Lys Thr Met Glu Glu Val Tyr Thr Asp Lys Ala Val Ser Asp
65 70 75 80
Lys Glu Gly Lys Tyr Lys Phe Ile Val His Asp Asp His Arg Asp Gln
85 90 95
Met Cys Asp Val Leu Leu Val Lys Ser Ser Asp Lys Thr Cys Ser Lys
100 105 110
Ile Ser Val Gly Arg Glu Lys Ser Arg Val Ile Leu Asn His Tyr Ser
115 120 125
Gly Ile Ala Ser Gln Ile Arg His Ala Asn Asn Met Gly Phe Glu Lys
130 135 140
Glu Val Ser Asp Val Phe Cys Ser Ala Leu Phe Gln Lys Tyr Met Val
145 150 155 160
Asp Glu Asp Glu Asp Asp Ile Lys Asn His Leu
165 170
```

(2) INFORMATION FOR SEQ ID NO:2534:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1573608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2534:

```
Met Leu Leu Val Leu Cys Ile Leu Pro Ala Ile Ala Met Ala Ala Arg
1 5 10 15
Arg Ser Asn Ile Gly Lys Asn Thr Met Val Val Gln Gly Ser Thr Tyr
20 25 30
Cys Asp Ile Cys Lys Phe Gly Phe Glu Thr Pro Glu Ser Ser Tyr Phe
35 40 45
Ile Pro Gly Ala Thr Val Lys Leu Ser Cys Lys Asp Arg Lys Thr Met
50 55 60
Glu Glu Val Tyr Thr Asp Lys Ala Val Ser Asp Lys Glu Gly Lys Tyr
65 70 75 80
Lys Phe Ile Val His Asp Asp His Arg Asp Gln Met Cys Asp Val Leu
85 90 95
Leu Val Lys Ser Ser Asp Lys Thr Cys Ser Lys Ile Ser Val Gly Arg
100 105 110
Glu Lys Ser Arg Val Ile Leu Asn His Tyr Ser Gly Ile Ala Ser Gln
115 120 125
Ile Arg His Ala Asn Asn Met Gly Phe Glu Lys Glu Val Ser Asp Val
130 135 140
Phe Cys Ser Ala Leu Phe Gln Lys Tyr Met Val Asp Glu Asp Glu Asp
145 150 155 160
Asp Ile Lys Asn His Leu
165
```

(2) INFORMATION FOR SEQ ID NO:2535:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..154  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573609  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2535:  
Met Ala Ala Arg Arg Ser Asn Ile Gly Lys Asn Thr Met Val Val Gln  
1 5 10 15  
Gly Ser Thr Tyr Cys Asp Ile Cys Lys Phe Gly Phe Glu Thr Pro Glu  
20 25 30  
Ser Ser Tyr Phe Ile Pro Gly Ala Thr Val Lys Leu Ser Cys Lys Asp  
35 40 45  
Arg Lys Thr Met Glu Glu Val Tyr Thr Asp Lys Ala Val Ser Asp Lys  
50 55 60  
Glu Gly Lys Tyr Lys Phe Ile Val His Asp Asp His Arg Asp Gln Met  
65 70 75 80  
Cys Asp Val Leu Leu Val Lys Ser Ser Asp Lys Thr Cys Ser Lys Ile  
85 90 95  
Ser Val Gly Arg Glu Lys Ser Arg Val Ile Leu Asn His Tyr Ser Gly  
100 105 110  
Ile Ala Ser Gln Ile Arg His Ala Asn Asn Met Gly Phe Glu Lys Glu  
115 120 125  
Val Ser Asp Val Phe Cys Ser Ala Leu Phe Gln Lys Tyr Met Val Asp  
130 135 140  
Glu Asp Glu Asp Asp Ile Lys Asn His Leu  
145 150

(2) INFORMATION FOR SEQ ID NO:2536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1707 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1707  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2536:

|             |             |                |             |             |            |      |
|-------------|-------------|----------------|-------------|-------------|------------|------|
| atacacacaa  | ttcaatat    | ttt gacttcacat | agagagagat  | agagagatgg  | cgacggaaac | 60   |
| ggaagtgtga  | gtctccgttaa | cggtaagcaa     | cggcggaagc  | aaaggatgtt  | gcaagtacgg | 120  |
| gtgtcctggg  | tacgcgactc  | ctctcgccgc     | tatgtctggt  | ccatcgagga  | aacttatcta | 180  |
| cgtaaccgcc  | gtctacacccg | gaactggaa      | agataaaccc  | gattatttgg  | cgacggtgga | 240  |
| tgtagatcca  | agctcgccct  | cgtattcaag     | tggtattcat  | agattaccaa  | tgccctttgt | 300  |
| tggtgatgag  | cttcatcatt  | ctgggtggaa     | ctctttagat  | tcttgccatg  | gtgatgtctc | 360  |
| tggtgataga  | cgtttatctg  | tggtaccgtc     | tcttatatct  | ggtcgattt   | atgcgattga | 420  |
| tactaaggaa  | aacccgaggg  | ctccgtcttt     | gtataagtat  | gttgatccta  | aagagattgc | 480  |
| tgataagMac  | tggattggcg  | tttctcaca      | cggctcattg  | cctcgccacg  | ggcgagatct | 540  |
| tggtgtctcg  | tcttgagagt  | gaagagggga     | atgctaaggg  | gaatgggttt  | cttcttsttg | 600  |
| actctgattt  | taacatcaag  | aataggtggg     | agaaaccagg  | acatagtcc   | ttgatgggt  | 660  |
| atgatgttct  | agatgttttt  | ggtaccaacc     | tccgcacaag  | accatgatca  | gcacatcttg | 720  |
| gggagcacct  | aaagcctctc  | ctaaagggtt     | caatcttcag  | cacgttgctg  | atggcttgta | 780  |
| tggaagtcac  | ctacatgttt  | atagttggcc     | aggaggtgaa  | atgaaacaat  | taattgacct | 840  |
| tggaaccgact | ggtctctacc  | ctttggagat     | tagattcttg  | catgatccat  | ctaaagatac | 900  |
| agggtttgtt  | gggagtgcct  | gtcagagtaa     | tatgataaga  | tttttcaaga  | acagtgtatg | 960  |
| aacatggagc  | catgaggttg  | ttatatcggt     | taaaccgttg  | aaagtgcgaa  | actgggatac | 1020 |
| tcacagaatg  | ccgggggttaa | tcaccgactt     | cttgatctcc  | ctcgatgacc  | gatttatta  | 1080 |
| ctttgtgaac  | tggtccatag  | gagacattcg     | tcagttacaac | atagaggacc  | ctaaaaaccc | 1140 |
| tgtaattaaca | gggcaaat    | gggttggagg     | attactacaa  | aaggggcagtc | ctgttaaggc | 1200 |

ggtgtggagaa gacggaacaa ctttccagtt cgaggttctt cagatcaagg ggaatctttt 1260  
acgaggttga cctcaaatga ttcagctgag cctcgatggg aaacgattgt atgcaacaaa 1320  
ctcgcgtttt agcgcatggg atcgtcagtt ttatcctgaa atcatggaga aaggctcaca 1380  
cataattcag attgatgttg atacagaaaa aggtggtctc accataaacc ctgattttctt 1440  
tgtggacttt ggtgatgaac cagacggtcc ttactagcc caccagatga gatattccagg 1500  
tggagactgc acttccgata tctggatttg aatttggctt tgttttagtg gtgttttgg 1560  
ttaagttaa attgagtttt attatttggg tgtgttttag taCgagttga ataaaaaagg 1620  
gagtaagatg actcagacaa ttaacacttg ttgtacatt ttgactccta tgtgtcttaa 1680  
gtaataaac ttttacaat tcgactg

(2) INFORMATION FOR SEQ ID NO:2537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..275
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1573625
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2537:

Met Ile Ser Thr Ser Trp Gly Ala Pro Lys Ala Phe Ser Lys Gly Phe  
1 5 10 15  
Asn Leu Gln His Val Ala Asp Gly Leu Tyr Gly Ser His Leu His Val  
20 25 30  
Tyr Ser Trp Pro Gly Gly Glu Met Lys Gln Leu Ile Asp Leu Gly Pro  
35 40 45  
Thr Gly Leu Leu Pro Leu Glu Ile Arg Phe Leu His Asp Pro Ser Lys  
50 55 60  
Asp Thr Gly Phe Val Gly Ser Ala Leu Ser Ser Asn Met Ile Arg Phe  
65 70 75 80  
Phe Lys Asn Ser Asp Glu Thr Trp Ser His Glu Val Val Ile Ser Val  
85 90 95  
Lys Pro Leu Lys Val Glu Asn Trp Ile Leu Pro Glu Met Pro Gly Leu  
100 105 110  
Ile Thr Asp Phe Leu Ile Ser Leu Asp Asp Arg Phe Ile Tyr Phe Val  
115 120 125  
Asn Trp Leu His Gly Asp Ile Arg Gln Tyr Asn Ile Glu Asp Pro Lys  
130 135 140  
Asn Pro Val Leu Thr Gly Gln Ile Trp Val Gly Gly Leu Leu Gln Lys  
145 150 155 160  
Gly Ser Pro Val Lys Ala Val Gly Glu Asp Gly Asn Thr Phe Gln Phe  
165 170 175  
Glu Val Pro Gln Ile Lys Gly Lys Ser Leu Arg Gly Gly Pro Gln Met  
180 185 190  
Ile Gln Leu Ser Leu Asp Gly Lys Arg Leu Tyr Ala Thr Asn Ser Leu  
195 200 205  
Phe Ser Ala Trp Asp Arg Gln Phe Tyr Pro Glu Ile Met Glu Lys Gly  
210 215 220  
Ser His Ile Ile Gln Ile Asp Val Asp Thr Glu Lys Gly Gly Leu Thr  
225 230 235 240  
Ile Asn Pro Asp Phe Phe Val Asp Phe Gly Asp Glu Pro Asp Gly Pro  
245 250 255  
Ser Leu Ala His Glu Met Arg Tyr Pro Gly Gly Asp Cys Thr Ser Asp  
260 265 270  
Ile Trp Ile  
275

(2) INFORMATION FOR SEQ ID NO:2538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid

SEQUENCE 1573625

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..236  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2538:

Met Lys Gln Leu Ile Asp Leu Gly Pro Thr Gly Leu Leu Pro Leu Glu  
1 5 10 15  
Ile Arg Phe Leu His Asp Pro Ser Lys Asp Thr Gly Phe Val Gly Ser  
20 25 30  
Ala Leu Ser Ser Asn Met Ile Arg Phe Phe Lys Asn Ser Asp Glu Thr  
35 40 45  
Trp Ser His Glu Val Val Ile Ser Val Lys Pro Leu Lys Val Glu Asn  
50 55 60  
Trp Ile Leu Pro Glu Met Pro Gly Leu Ile Thr Asp Phe Leu Ile Ser  
65 70 75 80  
Leu Asp Asp Arg Phe Ile Tyr Phe Val Asn Trp Leu His Gly Asp Ile  
85 90 95  
Arg Gln Tyr Asn Ile Glu Asp Pro Lys Asn Pro Val Leu Thr Gly Gln  
100 105 110  
Ile Trp Val Gly Gly Leu Leu Gln Lys Gly Ser Pro Val Lys Ala Val  
115 120 125  
Gly Glu Asp Gly Asn Thr Phe Gln Phe Glu Val Pro Gln Ile Lys Gly  
130 135 140  
Lys Ser Leu Arg Gly Gly Pro Gln Met Ile Gln Leu Ser Leu Asp Gly  
145 150 155 160  
Lys Arg Leu Tyr Ala Thr Asn Ser Leu Phe Ser Ala Trp Asp Arg Gln  
165 170 175  
Phe Tyr Pro Glu Ile Met Glu Lys Gly Ser His Ile Ile Gln Ile Asp  
180 185 190  
Val Asp Thr Glu Lys Gly Gly Leu Thr Ile Asn Pro Asp Phe Phe Val  
195 200 205  
Asp Phe Gly Asp Glu Pro Asp Gly Pro Ser Leu Ala His Glu Met Arg  
210 215 220  
Tyr Pro Gly Gly Asp Cys Thr Ser Asp Ile Trp Ile  
225 230 235

(2) INFORMATION FOR SEQ ID NO:2539:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 199 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..199  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2539:

Met Ile Arg Phe Phe Lys Asn Ser Asp Glu Thr Trp Ser His Glu Val  
1 5 10 15  
Val Ile Ser Val Lys Pro Leu Lys Val Glu Asn Trp Ile Leu Pro Glu  
20 25 30  
Met Pro Gly Leu Ile Thr Asp Phe Leu Ile Ser Leu Asp Asp Arg Phe  
35 40 45  
Ile Tyr Phe Val Asn Trp Leu His Gly Asp Ile Arg Gln Tyr Asn Ile  
50 55 60  
Glu Asp Pro Lys Asn Pro Val Leu Thr Gly Gln Ile Trp Val Gly Gly  
65 70 75 80  
Leu Leu Gln Lys Gly Ser Pro Val Lys Ala Val Gly Glu Asp Gly Asn

85 90 95  
Thr Phe Gln Phe Glu Val Pro Gln Ile Lys Gly Lys Ser Leu Arg Gly  
100 105 110  
Gly Pro Gln Met Ile Gln Leu Ser Leu Asp Gly Lys Arg Leu Tyr Ala  
115 120 125  
Thr Asn Ser Leu Phe Ser Ala Trp Asp Arg Gln Phe Tyr Pro Glu Ile  
130 135 140  
Met Glu Lys Gly Ser His Ile Ile Gln Ile Asp Val Asp Thr Glu Lys  
145 150 155 160  
Gly Gly Leu Thr Ile Asn Pro Asp Phe Phe Val Asp Phe Gly Asp Glu  
165 170 175  
Pro Asp Gly Pro Ser Leu Ala His Glu Met Arg Tyr Pro Gly Gly Asp  
180 185 190  
Cys Thr Ser Asp Ile Trp Ile  
195

(2) INFORMATION FOR SEQ ID NO:2540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..777

(D) OTHER INFORMATION: / Ceres Seq. ID 1573628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2540:

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| atcttcacaa | ttttttttcg  | tctctcaaac | caacgcaaaa | gaacaatgtc | taacgttgtta | 60  |
| gtaatcgccg | ttgtttctcat | cgtagcatcg | ctaacaggac | atgtgtcagc | acaaatggat  | 120 |
| atgtctccgt | cgctcaggacc | atcggttgca | ccagactgca | tggcgaacct | aatgaacatg  | 180 |
| acaggctgtc | tctgtacgt   | tacggtcgga | gaaggtggtg | gtgcgagcaa | gccggacaag  | 240 |
| acgtgtgtgc | cgcgctacgc  | ggggctagtg | gagagctcgc | cgcaatgctt | atgttacctc  | 300 |
| ctctccgggt | acatggcgccg | acaaacttga | atcaagattg | ataaggcaaa | ggctctcaaa  | 360 |
| cttcccgga  | tttgcggcgt  | gatcactccc | gatccctcac | tttgtctct  | ttttggaatt  | 420 |
| cctgttgga  | cacctgtagc  | tatgggagac | gaggagacct | ccccagccta | tgctccaggt  | 480 |
| tcgatgtcag | aatcaccagg  | aggatttggg | tcgggtCctt | cggttagtag | aggagcgat   | 540 |
| gcaccaagca | gtgcacctta  | ttctcgtttt | ctcaacttta | taattttccc | attagctttt  | 600 |
| gcattttaca | tctttttctg  | atttcattct | cttccaacca | ttacaacaac | cattattttg  | 660 |
| tatgtatttt | cttaaaaagag | tattattgct | ttgttaggtc | atgttcttga | attttact    | 720 |
| ttgtgtatcc | acggattatt  | tcttcattca | tcttattgaa | taaagattgt | ttttttt     |     |

(2) INFORMATION FOR SEQ ID NO:2541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1573629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2541:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Phe | Thr | Ile | Phe | Phe | Arg | Leu | Ser | Asn | Gln | Arg | Lys | Arg | Thr | Met |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |     |
| Ser | Asn | Val | Val | Val | Ile | Ala | Val | Val | Leu | Ile | Val | Ala | Ser | Leu | Thr |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Gly | His | Val | Ser | Ala | Gln | Met | Asp | Met | Ser | Pro | Ser | Ser | Gly | Pro | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Gly | Ala | Pro | Asp | Cys | Met | Ala | Asn | Leu | Met | Asn | Met | Thr | Gly | Cys | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ser | Tyr | Val | Thr | Val | Gly | Glu | Gly | Gly | Ala | Ala | Lys | Pro | Asp | Lys |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Cys | Cys | Pro | Ala | Leu | Ala | Gly | Leu | Val | Glu | Ser | Ser | Pro | Gln | Cys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Cys | Tyr | Leu | Leu | Ser | Gly | Asp | Met | Ala | Ala | Gln | Leu | Gly | Ile | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Asp | Lys | Ala | Lys | Ala | Leu | Lys | Leu | Pro | Gly | Val | Cys | Gly | Val | Ile |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Pro | Asp | Pro | Ser | Leu | Cys | Ser | Leu | Phe | Gly | Ile | Pro | Val | Gly | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Val | Ala | Met | Gly | Asp | Glu | Gly | Ala | Ser | Pro | Ala | Tyr | Ala | Pro | Gly |
|     | 145 |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Met | Ser | Glu | Ser | Pro | Gly | Gly | Phe | Gly | Ser | Gly | Pro | Ser | Ala | Ser |
|     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |     |
| Arg | Gly | Ser | Asp | Ala | Pro | Ser | Ser | Ala | Pro | Tyr | Ser | Arg | Phe | Leu | Asn |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Leu | Ile | Ile | Phe | Pro | Leu | Ala | Phe | Ala | Phe | Tyr | Ile | Phe | Cys |     |     |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1573630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2542:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Asn | Val | Val | Val | Ile | Ala | Val | Val | Leu | Ile | Val | Ala | Ser | Leu |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Thr | Gly | His | Val | Ser | Ala | Gln | Met | Asp | Met | Ser | Pro | Ser | Ser | Gly | Pro |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ser | Gly | Ala | Pro | Asp | Cys | Met | Ala | Asn | Leu | Met | Asn | Met | Thr | Gly | Cys |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Leu | Ser | Tyr | Val | Thr | Val | Gly | Glu | Gly | Gly | Gly | Ala | Ala | Lys | Pro | Asp |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Lys | Thr | Cys | Cys | Pro | Ala | Leu | Ala | Gly | Leu | Val | Glu | Ser | Ser | Pro | Gln |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Cys | Leu | Cys | Tyr | Leu | Leu | Ser | Gly | Asp | Met | Ala | Ala | Gln | Leu | Gly | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Ile | Asp | Lys | Ala | Lys | Ala | Leu | Lys | Leu | Pro | Gly | Val | Cys | Gly | Val |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ile | Thr | Pro | Asp | Pro | Ser | Leu | Cys | Ser | Leu | Phe | Gly | Ile | Pro | Val | Gly |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Ala | Pro | Val | Ala | Met | Gly | Asp | Glu | Gly | Ala | Ser | Pro | Ala | Tyr | Ala | Pro |
|     | 130 |     |     | 135 |     |     |     |     |     |     | 140 |     |     |     |     |
| Gly | Ser | Met | Ser | Glu | Ser | Pro | Gly | Gly | Phe | Gly | Ser | Gly | Pro | Ser | Ala |
|     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |     |
| Ser | Arg | Gly | Ser | Asp | Ala | Pro | Ser | Ser | Ala | Pro | Tyr | Ser | Arg | Phe | Leu |
|     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |     |
| Asn | Leu | Ile | Ile | Phe | Pro | Leu | Ala | Phe | Ala | Phe | Tyr | Ile | Phe | Cys |     |
|     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2543:

(2) INFORMATION FOR SEQ ID NO:2544:

(A) LENGTH: 788 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
```

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:
```

(A) NAME/KEY: -

(B) LOCATION: 1..788

(D) OTHER INFORMATION: / Ceres Seq. ID 1573632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2544:

|            |             |             |             |             |             |     |
|------------|-------------|-------------|-------------|-------------|-------------|-----|
| atttatcttc | aCaatttttG  | tttgcgtctct | caaaccaacg  | caaaagaaca  | atgtctaacg  | 60  |
| ttgtagtaat | cgcctgtgtt  | ctcatctcgt  | catcgctaac  | aggacatggt  | tcgcacacaa  | 120 |
| tgtgatgttc | ctcgtcgtca  | ggaccatcga  | gtgcaccaga  | ctgcgatggt  | aacctaatga  | 180 |
| acatgacagg | ctgtctctcgc | tacgttaacg  | tgcggagaag  | tgggtgttgG  | gccaaagccgg | 240 |
| acaagaagtc | tgtgtccggcg | tacGcggggg  | taagtggaaag | ctgcgccaca  | tgtgatgtt   | 300 |
| acotctctct | cggtagacatg | cgccgaccaa  | tgtgaataca  | tattcaattg  | gccaaagttct | 360 |
| tcacaactct | cggagtttgc  | gcgctgatca  | cttcgcgatc  | gtatcgtatg  | tcctatgttc  | 420 |
| gaattctcgt | tggagcaact  | gtagctatca  | gagacgagg   | agcctcccc   | gcctatgtct  | 480 |
| caggttgcag | gtcagggtca  | gataccaccg  | gaggatgttg  | tgcgggtCct  | tcggctagta  | 540 |
| gagggagaca | tgacccaacc  | agtgacacct  | attctcgttt  | tctcaattct  | ataattttcc  | 600 |
| cattagcttt | tgcattttac  | atctttttct  | gatttcaatc  | ttctccaacc  | attaacaaca  | 660 |
| ccattatttt | ttagtatttt  | ctcttaaaaga | gtattattgc  | ttttgtaggc  | tatgtctctg  | 720 |
| aattttatcc | tttgtgtatc  | caacgattat  | ttcttcattc  | atctctattga | ataaagattg  | 780 |
| ttttttttc  |             |             |             |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2545:

### (i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..209

(D) OTHER INFORMATION: / Ceres Seq. ID 1573633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2545:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Ser | Ser | Gln | Phe | Leu | Phe | Arg | Leu | Ser | Asn | Gln | Arg | Lys | Arg | Thr |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Met | Ser | Asn | Val | Val | Val | Ile | Ala | Val | Val | Leu | Ile | Val | Ala | Ser | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Thr | Gly | His | Val | Ser | Ala | Gln | Met | Asp | Met | Ser | Pro | Ser | Ser | Gly | Pro |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |  |
| Ser | Gly | Ala | Pro | Asp | Cys | Met | Ala | Asn | Leu | Met | Asn | Met | Thr | Gly | Cys |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Leu | Ser | Tyr | Val | Thr | Val | Gly | Glu | Gly | Gly | Gly | Ala | Ala | Lys | Pro | Asp |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Lys | Thr | Cys | Cys | Pro | Ala | Leu | Ala | Gly | Leu | Val | Glu | Ser | Ser | Pro | Gln |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Cys | Leu | Cys | Tyr | Leu | Leu | Ser | Gly | Asp | Met | Ala | Ala | Gln | Leu | Gly | Ile |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Lys | Ile | Asp | Lys | Ala | Lys | Ala | Leu | Lys | Leu | Pro | Gly | Val | Cys | Gly | Val |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ile | Thr | Ser | Asp | Pro | Ser | Leu | Cys | Ser | Leu | Phe | Gly | Ile | Pro | Val | Gly |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ala | Pro | Val | Ala | Met | Gly | Asp | Glu | Gly | Ala | Ser | Pro | Ala | Tyr | Ala | Pro |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Gly | Ser | Met | Ser | Gly | Ala | Glu | Ser | Pro | Gly | Gly | Phe | Gly | Ser | Gly | Pro |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Ser | Ala | Ser | Arg | Gly | Ser | Asp | Ala | Pro | Ser | Ser | Ala | Pro | Tyr | Ser | Arg |  |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |
| Phe | Leu | Asn | Leu | Ile | Ile | Phe | Pro | Leu | Ala | Phe | Ala | Phe | Tyr | Ile | Phe |  |
|     |     |     | 195 |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |
| Cys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2546:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1573634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2546:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Asn | Val | Val | Val | Ile | Ala | Val | Val | Leu | Ile | Val | Ala | Ser | Leu |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Thr | Gly | His | Val | Ser | Ala | Gln | Met | Asp | Met | Ser | Pro | Ser | Ser | Gly | Pro |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Ser | Gly | Ala | Pro | Asp | Cys | Met | Ala | Asn | Leu | Met | Asn | Met | Thr | Gly | Cys |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu | Ser | Tyr | Val | Thr | Val | Gly | Glu | Gly | Gly | Gly | Ala | Ala | Lys | Pro | Asp |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Lys | Thr | Cys | Cys | Pro | Ala | Leu | Ala | Gly | Leu | Val | Glu | Ser | Ser | Pro | Gln |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Cys | Leu | Cys | Tyr | Leu | Leu | Ser | Gly | Asp | Met | Ala | Ala | Gln | Leu | Gly | Ile |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Lys | Ile | Asp | Lys | Ala | Lys | Ala | Leu | Lys | Leu | Pro | Gly | Val | Cys | Gly | Val |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| Ile | Thr | Ser | Asp | Pro | Ser | Leu | Cys | Ser | Leu | Phe | Gly | Ile | Pro | Val | Gly |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ala | Pro | Val | Ala | Met | Gly | Asp | Glu | Gly | Ala | Ser | Pro | Ala | Tyr | Ala | Pro |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |  |



Gly Ser Met Ser Gly Ala Glu Ser Pro Gly Gly Phe Gly Ser Gly Pro  
145 150 155 160  
Ser Ala Ser Arg Gly Ser Asp Ala Pro Ser Ser Ala Pro Tyr Ser Arg  
165 170 175  
Phe Leu Asn Leu Ile Ile Phe Pro Leu Ala Phe Ala Phe Tyr Ile Phe  
180 185 190

Cys

(2) INFORMATION FOR SEQ ID NO:2547:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1573635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2547:

Met Asp Met Ser Pro Ser Ser Gly Pro Ser Gly Ala Pro Asp Cys Met  
1 5 10 15  
Ala Asn Leu Met Asn Met Thr Gly Cys Leu Ser Tyr Val Thr Val Gly  
20 25 30  
Glu Gly Gly Gly Ala Ala Lys Pro Asp Lys Thr Cys Cys Pro Ala Leu  
35 40 45  
Ala Gly Leu Val Glu Ser Ser Pro Gln Cys Leu Cys Tyr Leu Leu Ser  
50 55 60  
Gly Asp Met Ala Ala Gln Leu Gly Ile Lys Ile Asp Lys Ala Lys Ala  
65 70 75 80  
Leu Lys Leu Pro Gly Val Cys Gly Val Ile Thr Ser Asp Pro Ser Leu  
85 90 95  
Cys Ser Leu Phe Gly Ile Pro Val Gly Ala Pro Val Ala Met Gly Asp  
100 105 110  
Glu Gly Ala Ser Pro Ala Tyr Ala Pro Gly Ser Met Ser Gly Ala Glu  
115 120 125  
Ser Pro Gly Gly Phe Gly Ser Gly Pro Ser Ala Ser Arg Gly Ser Asp  
130 135 140  
Ala Pro Ser Ser Ala Pro Tyr Ser Arg Phe Leu Asn Leu Ile Ile Phe  
145 150 155 160  
Pro Leu Ala Phe Ala Phe Tyr Ile Phe Cys  
165 170

(2) INFORMATION FOR SEQ ID NO:2548:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1403 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1403

(D) OTHER INFORMATION: / Ceres Seq. ID 1573636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2548:

aaaaatTTTTT aaaggGcaag acctcctctg ttccatatt ctcaccacag aagaactctt 60  
gagggtttct ctttctctca coattggcgaa accggtgttc attgaagtgt ataattctaa 120  
tgggaaatcac agagttgtta gcacaaaacc gatgcctgga actcgctgga tcaatctctt 180  
ggtagaccGaa ggttgtcgcg ttgagatagt tcatttgaag aagacaatct tgctctgtaga 240  
agatatcatt gatctgagtc gagacaagtg tgatggagtc atcggtcagt tgacggaaga 300  
ttggggagag actctgttct cagctttgag caaagctgga gggaaagctt tcaagtaaac 360  
ggccgttggt tataacaacg ttgatgttga agctgccaat aagtatggaa ttgctgtcgg 420

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| taaacactccg | ggagtggtga  | ctgagacgac | ggctgaacta  | gctgcttctc  | ttctcttggc  | 480  |
| tgctgcgaaga | agaattgttg  | aagccgacga | attcatgaga  | ggtgctgtgt  | acgagggatg  | 540  |
| gcttctctcat | ctgtttgttg  | ggaacttact | taaaaggacag | actgttgagc  | ttattggagc  | 600  |
| tggaacgtatt | ggactctgctt | atgctagaa  | gatggtggaa  | gggttcaaga  | tgaatttgat  | 660  |
| ctactttgat  | ctttaccaat  | ccactctgct | tgagaaatct  | gtgcacagctt | atggacagtt  | 720  |
| cttgaaaaga  | aatggagaa   | aaactgtgac | atggaaaacga | gcttctgtcca | tggaaggaggt | 780  |
| gctgcgtgag  | gctgatctga  | taagtcttca | cccggtgctg  | gacaaaacca  | cttaccatct  | 840  |
| tgtaacaacag | gagaggcttg  | ccatgatgaa | aaaggaagca  | atccttgtga  | actgcagcag  | 900  |
| aggtcctgtg  | atcgatgagg  | cagcttttgt | cgaacatctc  | aaagagaacc  | cgatgttccg  | 960  |
| agttgtctc   | gatgtgttgc  | aggaagagcc | attcatgaaa  | ccagggtctg  | ctgatatgaa  | 1020 |
| aaacgctatt  | gttcttctc   | acattgcttc | tgcttccaag  | tggactctgt  | aaggaatggc  | 1080 |
| tNacgcttgc  | agctctcaac  | gttctcgaa  | gagtcacaag  | gtacccgatt  | tggcatgacc  | 1140 |
| cgaaacgagt  | cgaatccatt  | ttgaacgaaa | acgcttcacc  | gcccactgcc  | agtcacaaga  | 1200 |
| tcgtcaactc  | aaagggccta  | ggattgcctg | ttctgaagct  | atgagttaag  | tatgaagaag  | 1260 |
| gggagatttg  | gaagaatcct  | tttagtgaa  | atatgatggt  | gtcaagttgt  | gtttatgtat  | 1320 |
| tgtatatgaa  | acaaccatgt  | tggatcatat | aatcactcc   | tttaaaagt   | tacattgttg  | 1380 |
| atgagtctat  | tagacgatta  | ccc        |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2549:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..378

(D) OTHER INFORMATION: / Ceres Seq. ID 1573637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2549:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Phe | Phe | Lys | Arg | Gln | Asp | Leu | Leu | Cys | Phe | His | Ile | Leu | Thr | Thr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Glu | Glu | Leu | Leu | Arg | Leu | Ser | Leu | Phe | Ser | Thr | Met | Ala | Lys | Pro | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ile | Glu | Val | Tyr | Asn | Pro | Asn | Gly | Lys | Tyr | Arg | Val | Val | Ser | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Pro | Met | Pro | Gly | Thr | Arg | Trp | Ile | Asn | Leu | Leu | Val | Asp | Gln | Gly |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Cys | Arg | Val | Glu | Ile | Cys | His | Leu | Lys | Lys | Thr | Ile | Leu | Ser | Val | Glu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Ile | Ile | Asp | Leu | Ile | Gly | Asp | Lys | Cys | Asp | Gly | Val | Ile | Gly | Gln |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Thr | Glu | Asp | Trp | Gly | Glu | Thr | Leu | Phe | Ser | Ala | Leu | Ser | Lys | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Gly | Lys | Ala | Phe | Ser | Asn | Met | Ala | Val | Gly | Tyr | Asn | Asn | Val | Asp |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Val | Glu | Ala | Ala | Asn | Lys | Tyr | Gly | Ile | Ala | Val | Gly | Asn | Thr | Pro | Gly |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Val | Leu | Thr | Glu | Thr | Thr | Ala | Glu | Leu | Ala | Ala | Ser | Leu | Ser | Leu | Ala |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ala | Ala | Arg | Arg | Ile | Val | Glu | Ala | Asp | Glu | Phe | Met | Arg | Gly | Gly | Leu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Tyr | Glu | Gly | Trp | Leu | Pro | His | Leu | Phe | Val | Gly | Asn | Leu | Leu | Lys | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gln | Thr | Val | Gly | Val | Ile | Gly | Ala | Gly | Arg | Ile | Gly | Ser | Ala | Tyr | Ala |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Met | Met | Val | Glu | Gly | Phe | Lys | Met | Asn | Leu | Ile | Tyr | Phe | Asp | Leu |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Tyr | Gln | Ser | Thr | Arg | Leu | Glu | Lys | Phe | Val | Thr | Ala | Tyr | Gly | Gln | Phe |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Leu | Lys | Ala | Asn | Gly | Glu | Gln | Pro | Val | Thr | Trp | Lys | Arg | Ala | Ser | Ser |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |

Met Glu Glu Val Leu Arg Glu Ala Asp Leu Ile Ser Leu His Pro Val  
260 265 270  
Leu Asp Lys Thr Thr Tyr His Leu Val Asn Lys Glu Arg Leu Ala Met  
275 280 285  
Met Lys Lys Glu Ala Ile Leu Val Asn Cys Ser Arg Gly Pro Val Ile  
290 295 300  
Asp Glu Ala Ala Leu Val Glu His Leu Lys Glu Asn Pro Met Phe Arg  
305 310 315 320  
Val Gly Leu Asp Val Phe Glu Glu Glu Pro Phe Met Lys Pro Gly Leu  
325 330 335  
Ala Asp Met Lys Asn Ala Ile Val Val Pro His Ile Ala Ser Ala Ser  
340 345 350  
Lys Trp Thr Arg Glu Gly Met Ala Xaa Ala Cys Ser Ser Gln Arg Pro  
355 360 365  
Arg Lys Ser Gln Arg Val Pro Asp Leu Ala  
370 375

(2) INFORMATION FOR SEQ ID NO:2550:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..351

(D) OTHER INFORMATION: / Ceres Seq. ID 1573638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2550:

Met Ala Lys Pro Val Ser Ile Glu Val Tyr Asn Pro Asn Gly Lys Tyr  
1 5 10 15  
Arg Val Val Ser Thr Lys Pro Met Pro Gly Thr Arg Trp Ile Asn Leu  
20 25 30  
Leu Val Asp Gln Gly Cys Arg Val Glu Ile Cys His Leu Lys Lys Thr  
35 40 45  
Ile Leu Ser Val Glu Asp Ile Ile Asp Leu Ile Gly Asp Lys Cys Asp  
50 55 60  
Gly Val Ile Gly Gln Leu Thr Glu Asp Trp Gly Glu Thr Leu Phe Ser  
65 70 75 80  
Ala Leu Ser Lys Ala Gly Gly Lys Ala Phe Ser Asn Met Ala Val Gly  
85 90 95  
Tyr Asn Asn Val Asp Val Glu Ala Ala Asn Lys Tyr Gly Ile Ala Val  
100 105 110  
Gly Asn Thr Pro Gly Val Leu Thr Glu Thr Thr Ala Glu Leu Ala Ala  
115 120 125  
Ser Leu Ser Leu Ala Ala Ala Arg Arg Ile Val Glu Ala Asp Glu Phe  
130 135 140  
Met Arg Gly Gly Leu Tyr Glu Gly Trp Leu Pro His Leu Phe Val Gly  
145 150 155 160  
Asn Leu Leu Lys Gly Gln Thr Val Gly Val Ile Gly Ala Gly Arg Ile  
165 170 175  
Gly Ser Ala Tyr Ala Arg Met Met Val Glu Gly Phe Lys Met Asn Leu  
180 185 190  
Ile Tyr Phe Asp Leu Tyr Gln Ser Thr Arg Leu Glu Lys Phe Val Thr  
195 200 205  
Ala Tyr Gly Gln Phe Leu Lys Ala Asn Gly Glu Gln Pro Val Thr Trp  
210 215 220  
Lys Arg Ala Ser Ser Met Glu Glu Val Leu Arg Glu Ala Asp Leu Ile  
225 230 235 240  
Ser Leu His Pro Val Leu Asp Lys Thr Thr Tyr His Leu Val Asn Lys  
245 250 255  
Glu Arg Leu Ala Met Met Lys Lys Glu Ala Ile Leu Val Asn Cys Ser

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Gly | Pro | Val | Ile | Asp | Glu | Ala | Ala | Leu | Val | Glu | His | Leu | Lys | Glu |
| 275 |     |     |     |     |     |     | 260 |     |     |     |     | 285 |     |     |     |
| Asn | Pro | Met | Phe | Arg | Val | Gly | Leu | Asp | Val | Phe | Glu | Glu | Glu | Pro | Phe |
| 290 |     |     |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Met | Lys | Pro | Gly | Leu | Ala | Asp | Met | Lys | Asn | Ala | Ile | Val | Val | Pro | His |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ile | Ala | Ser | Ala | Ser | Lys | Trp | Thr | Arg | Glu | Gly | Met | Ala | Xaa | Ala | Cys |
|     |     |     |     |     | 325 |     |     |     | 330 |     |     |     |     | 335 |     |
| Ser | Ser | Gln | Arg | Pro | Arg | Lys | Ser | Gln | Arg | Val | Pro | Asp | Leu | Ala |     |
|     |     |     |     |     | 340 |     |     | 345 |     |     |     |     | 350 |     |     |

(2) INFORMATION FOR SEQ ID NO:2551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..328

(D) OTHER INFORMATION: / Ceres Seq. ID 1573639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2551:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Gly | Thr | Arg | Trp | Ile | Asn | Leu | Leu | Val | Asp | Gln | Gly | Cys | Arg |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Glu | Ile | Cys | His | Leu | Lys | Lys | Thr | Ile | Leu | Ser | Val | Glu | Asp | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Asp | Leu | Ile | Gly | Asp | Lys | Cys | Asp | Gly | Val | Ile | Gly | Gln | Leu | Thr |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Glu | Asp | Trp | Gly | Glu | Thr | Leu | Phe | Ser | Ala | Leu | Ser | Lys | Ala | Gly | Gly |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Ala | Phe | Ser | Asn | Met | Ala | Val | Gly | Tyr | Asn | Asn | Val | Asp | Val | Glu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Ala | Asn | Lys | Tyr | Gly | Ile | Ala | Val | Gly | Asn | Thr | Pro | Gly | Val | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Thr | Glu | Thr | Thr | Ala | Glu | Leu | Ala | Ala | Ser | Leu | Ser | Leu | Ala | Ala |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Arg | Ile | Val | Glu | Ala | Asp | Glu | Phe | Met | Arg | Gly | Gly | Leu | Tyr | Glu |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Trp | Leu | Pro | His | Leu | Phe | Val | Gly | Asn | Leu | Leu | Lys | Gly | Gln | Thr |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Gly | Val | Ile | Gly | Ala | Gly | Arg | Ile | Gly | Ser | Ala | Tyr | Ala | Arg | Met |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Met | Val | Glu | Gly | Phe | Lys | Met | Asn | Leu | Ile | Tyr | Phe | Asp | Leu | Tyr | Gln |
|     |     |     |     |     | 165 |     |     |     | 170 |     |     |     | 175 |     |     |
| Ser | Thr | Arg | Leu | Glu | Lys | Phe | Val | Thr | Ala | Tyr | Gly | Gln | Phe | Leu | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Asn | Gly | Glu | Gln | Pro | Val | Thr | Trp | Lys | Arg | Ala | Ser | Ser | Met | Glu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Val | Leu | Arg | Glu | Ala | Asp | Leu | Ile | Ser | Leu | His | Pro | Val | Leu | Asp |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Thr | Thr | Tyr | His | Leu | Val | Asn | Lys | Glu | Arg | Leu | Ala | Met | Met | Lys |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Lys | Glu | Ala | Ile | Leu | Val | Asn | Cys | Ser | Arg | Gly | Pro | Val | Ile | Asp | Glu |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Ala | Ala | Leu | Val | Glu | His | Leu | Lys | Glu | Asn | Pro | Met | Phe | Arg | Val | Gly |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Leu | Asp | Val | Phe | Glu | Glu | Glu | Pro | Phe | Met | Lys | Pro | Gly | Leu | Ala | Asp |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Met | Lys | Asn | Ala | Ile | Val | Val | Pro | His | Ile | Ala | Ser | Ala | Ser | Lys | Trp |
| 290 |     |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |

Thr Arg Glu Gly Met Ala Xaa Ala Cys Ser Ser Gln Arg Pro Arg Lys  
305 310 315 320  
Ser Gln Arg Val Pro Asp Leu Ala  
325

(2) INFORMATION FOR SEQ ID NO:2552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1318
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2552:

```
aaaaccocaaa cccctactca cttttttcac attctttctc tctctcgata tcatctaaat 60
ctctctcttg atctcaattt cgcacaaatgg ctgacaaaga gatcagaatc ggaatcaacg 120
gtttcggaag aatcggtcgt ttggttgcta gagttgtctc tcagagggat gatgttgagc 180
tcgtcgctgt taacgatcct ttcatacaca ccgagtatcat gacatacatg ttttaagtatg 240
acagtgttca cggctcagtg aagcaccatg agcttaagggt gaaggatgac aaaactcttc 300
ctttcgtgtg gaagccagtc actgttttgc gcatcaggaa cctcgaggac atccccatggg 360
gtgaggtcgg agctgacttt gttgttgagt ctactggtgt cttcactgac aaagacaagg 420
ctgctgctca cttgaagggt ggtgctaaaa aggttgtcat ctctgcccc aacaaagatg 480
cgccccatgt cgttgttggt gtcAacgagc acgagtacaa gtctgacctt gacattgttt 540
ccaaacgtag ttgaccacct aactgccttg ctctctctgc caaggttatt aatgacaggt 600
ttggcattgt tgagggactc atgaccactg tccactctat cactgctact cagaagacag 660
ttgatgttcc atcaatgaag gactggagag gtggaagagc tgcttccttc aacattatc 720
ctagacgacac tgggtgccgc aaggtcgttg gaaaagtgtt gccatccctc aatggaaaat 780
tgacccgaat gtctttccgt gtcccaacgc ttgatgtctc agttgttgat ctcaccgtta 840
gacttgagaa agctgcaaca tacgacgaaa tcaagaaggc catcaaggag gaatctgaag 900
gcacaaatgaa gggaaatttg ggatacaact aggatgatgt ttgtctacc gacttttgtt 960
gtgacaacag gtcaagcatt ttcatgacca aggtcgggat tgcattgagc gacaaattgt 1020
tgaagtgtgt gtcatggtac gacaaacgaat ggggttacag tttcgtgtc ttgacctta 1080
tcgttccatc gtcaaaagcc taagcttaca ccggcgagag tttgtgtgtg gttgagttc 1140
tactgttctg aataaaaaaa aggagaaaaa aaaactcgag ttgttatgtt ttttcaactg 1200
ttccatgcgc agtcatgaga ttgttagct tttgtcttt tgctttctct taatgtttcc 1260
ctgctttatt tactgaaacc attggtttg tttttatgt taattaagtt tttagtcc
```

(2) INFORMATION FOR SEQ ID NO:2553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..338
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2553:

```
Met Ala Asp Lys Lys Ile Arg Ile Gly Ile Asn Gly Phe Gly Arg Ile
1 5 10 15
Gly Arg Leu Val Ala Arg Val Val Leu Gln Arg Asp Asp Val Glu Leu
20 25 30
Val Ala Val Asn Asp Pro Phe Ile Thr Thr Glu Tyr Met Thr Tyr Met
35 40 45
Phe Lys Tyr Asp Ser Val His Gly Gln Trp Lys His His Glu Leu Lys
50 55 60
Val Lys Asp Asp Lys Thr Leu Leu Phe Gly Glu Lys Pro Val Thr Val
65 70 75 80
Phe Gly Ile Arg Asn Pro Glu Asp Ile Pro Trp Gly Glu Ala Gly Ala
```

# 1. Introduction

(i) SEQUENCE CHARACTERISTICS:

- ```
(17) (A) LENGTH: 294 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..294
      (D) OTHER INFORMATION: / Ceres Seq. ID 1573642
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2554:																	
Met	Thr	Tyr	Met	Phe	Lys	Tyr	Asp	Ser	Val	His	Gly	Gln	Trp	Lys	His		
1			5						10					15			
His	Glu	Leu	Lys	Val	Lys	Asp	Asp	Lys	Thr	Leu	Leu	Phe	Gly	Glu	Lys		
			20					25						30			
Pro	Val	Thr	Val	Phe	Gly	Ile	Arg	Asn	Pro	Glu	Asp	Ile	Pro	Trp	Gly		
			35				40							45			
Glu	Ala	Gly	Ala	Asp	Phe	Val	Val	Glu	Ser	Thr	Gly	Val	Phe	Thr	Asp		
			50				55					60					
Lys	Asp	Lys	Ala	Ala	Ala	His	Leu	Lys	Gly	Gly	Ala	Lys	Lys	Val	Val		
65					70						75				80		
Ile	Ser	Ala	Pro	Ser	Lys	Asp	Ala	Pro	Met	Phe	Val	Val	Gly	Val	Asn		
				85					90						95		
Glu	His	Glu	Tyr	Lys	Ser	Asp	Leu	Asp	Ile	Val	Ser	Asn	Ala	Ser	Cys		
			100					105					110				
Thr	Thr	Asn	Cys	Leu	Ala	Pro	Leu	Ala	Lys	Val	Ile	Asn	Asp	Arg	Phe		
			115				120						125				

Gly Ile Val Glu Gly Leu Met Thr Thr Val His Ser Ile Thr Ala Thr
130 135 140
Gln Lys Thr Val Asp Gly Pro Ser Met Lys Asp Trp Arg Gly Gly Arg
145 150 155 160
Ala Ala Ser Phe Asn Ile Ile Pro Ser Ser Thr Gly Ala Ala Lys Ala
165 170 175
Val Gly Lys Val Leu Pro Ser Leu Asn Gly Lys Leu Thr Gly Met Ser
180 185 190
Phe Arg Val Pro Thr Val Asp Val Ser Val Val Asp Leu Thr Val Arg
195 200 205
Leu Glu Lys Ala Ala Thr Tyr Asp Glu Ile Lys Lys Ala Ile Lys Glu
210 215 220
Glu Ser Glu Gly Lys Met Lys Gly Ile Leu Gly Tyr Thr Glu Asp Asp
225 230 235 240
Val Val Ser Thr Asp Phe Val Gly Asp Asn Arg Ser Ser Ile Phe Asp
245 250 255
Ala Lys Ala Gly Ile Ala Leu Ser Asp Lys Phe Val Lys Leu Val Ser
260 265 270
Trp Tyr Asp Asn Glu Trp Gly Tyr Ser Ser Arg Val Val Asp Leu Ile
275 280 285
Val His Met Ser Lys Ala
290

(2) INFORMATION FOR SEQ ID NO:2555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..291
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2555:

Met Phe Lys Tyr Asp Ser Val His Gly Gln Trp Lys His His Glu Leu
1 5 10 15
Lys Val Lys Asp Asp Lys Thr Leu Leu Phe Gly Glu Lys Pro Val Thr
20 25 30
Val Phe Gly Ile Arg Asn Pro Glu Asp Ile Pro Trp Gly Glu Ala Gly
35 40 45
Ala Asp Phe Val Val Glu Ser Thr Gly Val Phe Thr Asp Lys Asp Lys
50 55 60
Ala Ala Ala His Leu Lys Gly Gly Ala Lys Lys Val Val Ile Ser Ala
65 70 75 80
Pro Ser Lys Asp Ala Pro Met Phe Val Val Gly Val Asn Glu His Glu
85 90 95
Tyr Lys Ser Asp Leu Asp Ile Val Ser Asn Ala Ser Cys Thr Thr Asn
100 105 110
Cys Leu Ala Pro Leu Ala Lys Val Ile Asn Asp Arg Phe Gly Ile Val
115 120 125
Glu Gly Leu Met Thr Thr Val His Ser Ile Thr Ala Thr Gln Lys Thr
130 135 140
Val Asp Gly Pro Ser Met Lys Asp Trp Arg Gly Gly Arg Ala Ala Ser
145 150 155 160
Phe Asn Ile Ile Pro Ser Ser Thr Gly Ala Ala Lys Ala Val Gly Lys
165 170 175
Val Leu Pro Ser Leu Asn Gly Lys Leu Thr Gly Met Ser Phe Arg Val
180 185 190
Pro Thr Val Asp Val Ser Val Val Asp Leu Thr Val Arg Leu Glu Lys
195 200 205
Ala Ala Thr Tyr Asp Glu Ile Lys Lys Ala Ile Lys Glu Glu Ser Glu

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210	215	220
Gly Lys Met Lys Gly Ile Leu Gly Tyr Thr Glu Asp Asp Val Val Ser		
225	230	235
Thr Asp Phe Val Gly Asp Asn Arg Ser Ser Ile Phe Asp Ala Lys Ala		
	245	250
Gly Ile Ala Leu Ser Asp Lys Phe Val Lys Leu Val Ser Trp Tyr Asp		
	260	265
Asn Glu Trp Gly Tyr Ser Ser Arg Val Val Asp Leu Ile Val His Met		
	275	280
Ser Lys Ala		285
290		

(2) INFORMATION FOR SEQ ID NO:2556:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 532 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..532
(D) OTHER INFORMATION: / Ceres Seq. ID 1573644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2556:

ataacacacaaa	tacacacacaaa	aaaaaaaaaac	agaaagtaac	atgagatctc	tcttattagc	60
cgtgtgacctg	gttctttgctt	tacactgcgg	tgaagcagcc	gtgtcttgca	acacggtgat	120
tgccgagctct	tacccttgct	tatctacgt	gactcagggc	ggaccggtcc	caaccctctg	180
ctgcaacgggt	ctcacacacac	tcaagagtc	ggctcaaaact	tctgtggacc	gtcaSgggGg	240
tctgtcgttg	catcaaatct	gctattggag	gactcactct	ctctccctaga	accatccaaa	300
atgcttttgg	attgccttct	aaatgtgtgt	tcatctccc	ttacaagttc	agcccttcac	360
ctgactgcga	cagtatccag	tgagacaagc	agaaaatctt	aaaggaagct	actacaagaa	420
ctataataac	ctaataatta	ataaatgagg	gcattgtgtt	gctagtgtct	aaAtgatgca	480
gtgatgtatt	Cgycattttg	aatgthctaa	tTctcagcag	gcacttatct	cc	

(2) INFORMATION FOR SEQ ID NO:2557:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..82
(D) OTHER INFORMATION: / Ceres Seq. ID 1573645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2557:

Met Arg Ser Leu Leu Ala Val Cys Leu Val Leu Ala Leu His Cys	
1	5 10 15
Gly Glu Ala Ala Val Ser Cys Asn Thr Val Ile Ala Asp Leu Tyr Pro	
	20 25 30
Cys Leu Ser Tyr Val Thr Gln Gly Gly Pro Val Pro Thr Leu Cys Cys	
	35 40 45
Asn Gly Leu Thr Thr Leu Lys Ser Gln Ala Gln Thr Ser Val Asp Arg	
	50 55 60
Xaa Gly Gly Leu Ser Leu His Gln Ile Cys Tyr Trp Arg Thr His Ser	
65	70 75 80
Leu Ser	

(2) INFORMATION FOR SEQ ID NO:2558:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 533 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1.533
(D) OTHER INFORMATION: / Ceres Seq. ID 1573646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2558:

ataacacaaa	tacacacaaa	aaaaaandRaa	Wacagaaagt	aacatgagat	ctctcttatt	60
agccgtgtgc	ctggttcttg	ctttacactg	cggtgaagca	gccgtgtctt	gcaacacggt	120
gattgaggat	ctttaccctt	gcttatccta	cggtgactcag	ggcggaacgg	tcccaacctt	180
ctgctgcac	ggctctacaa	cactcaagag	tcaggctcaa	acttctgtgg	accgtcaggg	240
gNgctgtctg	ttgcatcaaa	tctgctattg	gaggactcac	tctctctctt	agaaccatcc	300
aaaatgcttt	ggaattgcct	tctaaatgtg	gtgtcgatct	cccttacaag	ttcagccctt	360
ccactgactg	cgacagtatc	cagtgcagaca	agcagaaaaa	cttaaaggaa	gctactacaa	420
gaactataat	aaactaataa	ttaataaatt	agggcattgg	ttgtctagtt	gctaattgat	480
cagtgcagta	ttgtcatttt	gaatgttcta	atacgcag	gcatttatct	ctg	

(2) INFORMATION FOR SEQ ID NO:2559:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1.82
(D) OTHER INFORMATION: / Ceres Seq. ID 1573647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2559:

Met	Arg	Ser	Leu	Leu	Ala	Val	Cys	Leu	Val	Leu	Ala	Leu	His	Cys
1		5					10					15		
Gly	Glu	Ala	Ala	Val	Ser	Cys	Asn	Thr	Val	Ile	Ala	Asp	Leu	Tyr
		20					25					30		Pro
Cys	Leu	Ser	Tyr	Val	Thr	Gln	Gly	Gly	Pro	Val	Pro	Thr	Leu	Cys
		35				40					45			Cys
Asn	Gly	Leu	Thr	Thr	Leu	Lys	Ser	Gln	Ala	Gln	Thr	Ser	Val	Asp
		50				55					60			Arg
Gln	Gly	Xaa	Leu	Ser	Leu	His	Gln	Ile	Cys	Tyr	Trp	Arg	Thr	His
		65				70				75				Ser
Leu	Ser													

(2) INFORMATION FOR SEQ ID NO:2560:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 896 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..896
(D) OTHER INFORMATION: / Ceres Seq. ID 1573648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2560:

accattaggg	ctctctctaa	attctcag	ctcgtgagaa	tgtctatcgt	cttcacggag	60
ctcaatcgaa	gatgttaacg	gcagatatca	caccgaatca	ttcaatctac	atccaGaaac	120
ctcaatgaaa	ggatcaagaa	agaggaaattg	aagagatctc	tttactgttt	gttctctcag	180
tttgggagaa	tacttgcattg	ggttgccttg	aagactccga	agctccgagg	acaagcttgg	240
gttactttta	gtgaagtcac	tgctgctggt	catgctgttc	gtcagatgca	aaattttccc	300
ttvtatgata	aaaccaatg	cttacaatat	gcaaaagcaa	agtcagattg	tctagctaaa	360
gctgagggaa	ctttgcttcc	aaaagataag	aagaggaagc	aagaagaaaa	agttgaaaga	420
aagcgtgaag	aatcccaacg	accaaacaca	gctaattggtc	caagtgcata	tggtccaaat	480
gccaaataacg	gagtcctcgt	gccttcgttc	cagccgagcg	ggcaagaaac	aatgccacca	540

aacaacatac tcttcattca gaatctccca cagcagacaa caagcatgat gctccagctt 600
ctcttcgaac agtaccctgg attcaaaagc ataagaatga tcgacgcaaa accaggaatc 660
gcggttttag agtacgaaga cgaatgttcaa gcttccatag ctatgcaacc tcttcaaggt 720
tccaaaatca ctccccagaa tccaatggct atctctttcg ccaagaaatg ataagatct 780
tggttttggt tggtttgtgt cctttaagac gatagtactg gaccaaccaaa acctgggtgt 840
tataaccaac caacggttct attggttaac ggattaatcc gggtttggtt taateg

(2) INFORMATION FOR SEQ ID NO:2561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1573649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2561:

Met	Gln	Asn	Phe	Pro	Xaa	Tyr	Asp	Lys	Pro	Met	Arg	Leu	Gln	Tyr	Ala
1		5						10					15		
Lys	Ala	Lys	Ser	Asp	Cys	Leu	Ala	Lys	Ala	Glu	Gly	Thr	Phe	Val	Pro
		20						25					30		
Lys	Asp	Lys	Lys	Arg	Lys	Gln	Glu	Glu	Lys	Val	Glu	Arg	Lys	Arg	Glu
		35				40					45				
Glu	Ser	Gln	Arg	Pro	Asn	Thr	Ala	Asn	Gly	Pro	Ser	Ala	Asn	Gly	Pro
		50				55					60				
Ser	Ala	Asn	Asn	Gly	Val	Pro	Ala	Pro	Ser	Phe	Gln	Pro	Ser	Gly	Gln
		65			70					75				80	
Glu	Thr	Met	Pro	Pro	Asn	Asn	Ile	Leu	Phe	Ile	Gln	Asn	Leu	Pro	His
			85					90					95		
Glu	Thr	Thr	Ser	Met	Met	Leu	Gln	Leu	Leu	Phe	Glu	Gln	Tyr	Pro	Gly
			100					105					110		
Phe	Lys	Glu	Ile	Arg	Met	Ile	Asp	Ala	Lys	Pro	Gly	Ile	Ala	Phe	Val
			115				120					125			
Glu	Tyr	Glu	Asp	Asp	Val	Gln	Ala	Ser	Ile	Ala	Met	Gln	Pro	Leu	Gln
		130				135					140				
Gly	Phe	Lys	Ile	Thr	Pro	Gln	Asn	Pro	Met	Val	Ile	Ser	Phe	Ala	Lys
					150					155					160
Lys															

(2) INFORMATION FOR SEQ ID NO:2562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1573650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2562:

Met	Arg	Leu	Gln	Tyr	Ala	Lys	Ala	Lys	Ser	Asp	Cys	Leu	Ala	Lys	Ala
1			5					10					15		
Glu	Gly	Thr	Phe	Val	Pro	Lys	Asp	Lys	Lys	Arg	Lys	Gln	Glu	Glu	Lys
			20					25					30		
Val	Glu	Arg	Lys	Arg	Glu	Glu	Ser	Gln	Arg	Pro	Asn	Thr	Ala	Asn	Gly
			35				40					45			
Pro	Ser	Ala	Asn	Gly	Pro	Ser	Ala	Asn	Asn	Gly	Val	Pro	Ala	Pro	Ser
			50				55				60				
Phe	Gln	Pro	Ser	Gly	Gln	Glu	Thr	Met	Pro	Pro	Asn	Asn	Ile	Leu	Phe

65	70	75	80
Ile Gln Asn Leu Pro His Glu Thr Thr Ser Met Met Leu Gln Leu Leu			
	85	90	95
Phe Glu Gln Tyr Pro Gly Phe Lys Glu Ile Arg Met Ile Asp Ala Lys			
	100	105	110
Pro Gly Ile Ala Phe Val Glu Tyr Glu Asp Asp Val Gln Ala Ser Ile			
	115	120	125
Ala Met Gln Pro Leu Gln Gly Phe Lys Ile Thr Pro Gln Asn Pro Met			
	130	135	140
Val Ile Ser Phe Ala Lys Lys			
	145	150	

(2) INFORMATION FOR SEQ ID NO:2563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1070 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1070
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2563:

acatttttca	cgctctcgac	aactctcttc	tctccaaccc	aaattctctt	cttctcaacc	60
tcgtctcttc	cgctctcttc	ctccaacatt	tctccgatca	ttgatgggtt	cgctctcttc	120
ttctctctct	tctctctcga	agcttctctt	tcgtcaacac	tttgagaacg	aatcttccac	180
ctttactatt	cttctcgccg	acgtttctca	tcctgataaa	cctgctttgt	tgattgatcc	240
ggtggacaag	actgtggata	gagacttgaa	actgattgat	gagttaggat	taaagcttat	300
ctatgctatg	aacactcatg	tctatgctga	tcagtcaact	ggctactggc	ttcttaagac	360
gaagctcccg	ggtgtgaaat	ccgttatctc	gaaagcaagt	gggtccaaag	ctgatttggg	420
ctctgaacct	ggtgacaag	tatctattgg	tgatatatac	cttgagggtc	gtgctacacc	480
tggaacaact	acaggatgtg	ttacatatgt	gactgggtga	ggagctgac	agccccaacc	540
aagaatggct	tttaccgggg	atgctgtact	cctcgggtgt	tggtgggagg	ctgacttttc	600
gggagggaag	tcagatcaac	ctcaccgagc	tgatattcca	cagatatttt	cattgccaaa	660
ggacacattg	atctatccag	ctcaccgact	caaaggtttc	gaggtaaagta	cagttggaga	720
agagatgcaa	cacaaccgcc	gtctaaactaa	agataaagaa	acattcaaaa	ccattatgtc	780
aaatctgaat	ctgtcgtatc	ogaagatgat	tgatgttgca	gtaccagcaa	atatgtgtct	840
tggtgtacaa	gatgtgcctt	ctcaagccaa	ctaaaaaaaa	ctcttaccata	taatgtttgt	900
ctttttatcg	atgtcattct	atatattacca	aagccaataa	aaactcttga	gagtaatttc	960
tacaataaga	tttgcctccg	tttagataaa	gttcatttaga	aaattgtgta	aattagattg	1020
aaactgttga	attgtttatg	aagatgaaga	cagtattttgc	gtgttcagac		

(2) INFORMATION FOR SEQ ID NO:2564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..290
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2564:

His Phe Ser Arg Leu Arg Gln Leu Leu Leu Leu Gln Pro Lys Phe Leu			
1	5	10	15
Ser Ser Gln Pro Arg Pro Leu Arg Ser Pro Pro Thr Phe Leu Arg			
	20	25	30
Ser Leu Met Gly Ser Ser Ser Phe Ser Ser Ser Ser Lys Leu			
	35	40	45
Leu Phe Arg Gln Leu Phe Glu Asn Glu Ser Ser Thr Phe Thr Tyr Leu			
	50	55	60

Leu Ala Asp Val Ser His Pro Asp Lys Pro Ala Leu Leu Ile Asp Pro
65 70 75 80
Val Asp Lys Thr Val Asp Arg Asp Leu Lys Leu Ile Asp Glu Leu Gly
85 90 95
Leu Lys Leu Ile Tyr Ala Met Asn Thr His Val His Ala Asp His Val
100 105 110
Thr Gly Thr Gly Leu Leu Lys Thr Lys Leu Pro Gly Val Lys Ser Val
115 120 125
Ile Ser Lys Ala Ser Gly Ser Lys Ala Asp Leu Phe Leu Glu Pro Gly
130 135 140
Asp Lys Val Ser Ile Gly Asp Ile Tyr Leu Glu Val Arg Ala Thr Pro
145 150 155 160
Gly His Thr Thr Gly Cys Val Thr Tyr Val Thr Gly Glu Gly Ala Asp
165 170 175
Gln Pro Gln Pro Arg Met Ala Phe Thr Gly Asp Ala Val Leu Ile Arg
180 185 190
Gly Cys Gly Arg Thr Asp Phe Gln Gly Gly Ser Ser Asp Gln Leu Tyr
195 200 205
Glu Ser Val His Ser Gln Ile Phe Ser Leu Pro Lys Asp Thr Leu Ile
210 215 220
Tyr Pro Ala His Asp Tyr Lys Gly Phe Glu Val Ser Thr Val Gly Glu
225 230 235 240
Glu Met Gln His Asn Pro Arg Leu Thr Lys Asp Lys Glu Thr Phe Lys
245 250 255
Thr Ile Met Ser Asn Leu Asn Leu Ser Tyr Pro Lys Met Ile Asp Val
260 265 270
Ala Val Pro Ala Asn Met Val Cys Gly Leu Gln Asp Val Pro Ser Gln
275 280 285
Ala Asn
290

(2) INFORMATION FOR SEQ ID NO:2565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1573653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2565:

Met Gly Ser Ser Ser Phe Ser Ser Ser Ser Lys Leu Leu Phe
1 5 10 15
Arg Gln Leu Phe Glu Asn Glu Ser Ser Thr Phe Thr Tyr Leu Leu Ala
20 25 30
Asp Val Ser His Pro Asp Lys Pro Ala Leu Leu Ile Asp Pro Val Asp
35 40 45
Lys Thr Val Asp Arg Asp Leu Lys Leu Ile Asp Glu Leu Gly Leu Lys
50 55 60
Leu Ile Tyr Ala Met Asn Thr His Val His Ala Asp His Val Thr Gly
65 70 75 80
Thr Gly Leu Leu Lys Thr Lys Leu Pro Gly Val Lys Ser Val Ile Ser
85 90 95
Lys Ala Ser Gly Ser Lys Ala Asp Leu Phe Leu Glu Pro Gly Asp Lys
100 105 110
Val Ser Ile Gly Asp Ile Tyr Leu Glu Val Arg Ala Thr Pro Gly His
115 120 125
Thr Thr Gly Cys Val Thr Tyr Val Thr Gly Glu Gly Ala Asp Gln Pro
130 135 140
Gln Pro Arg Met Ala Phe Thr Gly Asp Ala Val Leu Ile Arg Gly Cys

145				150					155				160
Gly	Arg	Thr	Asp	Phe	Gln	Gly	Gly	Ser	Ser	Asp	Gln	Leu	Tyr
				165					170				175
Val	His	Ser	Gln	Ile	Phe	Ser	Leu	Pro	Lys	Asp	Thr	Leu	Ile
			180					185				190	195
Ala	His	Asp	Tyr	Lys	Gly	Phe	Glu	Val	Ser	Thr	Val	Gly	Glu
		195					200				205		210
Gln	His	Asn	Pro	Arg	Leu	Thr	Lys	Asp	Lys	Glu	Thr	Phe	Lys
					215					220		225	230
Met	Ser	Asn	Leu	Asn	Leu	Ser	Tyr	Pro	Lys	Met	Ile	Asp	Val
										235		240	245
Pro	Ala	Asn	Met	Val	Cys	Gly	Leu	Gln	Asp	Val	Pro	Ser	Gln
				245				250					255

(2) INFORMATION FOR SEQ ID NO:2566:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..188

(D) OTHER INFORMATION: / Ceres Seq. ID 1573654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2566:

Met	Asn	Thr	His	Val	His	Ala	Asp	His	Val	Thr	Gly	Thr	Gly	Leu	Leu
1			5						10					15	
Lys	Thr	Lys	Leu	Pro	Gly	Val	Lys	Ser	Val	Ile	Ser	Lys	Ala	Ser	Gly
			20					25					30		
Ser	Lys	Ala	Asp	Leu	Phe	Leu	Glu	Pro	Gly	Asp	Lys	Val	Ser	Ile	Gly
		35				40					45				
Asp	Ile	Tyr	Leu	Glu	Val	Arg	Ala	Thr	Pro	Gly	His	Thr	Thr	Gly	Cys
	50				55						60				
Val	Thr	Tyr	Val	Thr	Gly	Glu	Gly	Ala	Asp	Gln	Pro	Gln	Pro	Arg	Met
	65			70					75					80	
Ala	Phe	Thr	Gly	Asp	Ala	Val	Leu	Ile	Arg	Gly	Cys	Gly	Arg	Thr	Asp
			85						90					95	
Phe	Gln	Gly	Gly	Ser	Ser	Asp	Gln	Leu	Tyr	Glu	Ser	Val	His	Ser	Gln
			100					105					110		
Ile	Phe	Ser	Leu	Pro	Lys	Asp	Thr	Leu	Ile	Tyr	Pro	Ala	His	Asp	Tyr
			115				120					125			
Lys	Gly	Phe	Glu	Val	Ser	Thr	Val	Gly	Glu	Glu	Met	Gln	His	Asn	Pro
	130					135					140				
Arg	Leu	Thr	Lys	Asp	Lys	Glu	Thr	Phe	Lys	Thr	Ile	Met	Ser	Asn	Leu
	145			150						155				160	
Asn	Leu	Ser	Tyr	Pro	Lys	Met	Ile	Asp	Val	Ala	Val	Pro	Ala	Asn	Met
				165					170					175	
Val	Cys	Gly	Leu	Gln	Asp	Val	Pro	Ser	Gln	Ala	Asn				
			180					185							

(2) INFORMATION FOR SEQ ID NO:2567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1151 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1151

(D) OTHER INFORMATION: / Ceres Seq. ID 1573655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2567:

acacatcttta	aaaagtaaaa	acacattcat	ctatccaaca	aaaaaaaaaa	aaaaaggag	60
aaatgggaag	aatgatcat	agaatgggtg	gtgtcaatgg	cataactatg	cacattgcgc	120
agaaaggtcc	caaagaagga	cctgtggtgc	ttctctccca	tggtattccct	gatctctggt	180
acacgtggcg	tcaccagatt	agtgggttat	catctctagg	ttaccgcgct	gtatgctcag	240
acctcccgag	ctacggagac	tttgattcgc	cagagtcttt	ctccgagtac	acgtgtctta	300
acgtcggttg	ggacctcgta	gctctctcgg	acagtggtgc	tggaatcaaa	gagaagggtg	360
ttctgttcgg	tcattgattg	ggagccatta	tcggatggtt	ttctgttttg	tttcgacctg	420
aaaagattaa	cggctttgtg	tgtttgagtg	tgccgtatag	atcaagaaac	cctaaagtca	480
agcccgttca	agggttcaag	gctgtatttg	gagatgatta	ctacatttgt	agattttcag	540
aaccggggaa	gattgaagga	gagattgcaa	gtgcagatcc	aagaatatct	ctgagggaacc	600
ttcttcacag	gaggacactc	ggctccgcga	ttttacctaa	ggataatccc	tttggggaaa	660
aacctaaacc	taatagcgaa	aacattgaa	tgccctgaatg	gttttctaag	aaagatctcg	720
atttctatgt	ctccaaatct	gagaaggcag	gatttaccgg	tggtttgaac	tactacagag	780
ccatggatct	gaattgggag	ctcactgcac	catggaccgg	agctaagatt	caagtctccag	840
tgaagttcat	gacagggtgac	ttcgacatgg	tttaccaccac	accagggatg	aaagagtaca	900
ttcacgggtg	tggaattgct	gcagatgttc	caactcttca	agagatagtg	gtgattgaag	960
atgtctggKYM	Ytcgtttaacc	aagagaaacc	taagaggttc	actgctcaca	tcaatgactt	1020
cttcaccaag	cttcggggaca	acaacaaaag	cttttagagt	ttctgttttg	ttctattatg	1080
ttggctctca	aaacaagtgt	gtttcttgcat	gtgtgtgttc	gacaagattt	tgaataagac	1140
ttggcattat	g					

(2) INFORMATION FOR SEQ ID NO:2568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 356 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..356

(D) OTHER INFORMATION: / Ceres Seq. ID 1573656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2568:

Met	Glu	Gly	Ile	Asp	His	Arg	Met	Val	Ser	Val	Asn	Gly	Ile	Thr	Met
1				5					10					15	
His	Ile	Ala	Glu	Lys	Gly	Pro	Lys	Glu	Gly	Pro	Val	Val	Leu	Leu	
				20					25					30	
His	Gly	Phe	Pro	Asp	Leu	Trp	Tyr	Thr	Trp	Arg	His	Gln	Ile	Ser	Gly
				35					40					45	
Leu	Ser	Ser	Leu	Gly	Tyr	Arg	Ala	Val	Ala	Pro	Asp	Leu	Arg	Gly	Tyr
				50					55					60	
Gly	Asp	Ser	Asp	Ser	Pro	Glu	Ser	Phe	Ser	Glu	Tyr	Thr	Cys	Leu	Asn
				65					70					75	80
Val	Val	Gly	Asp	Leu	Val	Ala	Leu	Leu	Asp	Ser	Val	Ala	Gly	Asn	Gln
				85					90					95	
Glu	Lys	Val	Phe	Leu	Val	Gly	His	Asp	Trp	Gly	Ala	Ile	Ile	Gly	Trp
				100					105					110	
Phe	Leu	Cys	Leu	Phe	Arg	Pro	Glu	Lys	Ile	Asn	Gly	Phe	Val	Cys	Leu
				115					120					125	
Ser	Val	Pro	Tyr	Arg	Ser	Arg	Asn	Pro	Lys	Val	Lys	Pro	Val	Gln	Gly
				130					135					140	
Phe	Lys	Ala	Val	Phe	Gly	Asp	Asp	Tyr	Tyr	Ile	Cys	Arg	Phe	Gln	Glu
				145					150					155	160
Pro	Gly	Lys	Ile	Glu	Gly	Glu	Ile	Ala	Ser	Ala	Asp	Pro	Arg	Ile	Phe
				165					170					175	
Leu	Arg	Asn	Leu	Phe	Thr	Gly	Arg	Thr	Leu	Gly	Pro	Pro	Ile	Leu	Pro
				180					185					190	
Lys	Asp	Asn	Pro	Phe	Gly	Glu	Lys	Pro	Asn	Pro	Asn	Ser	Glu	Asn	Ile
				195					200					205	
Glu	Leu	Pro	Glu	Trp	Phe	Ser	Lys	Lys	Asp	Leu	Asp	Phe	Tyr	Val	Ser

(2) INFORMATION FOR SEQ ID NO:2569:

(A) LENGTH: 349 amino acids

(C) STRANDEDNESS:

MOLECULE TYPE: peptid

(A) NAME

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:2569:

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
Lys	Glu	Gly	Pro	Val	Val	Leu	Leu	Leu	His	Gly	Phe	Pro	Asp	Leu	Trp				
			20					25				30							
Tyr	Thr	Trp	Arg	His	Gln	Ile	Ser	Gly	Leu	Ser	Ser	Leu	Gly	Tyr	Arg				
		35					40					45							
Ala	Val	Ala	Pro	Asp	Leu	Arg	Gly	Tyr	Gly	Asp	Ser	Asp	Ser	Pro	Glu				
		50				55					60								
Ser	Phe	Ser	Glu	Tyr	Trp	Cys	Leu	Asn	Val	Val	Gly	Asp	Leu	Val	Ala				
65				70					75					80					
Leu	Leu	Asp	Ser	Val	Ala	Gly	Asn	Gln	Glu	Lys	Val	Phe	Leu	Val	Gly				
				85					90				95						
His	Asp	Trp	Gly	Ala	Ile	Ile	Gly	Trp	Phe	Leu	Cys	Leu	Phe	Arg	Pro				
			100					105					110						
Glu	Lys	Ile	Asn	Gly	Phe	Val	Cys	Leu	Ser	Val	Pro	Tyr	Arg	Ser	Arg				
		115					120					125							
Asn	Pro	Lys	Val	Lys	Pro	Val	Gln	Gly	Phe	Lys	Ala	Val	Phe	Gly	Asp				
		130				135					140								
Asp	Tyr	Tyr	Ile	Cys	Arg	Phe	Gln	Glu	Pro	Gly	Lys	Ile	Glu	Gly	Glu				
145				150						155				160					
Ile	Ala	Ser	Ala	Asp	Pro	Ile	Phe	Leu	Arg	Asn	Leu	Phe	Thr	Gly					
			165				170					175							
Arg	Thr	Leu	Gly	Pro	Pro	Ile	Leu	Pro	Lys	Asp	Asn	Pro	Phe	Gly	Glu				
		180					185					190							
Lys	Pro	Asn	Pro	Asn	Ser	Glu	Asn	Ile	Glu	Leu	Pro	Glu	Trp	Phe	Ser				
		195				200					205								
Lys	Lys	Asp	Leu	Asp	Phe	Tyr	Val	Ser	Lys	Phe	Glu	Lys	Ala	Gly	Phe				
		210				215				220									
Thr	Gly	Gly	Leu	Asn	Tyr	Tyr	Arg	Ala	Met	Asp	Leu	Asn	Trp	Glu	Leu				
225				230					235					240					

Thr Ala Pro Trp Thr Gly Ala Lys Ile Gln Val Pro Val Lys Phe Met
245 250 255
Thr Gly Asp Phe Asp Met Val Tyr Thr Thr Pro Gly Met Lys Glu Tyr
260 265 270
Ile His Gly Gly Gly Phe Ala Ala Asp Val Pro Thr Leu Gln Glu Ile
275 280 285
Val Val Ile Glu Asp Ala Xaa Xaa Ser Leu Thr Lys Arg Asn Leu Lys
290 295 300
Arg Ser Leu Leu Thr Ser Met Thr Ser Ser Pro Ser Phe Gly Thr Thr
305 310 315 320
Thr Lys Ala Phe Arg Val Leu Val Trp Phe Tyr Tyr Val Gly Ser Gln
325 330 335
Asn Lys Leu Val Leu Ala Cys Val Val Ser Thr Arg Phe
340 345

(2) INFORMATION FOR SEQ ID NO:2570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..341
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2570:

Met His Ile Ala Glu Lys Gly Pro Lys Glu Gly Pro Val Val Leu Leu
1 5 10 15
Leu His Gly Phe Pro Asp Leu Trp Tyr Thr Trp Arg His Gln Ile Ser
20 25 30
Gly Leu Ser Ser Leu Gly Tyr Arg Ala Val Ala Pro Asp Leu Arg Gly
35 40 45
Tyr Gly Asp Ser Asp Ser Pro Glu Ser Phe Ser Glu Tyr Thr Cys Leu
50 55 60
Asn Val Val Gly Asp Leu Val Ala Leu Leu Asp Ser Val Ala Gly Asn
65 70 75 80
Gln Glu Lys Val Phe Leu Val Gly His Asp Trp Gly Ala Ile Ile Gly
85 90 95
Trp Phe Leu Cys Leu Phe Arg Pro Glu Lys Ile Asn Gly Phe Val Cys
100 105 110
Leu Ser Val Pro Tyr Arg Ser Arg Asn Pro Lys Val Lys Pro Val Gln
115 120 125
Gly Phe Lys Ala Val Phe Gly Asp Asp Tyr Tyr Ile Cys Arg Phe Gln
130 135 140
Glu Pro Gly Lys Ile Glu Gly Glu Ile Ala Ser Ala Asp Pro Arg Ile
145 150 155 160
Phe Leu Arg Asn Leu Phe Thr Gly Arg Thr Leu Gly Pro Pro Ile Leu
165 170 175
Pro Lys Asp Asn Pro Phe Gly Glu Lys Pro Asn Pro Asn Ser Glu Asn
180 185 190
Ile Glu Leu Pro Glu Trp Phe Ser Lys Lys Asp Leu Asp Phe Tyr Val
195 200 205
Ser Lys Phe Glu Lys Ala Gly Phe Thr Gly Gly Leu Asn Tyr Tyr Arg
210 215 220
Ala Met Asp Leu Asn Trp Glu Leu Thr Ala Pro Trp Thr Gly Ala Lys
225 230 235 240
Ile Gln Val Pro Val Lys Phe Met Thr Gly Asp Phe Asp Met Val Tyr
245 250 255
Thr Thr Pro Gly Met Lys Glu Tyr Ile His Gly Gly Gly Phe Ala Ala
260 265 270
Asp Val Pro Thr Leu Gln Glu Ile Val Val Ile Glu Asp Ala Xaa Xaa

(2) INFORMATION FOR SEQ ID NO:2571:

(A) LENGTH: 1153 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: sing

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

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(11) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
```

(1X) FEATURE:
(7A) NAM

(A) NAME/REF: -
(B) LOCATION: 1

(D) OTHER INFORMATION

(D) OTHER INFORMATION: 7 Ceres Seq. ID 1973859
SEQUENCE DESCRIPTION: SEQ ID NO:2571:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:2571:
tctctctt gttctctctt attgctctct ccaacacacac a

atcttaaaaa	gtataaaacac	attcattcag	ccacaacaaa	aaaaaaaata	aagggaagaa	120
ggaagagatc	gatacatagac	tgtgtgagtg	caattgcgata	actatgcaca	tctccgagaa	120
agggtccaaa	gaaggacacgt	tgtgtctctc	ctctccatcg	tctccgtgat	ccgtacacgt	180
ggcgtcgata	gat tagtgctt	tatatcatct	taggttaccg	cgctgtagct	cagcaacctc	240
gaggctcagc	agactctgat	ctcgcaagct	ctttctccga	tcaacagctg	ctttaacctg	300
tctgggacat	ctgactgctct	ctggacagct	tgtctgaaa	tcaagaaagg	tgtttctcgt	360
cggtctgatg	tggggaagcca	tctatcggat	gtttctctcg	tgtttctcac	ctgaaaagat	420
taacggcttt	gttggtgttg	agtgctgcgt	atagatacct	gaagacctaa	agtcacagaa	480
gttcaagggt	tcaaggctgt	ttttggagat	gattactaca	ttttgtagat	tcaaggaaacg	540
gggaagatgt	aaggagagat	tgcgaagtca	gcacaaagaa	tatttctgag	gaacctcttc	600
acagggaagc	cactcgtctc	cgccgattta	cctaagagta	atcccctttg	ggaaaataact	660
aacccttaata	gcgaaaaactc	tgaattgctt	gaatggtttt	ctaaagaaga	tctcgattct	720
tatgtcttca	aacttcgaaa	ggcagagatt	accgggtgat	tgaactacta	cacagccgat	780
tgctgtaatt	gggagctcac	tgcacactcg	accggagcta	agattcaagt	tccagtgaa	840
tctcatgacg	tgactctcaa	catgtgtttac	accacacacg	ggatgaaaga	gtacattcac	900
gggtgtggat	tgtctgcgaa	tgtctcaaat	ctctaagaag	tatgtgtgtg	tgaagatgct	960
ggctcacttc	ttaacaaaga	gaacacctcaa	gaggtcta	ctgcattcaa	tgaactcttc	1020
accaactctc	gggacaacaa	aaaaagcttt	tagagtcttc	gtttcgtcat	attatgttgg	1080
ctctcaaaac	aagttggttc	tgtcatgtgt	tgtttcgaca	agattttgaa	taagactctg	1140
catctacata	ccg					

(2) INFORMATION FOR SEQ ID NO:2572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1573660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2572:

Met	Asp	Ser	Leu	Ile	Ser	Tyr	Thr	Trp	Arg	His	Gln	Ile	Ser	Gly	Leu
				5					10					15	
1	Ser	Ser	Leu	Gly	Tyr	Arg	Ala	Val	Ala	Pro	Asp	Leu	Arg	Gly	Tyr
				20					25					30	
Asp	Ser	Asp	Ser	Pro	Glu	Ser	Phe	Ser	Glu	Tyr	Thr	Cys	Leu	Asn	Val
				35								45			
Val	Gly	Asp	Leu	Val	Ala	Leu	Leu	Asp	Ser	Val	Ala	Gly	Asn	Gln	Arg
	50					55				60					

Arg Cys Phe Trp Ser Val Met Ile Gly Glu Pro Leu Ser Asp Gly Phe
65 70 75 80
Ser Val Cys Phe Asp Leu Lys Arg Leu Thr Ala Leu Trp Cys Leu Ser
85 90 95
Val Pro Tyr Arg Ser Arg Lys Pro
100

(2) INFORMATION FOR SEQ ID NO:2573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1573661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2573:

Met Asp Leu Asn Trp Glu Leu Thr Ala Pro Trp Thr Gly Ala Lys Ile
1 5 10 15
Gln Val Pro Val Lys Phe Met Thr Gly Asp Phe Asn Met Val Tyr Thr
20 25 30
Thr Pro Gly Met Lys Glu Tyr Ile His Gly Gly Phe Ala Ala Asp
35 40 45
Val Pro Thr Leu Gln Glu Ile Val Val Ile Glu Asp Ala Gly His Phe
50 55 60
Val Asn Gln Glu Lys Pro Gln Glu Val Thr Ala His Ile Asn Asp Phe
65 70 75 80
Phe Thr Asn Leu Arg Asp Asn Asn Lys Ser Phe
85 90

(2) INFORMATION FOR SEQ ID NO:2574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1573662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2574:

Met Thr Gly Asp Phe Asn Met Val Tyr Thr Thr Pro Gly Met Lys Glu
1 5 10 15
Tyr Ile His Gly Gly Phe Ala Ala Asp Val Pro Thr Leu Gln Glu
20 25 30
Ile Val Val Ile Glu Asp Ala Gly His Phe Val Asn Gln Glu Lys Pro
35 40 45
Gln Glu Val Thr Ala His Ile Asn Asp Phe Phe Thr Asn Leu Arg Asp
50 55 60
Asn Asn Lys Ser Phe
65

(2) INFORMATION FOR SEQ ID NO:2575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1155 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1155

(D) OTHER INFORMATION: / Ceres Seq. ID 1573663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2575:

acatcttataa	aagtaaaac	acattcatct	atccaacaaa	aaaaaaaaa	aaaaaggaga	60
aatgggaagga	atcgatcata	gaatgggtgag	tgtaaatggc	ataactatgc	acattgccga	120
gaaaggtccc	aaagaaggac	ctgtggtgct	tctctcccat	ggattcccta	atctctggtgta	180
cacgtggcgt	caccagatta	gtgggttatc	atctctaggt	taccgcgctg	tagctccaga	240
ctcccgaggc	tacggagact	ctgattcgcc	agagcttttc	tcggagtaca	cgtgtcttaa	300
cgtcgttggg	gacctcgtag	ctcttctgga	cagtggtgct	ggaatcaag	agaaggtggt	360
ctcgttcggt	catgattggg	gagccattat	cggatgggtt	ctctgtttgt	tccagactga	420
aaagattaac	ggcttttgtg	gtttgagtg	gccgtataga	tcaagaaacc	ctaaagtcaa	480
gccgttcaa	gggttcaagg	ctgtatttgg	agatgattac	tacattttga	gatttccaga	540
accggggaag	attgaaggag	agattgcaag	tgcatatcca	agaattattc	tgaggaaacct	600
cttcaacagg	aggacactcg	gtccgcgat	tttaacctaa	gataatccct	ttggggaaaaa	660
acctaacctc	aatacgcaaa	acattgaatt	gcctgaatgg	ttttctaaga	aagatctcga	720
ttcttatgtc	tccaaattcg	agaaggcagg	atttaccggt	ggattgaact	actacaagagc	780
catggatctg	aattgggagc	tcactgcacc	atggaccgga	gctgaagattc	aagttccagt	840
gaagttcatc	acaggtgact	tcgacatggt	ttacaccaca	ccagggatga	aagatgacat	900
tcacggtggt	ggattttgctg	cagatgttcc	aacttttcaa	gagatagttg	tgattgaaga	960
tgctgtTchc	ttcgttaacc	aagagaaacc	tcaagaggtc	actgctcaca	tcaatgacct	1020
cttcaaccaag	cttcgggaca	acaacaaaag	cttttagagt	ttcgttttgg	ttctattatg	1080
ttggctctca	aaacaagttg	gtttcttgc	gtgtgttttc	gacaagattt	tgaataagac	1140
ttggcattat	gaagc					

(2) INFORMATION FOR SEQ ID NO:2576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..331

(D) OTHER INFORMATION: / Ceres Seq. ID 1573664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2576:

Met	Glu	Gly	Ile	Asp	His	Arg	Met	Val	Ser	Val	Asn	Gly	Ile	Thr	Met
1				5				10					15		
His	Ile	Ala	Glu	Lys	Gly	Pro	Lys	Glu	Gly	Pro	Val	Val	Leu	Leu	Leu
			20					25					30		
His	Gly	Phe	Pro	Asn	Leu	Trp	Tyr	Thr	Trp	Arg	His	Gln	Ile	Ser	Gly
			35				40					45			
Leu	Ser	Ser	Leu	Gly	Tyr	Arg	Ala	Val	Ala	Pro	Asp	Leu	Arg	Gly	Tyr
			50				55				60				
Gly	Asp	Ser	Asp	Ser	Pro	Glu	Ser	Phe	Ser	Glu	Tyr	Thr	Cys	Leu	Asn
65				70				75					80		
Val	Val	Gly	Asp	Leu	Val	Ala	Leu	Leu	Asp	Ser	Val	Ala	Gly	Asn	Gln
			85					90					95		
Glu	Lys	Val	Phe	Leu	Val	Gly	His	Asp	Trp	Gly	Ala	Ile	Ile	Gly	Trp
			100					105					110		
Phe	Leu	Cys	Leu	Phe	Arg	Pro	Glu	Lys	Ile	Asn	Gly	Phe	Val	Cys	Leu
			115				120					125			
Ser	Val	Pro	Tyr	Arg	Ser	Arg	Asn	Pro	Lys	Val	Lys	Pro	Val	Gln	Gly
			130				135				140				
Phe	Lys	Ala	Val	Phe	Gly	Asp	Asp	Tyr	Tyr	Ile	Cys	Arg	Phe	Gln	Glu
145				150				155					160		
Pro	Gly	Lys	Ile	Glu	Gly	Glu	Ile	Ala	Ser	Ala	Asp	Pro	Arg	Ile	Phe
			165					170					175		
Leu	Arg	Asn	Leu	Phe	Thr	Gly	Arg	Thr	Leu	Gly	Pro	Pro	Ile	Leu	Pro
			180				185						190		
Lys	Asp	Asn	Pro	Phe	Gly	Glu	Lys	Pro	Asn	Pro	Asn	Ser	Glu	Asn	Ile
			195				200						205		

Glu Leu Pro Glu Trp Phe Ser Lys Lys Asp Leu Asp Phe Tyr Val Ser
210 215 220
Lys Phe Glu Lys Ala Gly Phe Thr Gly Gly Leu Asn Tyr Tyr Arg Ala
225 230 235 240
Met Asp Leu Asn Trp Glu Leu Thr Ala Pro Trp Thr Gly Ala Lys Ile
245 250 255
Gln Val Pro Val Lys Phe Met Thr Gly Asp Phe Asp Met Val Tyr Thr
260 265 270
Thr Pro Gly Met Lys Glu Tyr Ile His Gly Gly Gly Phe Ala Ala Asp
275 280 285
Val Pro Thr Leu Gln Glu Ile Val Val Ile Glu Asp Ala Gly Xaa Phe
290 295 300
Val Asn Gln Glu Lys Pro Gln Glu Val Thr Ala His Ile Asn Asp Phe
305 310 315 320
Phe Thr Lys Leu Arg Asp Asn Asn Lys Ser Phe
325 330

(2) INFORMATION FOR SEQ ID NO:2577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..324

(D) OTHER INFORMATION: / Ceres Seq. ID 1573665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2577:

Met Val Ser Val Asn Gly Ile Thr Met His Ile Ala Glu Lys Gly Pro
1 5 10 15
Lys Glu Gly Pro Val Val Leu Leu Leu His Gly Phe Pro Asn Leu Trp
20 25 30
Tyr Thr Trp Arg His Gln Ile Ser Gly Leu Ser Ser Leu Gly Tyr Arg
35 40 45
Ala Val Ala Pro Asp Leu Arg Gly Tyr Gly Asp Ser Asp Ser Pro Glu
50 55 60
Ser Phe Ser Glu Tyr Thr Cys Leu Asn Val Val Gly Asp Leu Val Ala
65 70 75 80
Leu Leu Asp Ser Val Ala Gly Asn Gln Glu Lys Val Phe Leu Val Gly
85 90 95
His Asp Trp Gly Ala Ile Ile Gly Trp Phe Leu Cys Leu Phe Arg Pro
100 105 110
Glu Lys Ile Asn Gly Phe Val Cys Leu Ser Val Pro Tyr Arg Ser Arg
115 120 125
Asn Pro Lys Val Lys Pro Val Gln Gly Phe Lys Ala Val Phe Gly Asp
130 135 140
Asp Tyr Tyr Ile Cys Arg Phe Gln Glu Pro Gly Lys Ile Glu Gly Glu
145 150 155 160
Ile Ala Ser Ala Asp Pro Arg Ile Phe Leu Arg Asn Leu Phe Thr Gly
165 170 175
Arg Thr Leu Gly Pro Pro Ile Leu Pro Lys Asp Asn Pro Phe Gly Glu
180 185 190
Lys Pro Asn Pro Asn Ser Glu Asn Ile Glu Leu Pro Glu Trp Phe Ser
195 200 205
Lys Lys Asp Leu Asp Phe Tyr Val Ser Lys Phe Glu Lys Ala Gly Phe
210 215 220
Thr Gly Gly Leu Asn Tyr Tyr Arg Ala Met Asp Leu Asn Trp Glu Leu
225 230 235 240
Thr Ala Pro Trp Thr Gly Ala Lys Ile Gln Val Pro Val Lys Phe Met
245 250 255
Thr Gly Asp Phe Asp Met Val Tyr Thr Pro Gly Met Lys Glu Tyr

(2) INFORMATION FOR SEO ID NO:2578:

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(1x) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..316

(D) OTHER INFORMATION: / Ceres Seq. ID 1573666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2578:

Met	His	Ile	Ala	Glu	Lys	Gly	Pro	Lys	Glu	Gly	Pro	Val	Val	Leu	Leu
1			5					10						15	
Leu	His	Gly	Phe	Pro	Asn	Leu	Trp	Tyr	Thr	Trp	Arg	His	Gln	Ile	Ser
			20					25					30		
Gly	Leu	Ser	Ser	Leu	Gly	Tyr	Arg	Ala	Val	Ala	Pro	Asp	Leu	Arg	Gly
		35				40					45				
Tyr	Gly	Asp	Ser	Asp	Ser	Pro	Glu	Ser	Phe	Ser	Glu	Tyr	Thr	Cys	Leu
		50				55					60				
Asn	Val	Val	Gly	Asp	Leu	Val	Ala	Leu	Leu	Asp	Ser	Val	Ala	Gly	Asn
65				70						75				80	
Gln	Glu	Lys	Val	Phe	Leu	Val	Gly	His	Asp	Trp	Gly	Ala	Ile	Ile	Gly
				85				90						95	
Trp	Phe	Leu	Cys	Leu	Phe	Arg	Pro	Glu	Lys	Ile	Asn	Gly	Phe	Val	Cys
			100					105					110		
Leu	Ser	Val	Pro	Tyr	Arg	Ser	Glu	Asn	Pro	Lys	Val	Lys	Pro	Val	Gln
		115					120					125			
Gly	Phe	Lys	Ala	Val	Phe	Gly	Asp	Asp	Tyr	Tyr	Ile	Cys	Arg	Phe	Gln
		130				135					140				
Glu	Pro	Gly	Lys	Ile	Glu	Gly	Glu	Ile	Ala	Ser	Ala	Asp	Pro	Arg	Ile
145				150						155				160	
Phe	Leu	Arg	Asn	Leu	Phe	Thr	Gly	Arg	Thr	Leu	Gly	Pro	Ser	Ile	Leu
				165				170						175	
Pro	Lys	Asp	Asn	Pro	Phe	Gly	Glu	Lys	Pro	Asn	Pro	Asn	Ser	Glu	Asn
			180					185					190		
Ile	Glu	Leu	Pro	Glu	Trp	Phe	Ser	Lys	Lys	Asp	Leu	Asp	Phe	Tyr	Val
		195				200						205			
Ser	Lys	Phe	Glu	Lys	Ala	Gly	Phe	Thr	Gly	Gly	Leu	Asn	Tyr	Tyr	Arg
		210				215					220				
Ala	Met	Asp	Leu	Asn	Trp	Glu	Leu	Thr	Ala	Pro	Trp	Thr	Gly	Ala	Lys
225				230						235				240	
Ile	Gln	Val	Pro	Val	Lys	Phe	Met	Thr	Gly	Asp	Phe	Asp	Met	Val	Tyr
				245				250						255	
Thr	Thr	Pro	Gly	Met	Lys	Glu	Tyr	Ile	His	Gly	Gly	Gly	Phe	Ala	Ala
			260					265					270		
Asp	Val	Pro	Thr	Leu	Gln	Glu	Ile	Val	Val	Ile	Glu	Asp	Ala	Gly	Xaa
		275				280						285			
Phe	Val	Asn	Gln	Glu	Lys	Pro	Gln	Glu	Val	Thr	Ala	His	Ile	Asn	Asp
		290				295					300				
Phe	Phe	Thr	Lys	Leu	Arg	Asp	Asn	Asn	Lys	Ser	Phe				
305				310						315					

(2) INFORMATION FOR SEQ ID NO:2579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2579:

aaagagaaMa	acgtatgagt	tgcttaaacc	ataaacctca	agctcaaaat	tttatcaacc	60
ttataaaagt	tcgtEWWtctc	gagattttga	atcttttcag	ctaaaaaaga	tcacagcttt	120
ttgcgttttc	tggatgagtt	tgagataaga	gaagatgaag	attcagtgta	acgtttgtga	180
ggcggcgga	gcgacgggtc	tatgwtgcgc	cgaaggagct	gctctttgt	gggcttgcca	240
tgagaaaatt	cacgccgcta	ataaactcgc	cggaaaaacat	cagagagtcc	ctctctctgc	300
ctctgcctct	tccataccca	aatgtgacat	ttgtcarraa	gcactctgat	tcttcttttg	360
tctgcaagat	agagcttttc	tatgtaggaa	atgtgatgtt	gcaatccaca	ctgtgaatcc	420
tcatgttttc	gctcaccaga	gRdtYcttM	ctcactggaa	tcaaaagtgg	tcttgaatct	480
atagacactg	gtcctcttac	taaatcctca	ctaccaatg	atgataaaac	catggagacc	540
aaaccttttg	ttaactctat	acctgagcct	caaaagatgg	cttcgatca	tcatcatcac	600
cagcagcagc	aggaacagca	ggaaggagtt	ataccgggaa	ctaaagtcaa	tgatcagaca	660
tcgacaaagc	tctctctcgt	aagtgcggga	tcaactactg	gaagcattcc	tcagtggcaa	720
atagaggaga	ttttcgggct	aaccgacttt	gatcagagct	atgaatacat	ggagaaatat	780
ggatcatcta	agggcgatac	tagtagacga	ggagattcag	acagttcttc	gatgatgaga	840
tctgcagaag	aagatgagga	agataacaat	aactgcttgg	gaggtgagac	atcatggggc	900
gtttcacaga	ttcaggtctc	acctacagcg	tctgttctaa	actggcctaa	gcattttcac	960
caccactctg	tgtttgttcc	ggacataact	tcttcaactc	cttataccgg	ttcatccccc	1020
aatcaaaagg	tggggaacg	cgccgcaacg	tcttagcatt	tgtaatatc	tttagccgcg	1080
ttgagaaaag	agattggcag	ctttctcagt	agatgtaaga	tcacataaat	gatttggaaa	1140
cttctaatgt	atgtagctgt	gagagtcggt	gttctttgtt	agctgaaaaa	acaaaaagat	1200
gtttatttgg	tcg					

(2) INFORMATION FOR SEQ ID NO:2580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2580:

Met	Lys	Ile	Gln	Cys	Asn	Val	Cys	Glu	Ala	Ala	Glu	Ala	Thr	Val	Leu	
1																
Xaa	Cys	Ala	Xaa	Glu	Ala	Ala	Leu	Cys	Trp	Ala	Cys	Asp	Glu	Lys	Ile	
His	Ala	Ala	Asn	Lys	Leu	Ala	Gly	Lys	His	Gln	Arg	Val	Pro	Leu	Ser	
Ala	Ser	Ala	Ser	Ser	Ile	Pro	Lys	Cys	Asp	Ile	Cys	Xaa	Xaa	Ala	Ser	
Gly	Phe	Phe	Phe	Cys	Leu	Gln	Asp	Arg	Ala	Leu	Cys	Arg	Lys	Cys		
Asp	Val	Ala	Ile	His	Thr	Val	Asn	Pro	His	Val	Ser	Ala	His	Gln	Xaa	
Xaa	Xaa	Xaa	Ser	Leu	Glu	Ser	Lys	Leu	Val	Leu	Asn	Leu				

(2) INFORMATION FOR SEQ ID NO:2581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..174
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1573684
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2581:

```
Met Glu Thr Lys Pro Phe Val Gln Ser Ile Pro Glu Pro Gln Lys Met
1      5      10      15
Ala Phe Asp His His His Gln Gln Gln Glu Gln Gln Glu Gly
20     25     30
Val Ile Pro Gly Thr Lys Val Asn Asp Gln Thr Ser Thr Lys Leu Pro
35     40     45
Leu Val Ser Ser Gly Ser Thr Thr Gly Ser Ile Pro Gln Trp Gln Ile
50     55     60
Glu Glu Ile Phe Gly Leu Thr Asp Phe Asp Gln Ser Tyr Glu Tyr Met
65     70     75     80
Glu Asn Asn Gly Ser Ser Lys Ala Asp Thr Ser Arg Arg Gly Asp Ser
85     90     95
Asp Ser Ser Ser Met Met Arg Ser Ala Glu Glu Asp Gly Glu Asp Asn
100    105    110
Asn Asn Cys Leu Gly Gly Glu Thr Ser Trp Ala Val Pro Gln Ile Gln
115    120    125
Ser Pro Pro Thr Ala Ser Gly Leu Asn Trp Pro Lys His Phe His His
130    135    140
His Ser Val Phe Val Pro Asp Ile Thr Ser Ser Thr Pro Tyr Thr Gly
145    150    155    160
Ser Ser Pro Asn Gln Arg Val Gly Lys Arg Arg Arg Arg Phe
165    170
```

- (2) INFORMATION FOR SEQ ID NO:2582:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..159
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1573685
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2582:

```
Met Ala Phe Asp His His His His Gln Gln Gln Glu Gln Glu
1      5      10      15
Gly Val Ile Pro Gly Thr Lys Val Asn Asp Gln Thr Ser Thr Lys Leu
20     25     30
Pro Leu Val Ser Ser Gly Ser Thr Thr Gly Ser Ile Pro Gln Trp Gln
35     40     45
Ile Glu Glu Ile Phe Gly Leu Thr Asp Phe Asp Gln Ser Tyr Glu Tyr
50     55     60
Met Glu Asn Asn Gly Ser Ser Lys Ala Asp Thr Ser Arg Arg Gly Asp
65     70     75     80
Ser Asp Ser Ser Ser Met Met Arg Ser Ala Glu Glu Asp Gly Glu Asp
85     90     95
Asn Asn Asn Cys Leu Gly Gly Glu Thr Ser Trp Ala Val Pro Gln Ile
100    105    110
Gln Ser Pro Pro Thr Ala Ser Gly Leu Asn Trp Pro Lys His Phe His
115    120    125
His His Ser Val Phe Val Pro Asp Ile Thr Ser Ser Thr Pro Tyr Thr
```

130 135 140
Gly Ser Ser Pro Asn Gln Arg Val Gly Lys Arg Arg Arg Phe
145 150 155

(2) INFORMATION FOR SEQ ID NO:2583:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1583 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1583
(D) OTHER INFORMATION: / Ceres Seq. ID 1573701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2583:

```

aaaaaagcta gaaaaacctt tccaaaaaat gcaaaagaacc gtaacttagt cttcttcttta 60
ggggatttag cgtctttttac actctccagt ttcccggtaa ctgtttccgg cgagccccctt 120
atcttatttca ctttccggcga ctcttctctac gatgtgggca acacgaagtt cttctctgtcg 180
gagttcgaatc cagccaccac gtggccttac ggcgattcca tcgatgatcc ctccggctcgt 240
tggtctgacg gccacattgt cccagatttc gtccgtcgat tgattgtgca tcgtgaacgc 300
attctctccg tacttgatcc aaaagctgat ctttctcgtg gagcaagctt tgccattgct 360
ggagcagttt ttcttggatc tcaatctact actgcatcca tgaattttgg acaacagata 420
tcgaagtgtt tagagttaca taagcaatgg actgataaag aacgagcaga agctatatac 480
atggtaaaaca taggagctga ggactacttg aatttcgcaa aggcctcatcc aaatggcaat 540
actgtgggagc agctaaactga agttgcccac gttctccaaa ggataccaaag agagctcacg 600
agctgtgggagc agctaaactga agttgcccac gttctccaaa ggataccaaag agagctcacg 660
agctgtgggagc agctaaactga agttgcccac gttctccaaa ggataccaaag agagctcacg 720
tgtttaccga tagtgagaca agagttaaag accggtgaga attgtatgga gatggtcaac 780
ttcatgttga aaacgcacaa tgaaaggctt agtcgtttgc tcggtgcgat aaccgtaccg 840
atactgtacc gtggcttcgc gtacagcctc ttgtatttca atggtgaaat tctccggagg 900
atcaatgaac catcaactcca ttgatatact gatacaacga cttcttgcgt cggaactgga 960
tcgagaaagt catacgggtg cggttatagt aacgtgcgat ctaagctctg cagctaccag 1020
aaatcatttt tgttcttcga cggcgctcac aacacgcaga aaacgcgata agaaagttgct 1080
aatctgtttt attccggaga caaacatgtc gtctctccga tgaataataa ggatctcgta 1140
ggtaaaagcag cgaccgatct tcttgcaaaa gaaatctaga aatcccaact ggtgtctggt 1200
ctgtttcttt gaaataagta Ccaatgggtg ttgtgtgaaa ctgtaaaact ctgtattcaa 1260
cttcatatat atatgatgat aaagaaaaaa taacacgttt acattgcaaa aaaaaaaa 1320
aaaaaacgatg acaagaccaa cgtcaaggcc gctgggggta aggtcgccgc gcaagctggc 1380
gagataggtg cggaggccct ggagaggatg ttctgtctct tccccaccac caagacctac 1440
ttcccgcaat tcgacctgag ccacggctct gccaggtta agggccacgg caagaaggtg 1500
gccgacgcgc tgaccaacgc cgtggcgcac gtggacgaca tgcccaacgc gctgtccgcg 1560
ctgagcgacc tgcacgcgca agcacttcgg gtggacccGG Tcaacttcaa gctcctaagc

```

(2) INFORMATION FOR SEQ ID NO:2584:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 372 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..372
(D) OTHER INFORMATION: / Ceres Seq. ID 1573702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2584:

```

Lys Lys Ala Arg Lys Thr Phe Pro Lys Met Ala Lys Asn Arg Asn Leu
1 5 10 15
Val Phe Phe Leu Gly Val Leu Ala Ser Phe Thr Leu Ser Ser Phe Pro
20 25 30
Val Thr Val Ser Gly Glu Pro Pro Ile Leu Phe Thr Phe Gly Asp Ser
35 40 45
Ser Tyr Asp Val Gly Asn Thr Lys Phe Phe Ser Ser Glu Phe Asp Pro

```


50	55	60
Ala Thr Thr Trp Pro Tyr Gly Asp Ser Ile Asp Asp Pro Ser Gly Arg		
65	70	75
Trp Ser Asp Gly His Ile Val Pro Asp Phe Val Gly Arg Leu Ile Gly		
	85	90
His Arg Glu Pro Ile Pro Pro Val Leu Asp Pro Lys Ala Asp Leu Ser		
	100	105
Arg Gly Ala Ser Phe Ala Ile Ala Gly Ala Val Val Leu Gly Ser Gln		
	115	120
Ser Thr Thr Ala Ser Met Asn Phe Gly Gln Gln Ile Ser Lys Phe Leu		
	130	135
Glu Leu His Lys Gln Trp Thr Asp Lys Glu Arg Ala Glu Ala Ile Tyr		
	145	150
Met Val Asn Ile Gly Ala Glu Asp Tyr Leu Asn Phe Ala Lys Ala His		
	165	170
Pro Asn Ala Asn Thr Val Glu Gln Leu Thr Gln Val Ala His Val Leu		
	180	185
Gln Arg Ile Pro Arg Glu Leu Thr Ser Leu Tyr Arg Ala Gly Gly Ala		
	195	200
Arg Lys Phe Ala Val Gln Asn Leu Gly Pro Leu Gly Cys Leu Pro Ile		
	210	215
Val Arg Gln Glu Phe Lys Thr Gly Glu Asn Cys Met Glu Met Val Asn		
	225	230
Phe Met Val Lys Thr His Asn Glu Arg Leu Ser Arg Leu Leu Val Ala		
	245	250
Ile Thr Val Pro Ile Leu Tyr Arg Gly Phe Arg Tyr Ser Leu Phe Asp		
	260	265
Phe Asn Gly Glu Ile Leu Arg Arg Ile Asn Glu Pro Ser Leu His Gly		
	275	280
Tyr Thr Asp Thr Thr Thr Ser Cys Cys Gly Thr Gly Ser Arg Asn Ala		
	290	295
Tyr Gly Cys Gly Tyr Ser Asn Val His Ala Lys Leu Cys Ser Tyr Gln		
	305	310
Lys Ser Phe Leu Phe Phe Asp Gly Arg His Asn Thr Glu Lys Thr Asp		
	325	330
Glu Glu Val Ala Asn Leu Phe Tyr Ser Gly Asp Lys His Val Val Ser		
	340	345
Pro Met Asn Ile Lys Asp Leu Val Gly Lys Ala Ala Thr Asp Leu Leu		
	355	360
Ala Gln Glu Ile		
370		

(2) INFORMATION FOR SEQ ID NO:2585:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..363

(D) OTHER INFORMATION: / Ceres Seq. ID 1573703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2585:

Met Ala Lys Asn Arg Asn Leu Val Phe Phe Leu Gly Val Leu Ala Ser		
1	5	10
Phe Thr Leu Ser Ser Phe Pro Val Thr Val Ser Gly Glu Pro Pro Ile		
	20	25
Leu Phe Thr Phe Gly Asp Ser Ser Tyr Asp Val Gly Asn Thr Lys Phe		
	35	40
Phe Ser Ser Glu Phe Asp Pro Ala Thr Thr Trp Pro Tyr Gly Asp Ser		
	50	55
		60

```

Ile Asp Asp Pro Ser Gly Arg Trp Ser Asp Gly His Ile Val Pro Asp
65              70              75              80
Phe Val Gly Arg Leu Ile Gly His Arg Glu Pro Ile Pro Pro Val Leu
85
Asp Pro Lys Ala Asp Leu Ser Arg Gly Ala Ser Phe Ala Ile Ala Gly
100              105
Ala Val Val Leu Gly Ser Gln Ser Thr Thr Ala Ser Met Asn Phe Gly
115              120              125
Gln Gln Ile Ser Lys Phe Leu Glu Leu His Lys Gln Trp Thr Asp Lys
130              135
Glu Arg Ala Glu Ala Ile Tyr Met Val Asn Ile Gly Ala Glu Asp Tyr
145              150              155              160
Leu Asn Phe Ala Lys Ala His Pro Asn Ala Asn Thr Val Glu Gln Leu
165              170              175
Thr Gln Val Ala His Val Leu Gln Arg Ile Pro Arg Glu Leu Thr Ser
180              185
Leu Tyr Arg Ala Gly Gly Ala Arg Lys Phe Ala Val Gln Asn Leu Gly
195              200              205
Pro Leu Gly Cys Leu Pro Ile Val Arg Gln Glu Phe Lys Thr Gly Glu
210              215              220
Asn Cys Met Glu Met Val Asn Phe Met Val Lys Thr His Asn Glu Arg
225              230              235              240
Leu Ser Arg Leu Leu Val Ala Ile Thr Val Pro Ile Leu Tyr Arg Gly
245              250              255
Phe Arg Tyr Ser Leu Phe Asp Phe Asn Gly Glu Ile Leu Arg Arg Ile
260              265              270
Asn Glu Pro Ser Leu His Gly Tyr Thr Asp Thr Thr Thr Ser Cys Cys
275              280              285
Gly Thr Gly Ser Arg Asn Ala Tyr Gly Cys Gly Tyr Ser Asn Val His
290              295              300
Ala Lys Leu Cys Ser Tyr Gln Lys Ser Phe Leu Phe Phe Asp Gly Arg
305              310              315              320
His Asn Thr Glu Lys Thr Asp Glu Glu Val Ala Asn Leu Phe Tyr Ser
325              330              335
Gly Asp Lys His Val Val Ser Pro Met Asn Ile Lys Asp Leu Val Gly
340              345              350
Lys Ala Ala Thr Asp Leu Leu Ala Gln Glu Ile
355              360

```

(2) INFORMATION FOR SEQ ID NO:2586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..239
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2586:

```

Met Asn Phe Gly Gln Gln Ile Ser Lys Phe Leu Glu Leu His Lys Gln
1              5              10              15
Trp Thr Asp Lys Glu Arg Ala Glu Ala Ile Tyr Met Val Asn Ile Gly
20              25              30
Ala Glu Asp Tyr Leu Asn Phe Ala Lys Ala His Pro Asn Ala Asn Thr
35              40              45
Val Glu Gln Leu Thr Gln Val Ala His Val Leu Gln Arg Ile Pro Arg
50              55              60
Glu Leu Thr Ser Leu Tyr Arg Ala Gly Gly Ala Arg Lys Phe Ala Val
65              70              75              80
Gln Asn Leu Gly Pro Leu Gly Cys Leu Pro Ile Val Arg Gln Glu Phe

```

(2) INFORMATION FOR SEO ID NO:2587:

(A) LENGTH: 1188 base pairs

(B) TYPE: nucleic acid

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1188

(D) OTHER INFORMATION: / Ceres Seq. ID 1573705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2587:

atcattctcgc	gtttaactaca	aacacataaat	aaaaacaaga	gaaagagata	taatatgggt	60
gggtggggaca	tcgcagtagca	cgttggtgcc	ggatcgaacc	taatcttcc	gcgagagaga	120
caagaagaaga	cgaaacagct	ctttagctcgt	tgcttcaacc	tcggcataat	agctttgcgt	180
tcgaattggt	ccgcacattga	cgtcgtttgag	ctcgtcatta	gagaatttga	gacgcattat	240
ctgttttaatt	caggccgcgtg	atctctcttcg	acggagaaga	gacccgttga	gatggaagct	300
agcaattatgg	accgttcgaa	gagacgttcg	gggtcgcgtt	ccgggataac	cacccgtgaa	360
aatctcatat	ctcgttcgtc	tcgcgtcatg	gacaaactct	cccacttcta	cctctgcttc	420
tcaggttcgac	aggaatttcgc	ccgcacaacac	ggagttgaaa	ttgtggacaac	cgagctatctt	480
gtcacggcag	acaacgtga	aatgtctcaag	ttggccaagc	aaagtaactc	catcttggtt	540
gattaccgga	ttccgcgat	gggattgtgc	ggcccgagct	cgaccacgac	tccaatctga	600
atgaacgctg	ttccatcag	catcttacga	cGgggaaca	ctcgggtcgc	tttgtgttga	660
cgggaaagga	cattgtgcgc	ccgggacatc	cacgggttgt	ttaatgaac	agatgatggg	720
aaggatttgt	gactcgcgc	tgataggagc	cgggacgtat	cgctcgagct	tttgtgggtg	780
gtcgtctgat	ggagaaggag	aagcaattat	aagaagcaac	cttcgtcgtg	atgtctcagc	840
tgttatgacg	tataaaggac	ttaacctcca	agagccgatt	gattacgcta	tcaagcatcg	900
actttagaca	gggttcgctg	gcactcattg	tgctcgcggt	taagcagagg	ttgtttggcg	960
tttttaactc	aatgggatgt	tcacgggattg	tgcaactgag	gatgattcta	tggaactgct	1020
ttatttggag	tgaagaatat	tttagattaa	gaaatgtct	tactgattat	taactcgtca	1080
tcgctctatt	aattttggtta	ttcatattca	taaaagctga	gtagtataat	tagttctctc	1140
gtctatcaca	gtctataatt	tatttgttgt	taattcggtt	tcaaatgg		

(2) INFORMATION FOR SEQ ID NO:2588:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..219

1	Leu	1	Leu	5	Leu	5	Thr	5	Glu	10	Thr	10	His	10	Asn	10	Lys	15	Thr	15	Lys	15	Arg	15	Lys	15	Arg
Tyr	Asn	20	Met	20	Gly	20	Trp	20	Ala	25	Ile	25	Ala	25	Val	25	His	30	Gly	30	Gly	30	Ala	30	Gly	30	Ile
Asp	Pro	35	Asn	35	Leu	35	Pro	35	Ala	40	Glu	40	Arg	40	Gln	40	Glu	45	Ala	45	Lys	45	Gln	45	Leu	45	Leu
Thr	Arg	50	Cys	50	Leu	50	Asn	50	Leu	55	Gly	55	Ile	55	Ile	55	Ala	60	Leu	60	Arg	60	Ser	60	Asn	60	Val
Ala	Ile	65	Asp	65	Val	65	Val	65	Glu	70	Leu	70	Val	70	Ile	70	Arg	75	Glu	75	Leu	75	Glu	75	Thr	75	Asp
Leu	Phe	85	Asn	85	Ser	85	Gly	85	Arg	90	Gly	90	Ser	90	Ser	90	Leu	90	Thr	90	Glu	95	Lys	95	Gly	95	Thr
Glu	Met	100	Glu	100	Ala	100	Ser	100	Ile	105	Met	105	Asp	105	Gly	105	Thr	110	Lys	110	Arg	110	Arg	110	Cys	110	Gly
Val	Ser	115	Gly	115	Ile	115	Thr	115	Thr	120	Thr	120	Val	120	Lys	120	Asn	125	Pro	125	Ile	125	Ser	125	Leu	125	Ala
Val	Met	130	Asp	130	Lys	130	Ser	130	Pro	135	His	135	Ser	135	Tyr	135	Leu	140	Ala	140	Phe	140	Ser	140	Gly	140	Ala
Asp	Phe	145	Ala	145	Arg	145	Lys	145	Gln	150	Gly	150	Val	150	Glu	150	Ile	155	Val	155	Asp	155	Asn	155	Glu	155	Tyr
Val	Thr	165	Asp	165	Asp	165	Asn	165	Val	170	Gly	170	Met	170	Leu	170	Val	175	Leu	175	Ala	175	Lys	175	Glu	175	Ala
Ser	Ile	180	Leu	180	Phe	180	Asp	180	Tyr	185	Arg	185	Ile	185	Pro	185	Pro	190	Met	190	Gly	190	Cys	190	Ala	190	Gly
Ala	Ala	195	Thr	195	Asp	195	Ser	195	Pro	200	Ile	200	Gln	200	Met	200	Asn	205	Gly	205	Leu	205	Pro	205	Ile	205	Ser
Tyr	Ala	210	Pro	210	Gly	210	Asp	210	Ser	215	Arg	215	Val	215	Arg	215	Cys	215	Gly	215							

Met	Gly	Gly	Trp	Ala	Ile	Ala	Val	His	Gly	Gly	Ala	Gly	Ile	Asp	Pro
1			5						10					15	
Asn	Leu	Pro	Ala	Glu	Arg	Gln	Glu	Glu	Ala	Lys	Gln	Leu	Leu	Thr	Arg
			20					25					30		
Cys	Leu	Asn	Leu	Gly	Ile	Ile	Ala	Leu	Arg	Ser	Asn	Val	Ser	Ala	Ile
			35				40				45				
Asp	Val	Val	Glu	Leu	Val	Ile	Arg	Glu	Leu	Glu	Thr	Asp	Pro	Leu	Phe
			50			55					60				
Asn	Ser	Gly	Arg	Gly	Ser	Ser	Leu	Thr	Glu	Lys	Gly	Thr	Val	Glu	Met
65					70					75					80
Glu	Ala	Ser	Ile	Met	Asp	Gly	Thr	Lys	Arg	Arg	Cys	Gly	Ala	Val	Ser
				85				90						95	
Gly	Ile	Thr	Thr	Val	Lys	Asn	Pro	Ile	Ser	Leu	Ala	Arg	Leu	Val	Met
			100					105					110		
Asp	Lys	Ser	Pro	His	Ser	Tyr	Leu	Ala	Phe	Ser	Gly	Ala	Glu	Asp	Phe
			115				120					125			
Ala	Arg	Lys	Gln	Gly	Val	Glu	Ile	Val	Asp	Asn	Glu	Tyr	Phe	Val	Thr
			130			135					140				
Asp	Asp	Asn	Val	Gly	Met	Leu	Lys	Leu	Ala	Lys	Glu	Ala	Asn	Ser	Ile

145 150 155 160
Leu Phe Asp Tyr Arg Ile Pro Pro Met Gly Cys Ala Gly Ala Ala Ala
165 170 175
Thr Asp Ser Pro Ile Gln Met Asn Gly Leu Pro Ile Ser Ile Tyr Ala
180 185 190
Pro Gly Asp Ser Arg Val Arg Cys Gly
195 200

(2) INFORMATION FOR SEQ ID NO:2590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2590:

Met Glu Ala Ser Ile Met Asp Gly Thr Lys Arg Arg Cys Gly Ala Val
1 5 10 15
Ser Gly Ile Thr Thr Val Lys Asn Pro Ile Ser Leu Ala Arg Leu Val
20 25 30
Met Asp Lys Ser Pro His Ser Tyr Leu Ala Phe Ser Gly Ala Glu Asp
35 40 45
Phe Ala Arg Lys Gln Gly Val Glu Ile Val Asp Asn Glu Tyr Phe Val
50 55 60
Thr Asp Asp Asn Val Gly Met Leu Lys Leu Ala Lys Glu Ala Asn Ser
65 70 75 80
Ile Leu Phe Asp Tyr Arg Ile Pro Pro Met Gly Cys Ala Gly Ala Ala
85 90 95
Ala Thr Asp Ser Pro Ile Gln Met Asn Gly Leu Pro Ile Ser Ile Tyr
100 105 110
Ala Pro Gly Asp Ser Arg Val Arg Cys Gly
115 120

(2) INFORMATION FOR SEQ ID NO:2591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1048 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1048
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2591:

aacgcaattta	aattaatatt	tatggataat	atgggtaata	aataaggaac	ttctatttat	60
atcacaaaaa	gtcactgggt	ttcttcgtgt	gacttcacca	ctttctcacc	tcaccaaaaa	120
atggctctct	cactcttttc	agtctttatc	tttttccatg	tttttaccac	tggtgttttt	180
gtgtcttcaa	atgagggaatc	caaggcccta	gtttctttac	caacgcacca	acttccatcg	240
ccatctcctg	ctaccacaaac	gcggtcgcca	gctctcaaac	cgccgacgcc	gtgtacaaag	300
ccaccacgcg	tgccaaactac	tcctattaaa	ccaccaccca	caaaaacctcc	gggtcaaaCct	360
ccaactactt	cggttacacc	agtaaaacct	ccggtttcaa	ctcctccgat	caaaactaccg	420
ccgggtacaa	caactacgta	caaaacccca	acgccaacag	ttaaaccacc	gtccgtccaa	480
ccactactgt	acaaaacccc	actccaacg	gttaaaccac	ccactacatc	accggtttaa	540
ccaccacta	cgccaccagt	ccaatcacgc	ccggtccaac	caactacgta	caaaaccccca	600
acgtcacccg	ttaaaaccacc	caccacaact	ccaccgggta	aaacccccac	caacgacgcca	660
ccggtccaac	caactacgta	caatccccca	actacacgta	ttaaaccacc	tacagcgcgc	720
cctgtcaaac	ctccgacacc	acctcccgta	agaactcgga	tagattgcgt	gcctttatgt	780
gggacgaggt	gtgggcaaca	ctcgaggaag	aacgtatgta	tgagagcgctg	cgctacggtgc	840

tgctaccgtg gcaagtgtgt tccccaggc acctacggta ataaggagaa gtgtggatct 900
tgttacggca acatgaagac acgtggtgga aaatccaaat gtccttgaac ctttatatga 960
cgatggttgt taaacgaaat aatttaaatac aatggagttt ttataagttt gtaatgcgtt 1020
tgttttttgtt atagtaatat tgagttgg

(2) INFORMATION FOR SEQ ID NO:2592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..275

(D) OTHER INFORMATION: / Ceres Seq. ID 1573714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2592:

Met	Ala	Leu	Ser	Leu	Ser	Val	Phe	Ile	Phe	Phe	His	Val	Phe	Thr
1		5						10					15	
Asn	Val	Val	Phe	Ala	Ala	Ser	Asn	Glu	Glu	Ser	Lys	Ala	Leu	Val
		20						25				30		
Leu	Pro	Thr	Pro	Thr	Leu	Pro	Ser	Pro	Ser	Pro	Ala	Thr	Lys	Pro
		35				40					45			
Ser	Pro	Ala	Leu	Lys	Pro	Pro	Thr	Pro	Ser	Tyr	Lys	Pro	Pro	Thr
		50				55				60				
Pro	Thr	Thr	Pro	Ile	Lys	Pro	Pro	Thr	Thr	Lys	Pro	Pro	Val	Lys
65					70					75				80
Pro	Thr	Thr	Ser	Val	Thr	Pro	Val	Lys	Pro	Pro	Val	Ser	Thr	Pro
				85				90						95
Ile	Lys	Leu	Pro	Pro	Val	Gln	Pro	Pro	Thr	Tyr	Lys	Pro	Pro	Thr
		100				105						110		
Thr	Val	Lys	Pro	Pro	Ser	Val	Gln	Pro	Pro	Thr	Tyr	Lys	Pro	Thr
		115				120						125		
Pro	Thr	Val	Lys	Pro	Pro	Thr	Thr	Ser	Pro	Val	Lys	Pro	Pro	Thr
		130				135					140			
Pro	Pro	Val	Gln	Ser	Pro	Pro	Val	Gln	Pro	Pro	Thr	Tyr	Lys	Pro
145					150					155				160
Thr	Ser	Pro	Val	Lys	Pro	Pro	Thr	Thr	Thr	Pro	Pro	Val	Lys	Pro
				165						170				175
Thr	Thr	Thr	Pro	Pro	Val	Gln	Pro	Pro	Thr	Tyr	Asn	Pro	Pro	Thr
			180						185				190	
Pro	Val	Lys	Pro	Pro	Thr	Ala	Pro	Pro	Val	Lys	Pro	Pro	Thr	Pro
			195			200					205			
Pro	Val	Arg	Thr	Arg	Ile	Asp	Cys	Val	Pro	Leu	Cys	Gly	Thr	Arg
		210				215					220			
Gly	Gln	His	Ser	Arg	Lys	Asn	Val	Cys	Met	Arg	Ala	Cys	Val	Thr
225					230					235				240
Cys	Tyr	Arg	Cys	Lys	Cys	Val	Pro	Pro	Gly	Thr	Tyr	Gly	Asn	Lys
				245					250					255
Lys	Cys	Gly	Ser	Cys	Tyr	Ala	Asn	Met	Lys	Thr	Arg	Gly	Gly	Lys
			260					265					270	
Lys	Cys	Pro												
		275												

(2) INFORMATION FOR SEQ ID NO:2593:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 836 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..836

(D) OTHER INFORMATION: / Ceres Seq. ID 1573727

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2593:

cttttttttt	tgtctattat	ttttttgact	ttgatctccc	atcagttcat	cttctctttc	60
ttcttctgat	caacctatgg	tgtgtgtata	agtgtgtcag	tctctttacc	ttcctccaag	120
tcctctctct	ttctcaccaa	aatctctctc	gtatcccttc	aaaggatttt	cctcaagaag	180
agcacagtgt	gttacagaag	agttgtgtca	gtgaaggctc	aggtgacaac	agatactacc	240
gaggcaccac	cagttaaagt	agtcaaggag	tctaagaaac	aggaagaagg	gattgtgtgc	300
aacaaatttc	aacctaaaga	cccttacact	ggtcgtgtcc	ttttgaacac	caagatcacc	360
ggtgatgacg	ctcccggtga	gacttggcac	attgtcttca	ccaccgaagg	TGagWgNttc	420
cgtatagaga	aggacaatgc	ataggagagt	ttccagaggg	aatagacaag	aacgggaagc	480
cgcacaagct	cagcgtttac	tctatcgcca	gtagtcccat	tgtgtacttt	ggagactcca	540
agaccgtttc	ttctctgttc	aagagactag	tttacacaaa	tgatggcgga	gagattgtta	600
agggggctgt	ctccaacttc	ttgtgtgact	tgaagccggg	tgatgaagct	aagatcactg	660
gacctgttgg	caaggaatag	cttatgccaa	aagaccocaa	tgccaccatc	atcatgcttg	720
gaacaggaac	tggaaatagt	ccattcagat	cattttgtg	gaaaatgttc	tttgaggagc	780
acgaggacta	caagttcaat	ggtttggcgt	ggcttttctt	gggtgtacc	acaagc	

(2) INFORMATION FOR SEQ ID NO:2594:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1573728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2594:

Phe	Phe	Phe	Ala	Tyr	Tyr	Phe	Phe	Asp	Phe	Asp	Leu	Pro	Ser	Val	His	
1				5						10				15		
Leu	Leu	Leu	Leu	Leu	Leu	Ile	Asn	His	Gly	Cys	Cys	Tyr	Lys	Cys	Cys	
				20				25					30			
Ser	Leu	Phe	Thr	Phe	Leu	Gln	Val	Ile	Leu	Ser	Pro	His	Gln	Asn	Leu	
				35			40					45				
Leu	Cys	Ile	Pro	Ser	Lys	Asp	Phe	Pro	Gln	Glu	Glu	His	Ser	Val	Leu	
				50			55					60				
Gln	Lys	Ser	Cys	Val	Ser	Glu	Gly	Ser	Gly	Asp	Asn	Arg	Tyr	Tyr	Arg	
				65		70			75					80		
Gly	Thr	Thr	Ser													

(2) INFORMATION FOR SEQ ID NO:2595:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1573729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2595:

Met	Ala	Ala	Ala	Ile	Ser	Ala	Ala	Val	Ser	Leu	Pro	Ser	Ser	Lys	Ser	
1				5						10				15		
Ser	Ser	Leu	Leu	Thr	Lys	Ile	Ser	Ser	Val	Ser	Pro	Gln	Arg	Ile	Phe	
				20				25				30				
Leu	Lys	Lys	Ser	Thr	Val	Cys	Tyr	Arg	Arg	Val	Val	Ser	Val	Lys	Ala	
				35			40					45				
Gln	Val	Thr	Thr	Asp	Thr	Thr	Glu	Ala	Pro	Pro	Val	Lys	Val	Val	Lys	
				50			55				60					

Glu Ser Lys Lys Gln Glu Glu Gly Ile Val Val Asn Lys Phe Lys Pro
65 70 75 80
Lys Asn Pro Tyr Thr Gly Arg Cys Leu Leu Asn Thr Lys Ile Thr Gly
85 90 95
Asp Asp Ala Pro Gly Glu Thr Trp His Ile Val Phe Thr Thr Glu Gly
100 105 110
Glu Xaa Phe Arg Ile Glu Lys Asp Asn Arg
115 120

(2) INFORMATION FOR SEQ ID NO:2596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1275

(D) OTHER INFORMATION: / Ceres Seq. ID 1573730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2596:

```

aatctttttt tttttgttta ttattttttt gactttgac tcccatcagt tcatctcttt      60
cttctttctt tgatcaacca tgggtgtctg tataagtgtc gcagtctctt taccttcttc      120
caagtcattc tctctctcca ccaaaatctc ctctgtatcc cctcaaagga ttttctctaa      180
gaagagacaca gtgtgtttaca gaagagtgtt gtcagtgaa gctcagggtga caacagatac      240
taccgaggca ccaccaggtta aagtagtcaa ggaagtctaa aaacaggaga aagggattgt      300
tgtcaacaaa ttcaaacctta agaaccctta cactggctgc tgctttttga acaccaagat      360
caccgggtgat gacgtctccg gtgagacttg gcacattgtc ttcaccaccg aaggtgaggt      420
tcctgtataga gaaggacaat cgataggagt gattccagag ggaatagaca agaaccggaa      480
gcgcgacaag ctacagcttt actctatcgc gagttagtgc attggtgact ttggagactc      540
caagaccgtt tctctctgtg tcaagagact agttttacaa aatgatggcg gagagattgt      600
taagggggtc tgctccaact tcttgtgtga cttgaagcgg ggtgatgaag ctaagatcac      660
tggacctgtt ggcaaggaaa tgccttatgc aaaagaccoc aatgccacca tcatctgct      720
tggaacagga actggaatag ctccattcag atcatttttg tggaaaatgt tctttgagga      780
gcacgaggac tacaagtcca atggtttggc gtggtctttc ttgggtgtac ccagaagcag      840
ctcactgcta tacaaggagg agtttgagaa gatgaaggag aagaaccagc acaacttcag      900
gctggacttt gcggtgagca gagagcagac gaacgagaag ggagagaaaa tgtacattca      960
gacaagaatg ccagagtatg cagAaagagc tgtgggagtt gctgaagaaa gacaacacct      1020
tgtttttacat gtgtgtgtctt aagggtatgg agaagggat cgtatgacatt atggtctcgc      1080
ttgctgtcaa agatgggata gattgtgttg atacaagaa gcaatttgaag agggatgaac      1140
agtggaatgt tgaagtctac taaggaaagt tctgaggagg taattatata atgtagataa      1200
aaagcttcag atgcattgtg aaatcttcac atctgcttct tttttcttc tcaaggattt      1260
tcaatcaaaa catcc

```

(2) INFORMATION FOR SEQ ID NO:2597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..320

(D) OTHER INFORMATION: / Ceres Seq. ID 1573731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2597:

```

Met Ala Ala Ala Ile Ser Ala Ala Val Ser Leu Pro Ser Ser Lys Ser
1 5 10 15
Ser Ser Leu Leu Thr Lys Ile Ser Ser Val Ser Pro Gln Arg Ile Phe
20 25 30
Leu Lys Lys Ser Thr Val Cys Tyr Arg Arg Val Val Ser Val Lys Ala
35 40 45
Gln Val Thr Thr Asp Thr Thr Glu Ala Pro Pro Val Lys Val Val Lys

```


50	55	60
Glu Ser Lys Lys Gln	Glu Glu Gly Ile Val	Val Asn Lys Phe Lys Pro
65	70	75
Lys Asn Pro Tyr Thr	Gly Arg Cys Leu Leu	Asn Thr Lys Ile Thr Gly
85	90	95
Asp Asp Ala Pro Gly	Glu Thr Trp His Ile Val	Phe Thr Thr Glu Gly
100	105	110
Glu Val Pro Tyr Arg	Glu Gly Gln Ser Ile Gly	Val Ile Pro Glu Gly
115	120	125
Ile Asp Lys Asn Gly	Lys Pro His Lys Leu Arg	Leu Tyr Ser Ile Ala
130	135	140
Ser Ser Ala Ile Gly	Asp Phe Gly Asp Ser	Lys Thr Val Ser Leu Cys
145	150	155
Val Lys Arg Leu Val	Tyr Thr Asn Asp Gly	Gly Glu Ile Val Lys Gly
165	170	175
Val Cys Ser Asn Phe	Leu Cys Asp Leu Lys	Pro Gly Asp Glu Ala Lys
180	185	190
Ile Thr Gly Pro Val	Gly Lys Glu Met Leu Met	Pro Lys Asp Pro Asn
195	200	205
Ala Thr Ile Ile Met	Leu Gly Thr Gly Ile Ala	Pro Phe Arg
210	215	220
Ser Phe Leu Trp Lys	Met Phe Phe Glu Glu His	Glu Asp Tyr Lys Phe
225	230	235
Asn Gly Leu Ala Trp	Leu Phe Leu Gly Val Pro	Arg Ser Ser Ser Leu
245	250	255
Leu Tyr Lys Glu Glu	Phe Glu Lys Met Lys	Glu Lys Asn Pro Asp Asn
260	265	270
Phe Arg Leu Asp Phe	Ala Val Ser Arg Glu Gln	Thr Asn Glu Lys Gly
275	280	285
Glu Lys Met Tyr Ile	Gln Thr Arg Met Ala Glu	Tyr Ala Glu Arg Ala
290	295	300
Val Gly Val Ala Glu	Glu Arg Gln His Leu Cys	Leu His Val Trp Ser
305	310	315
		320

(2) INFORMATION FOR SEQ ID NO:2598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1339
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2598:

aattattact	ttaattctct	ttccgcctct	ctattcttct	tcttctttag	gatcaatcac	60
cggttagctt	tcttcccatc	cgctctctcg	tttacgacca	gtatacagag	gctggagctg	120
gggaagaaaa	ggattgtcta	tggaggggaga	cgctcggaata	ggttttggtat	gccagaatac	180
tatggatggg	aaggcgagta	atggaaatgg	tttagagaag	actgtacctt	ctgtgtgcct	240
taaggtctat	gcattgtgtac	ctgaggatga	tgctaagtgt	cactccactg	ttgtttctgg	300
gtggtttctg	gaacctcacc	ctcgctctgg	gaaaaaaggc	ggcaaaagcg	tctatttcaa	360
caaccttatg	tggccaggag	aagcacactc	actgaaagtt	gagaaaagtc	tgttcaaaga	420
caagtcgagt	tttcaggag	tcttagtggt	cgagtcagcc	acgtacggaa	aggtgcttgt	480
tctagatggg	atcgtaacgc	tgaccgaaaa	agatgaatgt	gcataccagg	agatgatagc	540
ccatctgcct	ttatgtctta	tattctcccc	taaaaatggt	ctgtgtgttg	gtggaggtga	600
tggtgtgtgt	tttcagagaa	ttctcgcaca	tagttcttgt	gaggttatgt	atatctgtga	660
gatagacaag	atggttatag	atgtgtctaa	gaagTtcTtc	cccgagttag	cggttggtgt	720
tgacgatcct	cggtgtcaac	ttcacattag	tgaatgtgct	gagttctctc	gtaaaatccc	780
tgaagggaag	tatgatgcga	tcattgttga	ttcttcagat	cccgtaggtc	ctgctcttgc	840

(2) INFORMATION FOR SEO ID NO:2599:

(A) LENGTH: 359 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..359

(D) OTHER INFORMATION: / Ceres Seq. ID 1573733

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:2599:

Met	Glu	Gly	Asp	Val	Gly	Ile	Gly	Leu	Val	Cys	Gln	Asn	Thr	Met	Asp
1				5				10						15	
Gly	Lys	Ala	Ser	Asn	Gly	Asn	Gly	Leu	Glu	Lys	Thr	Val	Pro	Ser	Cys
			20					25					30		
Cys	Leu	Lys	Ala	Met	Ala	Cys	Val	Pro	Glu	Asp	Asp	Ala	Lys	Cys	His
		35					40					45			
Ser	Thr	Val	Val	Ser	Gly	Trp	Phe	Ser	Glu	Pro	His	Pro	Arg	Ser	Gly
	50					55					60				
Lys	Lys	Gly	Gly	Lys	Ala	Val	Tyr	Phe	Asn	Asn	Pro	Met	Trp	Pro	Gly
65					70					75					80
Glu	Ala	His	Ser	Leu	Lys	Val	Glu	Lys	Val	Leu	Phe	Lys	Asp	Lys	Ser
				85					90					95	
Asp	Phe	Gln	Glu	Val	Leu	Val	Phe	Glu	Ser	Ala	Thr	Tyr	Gly	Lys	Val
		100						105					110		
Leu	Val	Leu	Asp	Gly	Ile	Val	Gln	Leu	Thr	Glu	Lys	Asp	Glu	Cys	Ala
		115					120					125			
Tyr	Gln	Glu	Met	Ile	Ala	His	Leu	Pro	Leu	Cys	Ser	Ile	Ser	Ser	Pro
	130					135					140				
Lys	Asn	Val	Leu	Val	Val	Gly	Gly	Gly	Asp	Gly	Gly	Val	Leu	Arg	Glu
145					150					155					160
Ile	Ser	Arg	His	Ser	Ser	Val	Glu	Val	Ile	Asp	Ile	Cys	Glu	Ile	Asp
				165					170					175	
Lys	Met	Val	Ile	Asp	Val	Ser	Lys	Lys	Phe	Phe	Pro	Glu	Leu	Ala	Val
			180					185					190		
Gly	Phe	Asp	Asp	Pro	Arg	Val	Gln	Leu	His	Ile	Ser	Asp	Ala	Ala	Glu
		195					200					205			
Phe	Leu	Arg	Lys	Ser	Pro	Glu	Gly	Lys	Tyr	Asp	Ala	Ile	Ile	Val	Asp
	210					215				220					
Ser	Ser	Asp	Pro	Val	Gly	Pro	Ala	Leu	Ala	Leu	Val	Glu	Lys	Pro	Phe
225					230					235					240
Phe	Glu	Thr	Leu	Ala	Arg	Ala	Leu	Lys	Pro	Gly	Gly	Val	Leu	Cys	Asn
				245					250					255	
Met	Ala	Glu	Ser	Met	Trp	Leu	His	Thr	His	Leu	Ile	Glu	Asp	Met	Ile
			260					265					270		
Ser	Ile	Cys	Arg	Gln	Thr	Phe	Lys	Ser	Val	His	Tyr	Ala	Trp	Ser	Ser
		275					280					285			
Val	Pro	Thr	Tyr	Pro	Ser	Gly	Val	Ile	Gly	Phe	Val	Leu	Cys	Ser	Thr
		290				295				300					
Glu	Gly	Pro	Ala	Val	Asp	Phe	Lys	Asn	Pro	Ile	Asn	Pro	Ile	Glu	Lys
305					310					315					320

Leu Asp Gly Ala Met Thr His Lys Arg Glu Leu Lys Phe Tyr Asn Ser
325 330 335
Asp Met His Arg Ala Ala Phe Ala Leu Pro Thr Phe Leu Arg Arg Glu
340 345 350
Val Ala Ser Leu Leu Ala Ser
355

(2) INFORMATION FOR SEQ ID NO:2600:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..345

(D) OTHER INFORMATION: / Ceres Seq. ID 1573734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2600:

Met Asp Gly Lys Ala Ser Asn Gly Asn Gly Leu Glu Lys Thr Val Pro
1 5 10 15
Ser Cys Cys Leu Lys Ala Met Ala Cys Val Pro Glu Asp Asp Ala Lys
20 25 30
Cys His Ser Thr Val Val Ser Gly Trp Phe Ser Glu Pro His Pro Arg
35 40 45
Ser Gly Lys Lys Gly Gly Lys Ala Val Tyr Phe Asn Asn Pro Met Trp
50 55 60
Pro Gly Glu Ala His Ser Leu Lys Val Glu Lys Val Leu Phe Lys Asp
65 70 75 80
Lys Ser Asp Phe Gln Glu Val Leu Val Phe Glu Ser Ala Thr Tyr Gly
85 90 95
Lys Val Leu Val Leu Asp Gly Ile Val Gln Leu Thr Glu Lys Asp Glu
100 105 110
Cys Ala Tyr Gln Glu Met Ile Ala His Leu Pro Leu Cys Ser Ile Ser
115 120 125
Ser Pro Lys Asn Val Leu Val Val Gly Gly Gly Asp Gly Gly Val Leu
130 135 140
Arg Glu Ile Ser Arg His Ser Ser Val Glu Val Ile Asp Ile Cys Glu
145 150 155 160
Ile Asp Lys Met Val Ile Asp Val Ser Lys Lys Phe Phe Pro Glu Leu
165 170 175
Ala Val Gly Phe Asp Asp Pro Arg Val Gln Leu His Ile Ser Asp Ala
180 185 190
Ala Glu Phe Leu Arg Lys Ser Pro Glu Gly Lys Tyr Asp Ala Ile Ile
195 200 205
Val Asp Ser Ser Asp Pro Val Gly Pro Ala Leu Ala Leu Val Glu Lys
210 215 220
Pro Phe Phe Glu Thr Leu Ala Arg Ala Leu Lys Pro Gly Gly Val Leu
225 230 235 240
Cys Asn Met Ala Glu Ser Met Trp Leu His Thr His Leu Ile Glu Asp
245 250 255
Met Ile Ser Ile Cys Arg Gln Thr Phe Lys Ser Val His Tyr Ala Trp
260 265 270
Ser Ser Val Pro Thr Tyr Pro Ser Gly Val Ile Gly Phe Val Leu Cys
275 280 285
Ser Thr Glu Gly Pro Ala Val Asp Phe Lys Asn Pro Ile Asn Pro Ile
290 295 300
Glu Lys Leu Asp Gly Ala Met Thr His Lys Arg Glu Leu Lys Phe Tyr
305 310 315 320
Asn Ser Asp Met His Arg Ala Ala Phe Ala Leu Pro Thr Phe Leu Arg
325 330 335
Arg Glu Val Ala Ser Leu Leu Ala Ser

340

345

(2) INFORMATION FOR SEQ ID NO:2601:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..323

(D) OTHER INFORMATION: / Ceres Seq. ID 1573735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2601:

Met	Ala	Cys	Val	Pro	Glu	Asp	Asp	Ala	Lys	Cys	His	Ser	Thr	Val	Val	
1			5					10						15		
Ser	Gly	Trp	Phe	Ser	Glu	Pro	His	Pro	Arg	Ser	Gly	Lys	Lys	Gly	Gly	
			20				25						30			
Lys	Ala	Val	Tyr	Phe	Asn	Asn	Pro	Met	Trp	Pro	Gly	Glu	Ala	His	Ser	
			35				40					45				
Leu	Lys	Val	Glu	Lys	Val	Leu	Phe	Lys	Asp	Lys	Ser	Asp	Phe	Gln	Glu	
			50			55				60						
Val	Leu	Val	Phe	Glu	Ser	Ala	Thr	Tyr	Gly	Lys	Val	Leu	Val	Leu	Asp	
65				70				75						80		
Gly	Ile	Val	Gln	Leu	Thr	Glu	Lys	Asp	Glu	Cys	Ala	Tyr	Gln	Glu	Met	
			85					90					95			
Ile	Ala	His	Leu	Pro	Leu	Cys	Ser	Ile	Ser	Ser	Pro	Lys	Asn	Val	Leu	
			100					105					110			
Val	Val	Gly	Gly	Gly	Asp	Gly	Gly	Val	Leu	Arg	Glu	Ile	Ser	Arg	His	
			115				120					125				
Ser	Ser	Val	Glu	Val	Ile	Asp	Ile	Cys	Glu	Ile	Asp	Lys	Met	Val	Ile	
			130			135					140					
Asp	Val	Ser	Lys	Lys	Phe	Phe	Pro	Glu	Leu	Ala	Val	Gly	Phe	Asp	Asp	
145				150						155				160		
Pro	Arg	Val	Gln	Leu	His	Ile	Ser	Asp	Ala	Ala	Glu	Phe	Leu	Arg	Lys	
			165					170					175			
Ser	Pro	Glu	Gly	Lys	Tyr	Asp	Ala	Ile	Ile	Val	Asp	Ser	Ser	Asp	Pro	
			180				185						190			
Val	Gly	Pro	Ala	Leu	Ala	Leu	Val	Glu	Lys	Pro	Phe	Phe	Glu	Thr	Leu	
			195				200					205				
Ala	Arg	Ala	Leu	Lys	Pro	Gly	Gly	Val	Leu	Cys	Asn	Met	Ala	Glu	Ser	
			210			215					220					
Met	Trp	Leu	His	Thr	His	Leu	Ile	Glu	Asp	Met	Ile	Ser	Ile	Cys	Arg	
225				230						235				240		
Gln	Thr	Phe	Lys	Ser	Val	His	Tyr	Ala	Trp	Ser	Ser	Val	Pro	Thr	Tyr	
			245					250					255			
Pro	Ser	Gly	Val	Ile	Gly	Phe	Val	Leu	Cys	Ser	Thr	Glu	Gly	Pro	Ala	
			260				265						270			
Val	Asp	Phe	Lys	Asn	Pro	Ile	Asn	Pro	Ile	Glu	Lys	Leu	Asp	Gly	Ala	
			275				280					285				
Met	Thr	His	Lys	Arg	Glu	Leu	Lys	Phe	Tyr	Asn	Ser	Asp	Met	His	Arg	
			290			295					300					
Ala	Ala	Phe	Ala	Leu	Pro	Thr	Phe	Leu	Arg	Arg	Glu	Val	Ala	Ser	Leu	
305				310						315				320		
Leu	Ala	Ser														

(2) INFORMATION FOR SEQ ID NO:2602:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1444 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1444

(D) OTHER INFORMATION: / Ceres Seq. ID 1573736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2602:

```
aaatatatcaaacacagagagattttgattccatttttat tactgttact atcatccaaa 60
acottgggtat tftagaccat gactctgttt tcaagatctca tcaaccttaa cctctcagac 120
tccactgataa aaatcattgc tgaatacata tgggttggtg gttctggaaat ggacatgaga 180
agcaaaagcca ggaactctacc tggaccagtg actgaccctt cgcagctacc aaagtggaaac 240
tatgatgtgtt caagcacagg acaagctcct ggtgaagaca gtgaagtcat ctatatagtta 300
ataatcttttc tttcttgatc ttttaataag tttctctoca ttgttttttt ttctgattct 360
tgtttactaa tcttttgtgt gtttgtataa ctttgtttag cctcgaagcc atattcaaa 420
atccttttcc tagaggaanaa aacattcttg tcatgtgcga tgcgtacact ccgcggggtg 480
aaccaatccc gactaaacaaa agacacgctg cggctaaggt ctttagcaac cctgatgttg 540
cagctgaagtt gccatggtat ggtattgagc aagaatacac ttactccaag aaagatgtga 600
ggtggcctgt tggttggcct attggcggtt atcccgcccc tcaggggaccg tactattgctg 660
gtattggagc agacaaatct tttggcagag atgttgttta tctcactac aaggcctgtt 720
tatacgctgt aatcaacatt agtggcatca atggagaagt catgcggggt cagtgggagt 780
tcagggtcgg tccagctgtt ggtatctcgg ctgctgatga aattttgggtc gctcgtttaca 840
ttttggagag gatacacagag attgctgggt tagtgggtatc ttttgaccgc aaaccgatttc 900
ccgggtgactg gaacgctgtt ggtgctcact gcaactacag taccaaagtca atgaggggaag 960
aaggcggttta cgagatcatc aagaaagcaa tgcataaatT gggactgaga cacaaagarc 1020
rcattgctgc ttacsgtgaa ggcaatgagc gtgctctcac aggacaccac gagactgctg 1080
acatacaaac tttctcttgg ggtgttgaga accgtggagc atcgatccga gtaggacgtg 1140
atcaggagaaa agaaagggaaa ggatactttg aggaacaggag ccagactctg aacatggatc 1200
cttaacattgt tacttccatg attgcagaga ccaccatcct ctggaatcct tgatgatcat 1260
cagatcaaga aaaaaatcttg aatgtcactc aaattttgtg ttcttgcaag atttcaagatt 1320
tgtgtctctc atcaagcaat gtcttaggat aagtcaaaaga ttgctctgc ttattctgct 1380
ttttatttacc ttcacatcct attgaaaaaa ttattgtgta ttattatga ataaacatta 1440
tctt
```

(2) INFORMATION FOR SEQ ID NO:2603:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..266

(D) OTHER INFORMATION: / Ceres Seq. ID 1573737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2603:

```
Met Cys Asp Ala Tyr Thr Pro Ala Gly Glu Pro Ile Pro Thr Asn Lys
1 5 10 15
Arg His Ala Ala Ala Lys Val Phe Ser Asn Pro Asp Val Ala Ala Glu
20 25 30
Val Pro Trp Tyr Gly Ile Glu Gln Glu Tyr Thr Leu Leu Gln Lys Asp
35 40 45
Val Arg Trp Pro Val Gly Trp Pro Ile Gly Gly Tyr Pro Gly Pro Gln
50 55 60
Gly Pro Tyr Tyr Cys Gly Ile Gly Ala Asp Lys Ser Phe Gly Arg Asp
65 70 75 80
Val Val Asp Ser His Tyr Lys Ala Cys Leu Tyr Ala Gly Ile Asn Ile
85 90 95
Ser Gly Ile Asn Gly Glu Val Met Pro Gly Gln Trp Glu Phe Gln Val
100 105 110
Gly Pro Ala Val Gly Ile Ser Ala Ala Asp Glu Ile Trp Val Ala Arg
115 120 125
Tyr Ile Leu Glu Arg Ile Thr Glu Ile Ala Gly Val Val Val Ser Phe
130 135 140
```

```

Asp Pro Lys Pro Ile Pro Gly Asp Trp Asn Gly Ala Gly Ala His Cys
145                      150                      155                      160
Asn Tyr Ser Thr Lys Ser Met Arg Glu Gly Tyr Glu Ile Ile
                      165                      170                      175
Lys Lys Ala Ile Asp Lys Leu Gly Leu Arg His Lys Xaa Xaa Ile Ala
                      180                      185                      190
Ala Tyr Xaa Glu Gly Asn Glu Arg Arg Leu Thr Gly His His Glu Thr
                      195                      200                      205
Ala Asp Ile Asn Thr Phe Leu Trp Gly Val Ala Asn Arg Gly Ala Ser
210                      215                      220
Ile Arg Val Gly Arg Asp Thr Glu Lys Glu Gly Lys Gly Tyr Phe Glu
225                      230                      235                      240
Asp Arg Arg Pro Ala Ser Asn Met Asp Pro Tyr Ile Val Thr Ser Met
                      245                      250                      255
Ile Ala Glu Thr Thr Ile Leu Trp Asn Pro
                      260                      265

```

(2) INFORMATION FOR SEQ ID NO:2604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2604:

```

Met Pro Gly Gln Trp Glu Phe Gln Val Gly Pro Ala Val Gly Ile Ser
1                      5                      10                      15
Ala Ala Asp Glu Ile Trp Val Ala Arg Tyr Ile Leu Glu Arg Ile Thr
20                      25                      30
Glu Ile Ala Gly Val Val Val Ser Phe Asp Pro Lys Pro Ile Pro Gly
35                      40                      45
Asp Trp Asn Gly Ala Gly Ala His Cys Asn Tyr Ser Thr Lys Ser Met
50                      55                      60
Arg Glu Glu Gly Gly Tyr Glu Ile Ile Lys Lys Ala Ile Asp Lys Leu
65                      70                      75                      80
Gly Leu Arg His Lys Xaa Xaa Ile Ala Ala Tyr Xaa Glu Gly Asn Glu
85                      90                      95
Arg Arg Leu Thr Gly His His Glu Thr Ala Asp Ile Asn Thr Phe Leu
100                      105                      110
Trp Gly Val Ala Asn Arg Gly Ala Ser Ile Arg Val Gly Arg Asp Thr
115                      120                      125
Glu Lys Glu Gly Lys Gly Tyr Phe Glu Asp Arg Arg Pro Ala Ser Asn
130                      135                      140
Met Asp Pro Tyr Ile Val Thr Ser Met Ile Ala Glu Thr Thr Ile Leu
145                      150                      155                      160
Trp Asn Pro

```

(2) INFORMATION FOR SEQ ID NO:2605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1464
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573751

aagttctact	gcgaagtttt	caacagattc	gccggagaat	cttcgaatac	acggcggaga	60
aatggtctct	taacgcctct	ctacacgatc	caacatcact	actcgtccct	ctctccgcgc	120
cttcagcgca	ttaattctca	ccgacacaac	cttcagatac	atcagagatt	tgcttccttt	180
caacagctca	ttaatgtgat	cacgctcaag	ctccgtcgca	ctatcagatc	ragagctgct	240
cgattttctc	agaanccatt	cgcttgatgc	gaactatgga	aatcgcmssc	gatctgcttt	300
acaacggcga	gctaattcca	gggttttgcg	atctctcaag	cggccaaaga	cggtgagtca	360
tagCGGAGGA	agctgcstact	ccgaagaaga	accgcatatt	tactgtctat	cgctgatact	420
gtatttttct	aggtcgtggt	gtgtcgcttc	atgaggtttt	ctcagagctt	atgggaagac	480
aagctgggttg	ttctaaaggg	aaagctggat	ctatgcaatt	ctataaaga	gaatcgtctc	540
tttaacggtg	tcatgggatt	gttggtgcct	aggttccatt	aggttggtgt	attgcttttg	600
ctcagaagta	taataaggaa	gaggtcgtct	caattgcttt	tatgttgtag	ggtgcgtgca	660
atccgggaca	gttgtttgaa	ctgttgataa	tttctgcctc	tggggatttg	ctcgaattaa	720
tgctctgcga	gacaatcacc	tgatggaatg	gaactcgtga	atggagagcc	gctaaagatc	780
ctctcttacta	caagcgtggt	tattatgttc	ctgaactcaa	gtgagatggt	atggatgcct	840
ttgtctgcac	agacactctc	aaattttgcta	agcagcatgc	gtgtggagaag	gggcccaata	900
ttcttgagat	ggacacatgc	aggtttaccag	ctgaactcat	gtctgactct	gggacacat	960
agaactcccg	agatgagata	ttcgtgtgtga	ggcaggaacg	ggatccaatt	gagagaataa	1020
agaactcgtg	actatctcat	gacctacgaa	ccgagaaaga	gcttaaggat	atggagaagg	1080
aaattagaaa	agaaagtaga	gacgcgctat	ccaaagctaa	ggatgtccca	atgccagagc	1140
ctcttgagct	ctttaccaat	gtgtatctgta	agggatttgg	caccgtatca	tttggaacctg	1200
acagaaaagt	agtcnaaagc	tcctcttcgt	gcatcatgag	ctcttgttgc	ttaaactgcc	1260
acgtgtctatg	agaaaatttg	ctgatagaga	aatctatgaa	tatgaataaa	gattctgtgtg	1320
tatactctct	ctctcccccc	ccccccccct	ttcgattttt	aatctctctg	tatctttttt	1380
tacaacataa	aggagaaaaa	tgttattctt	gtgaagcttt	agtatgtctg	tgtttaatat	1440
tcaacacatc	gaattgaagt	ctctct				

Met	Ala	Leu	Met	Arg	Arg	Met	Glu	Ile	Xaa	Xaa	Asp	Ser	Leu	Tyr	Lys
1				5					10				15		
Ala	Lys	Leu	Ile	Xaa	Gly	Phe	Cys	His	Leu	Tyr	Asp	Gly	Gln	Glu	Ala
			20					25					30		
Val	Ala	Ile	Gly	Xaa	Glu	Ala	Xaa	Ile	Thr	Lys	Lys	Asp	Ala	Ile	Ile
			35				40					45			
Thr	Ala	Tyr	Arg	Asp	His	Cys	Ile	Phe	Leu	Gly	Arg	Gly	Gly	Ser	Leu
			50			55					60				
His	Glu	Val	Phe	Ser	Glu	Leu	Met	Gly	Arg	Gln	Ala	Gly	Cys	Ser	Lys
65					70				75						80
Gly	Lys	Gly	Gly	Ser	Met	His	Phe	Tyr	Lys	Lys	Glu	Ser	Ser	Phe	Tyr
				85				90					95		
Gly	Gly	His	Gly	Ile	Val	Gly	Ala	Gln	Val	Pro	Leu	Gly	Cys	Gly	Ile
			100				105						110		
Ala	Phe	Ala	Gln	Lys	Tyr	Asn	Lys	Glu	Glu	Ala	Val	Thr	Phe	Ala	Leu
			115				120					125			
Tyr	Gly	Asp	Gly	Ala	Ala	Asn	Gln	Gly	Gln	Leu	Phe	Glu	Ala	Leu	Asn
			130			135					140				
Ile	Ser	Ala	Leu	Trp	Asp	Leu	Pro	Ala	Ile	Leu	Val	Cys	Glu	Asn	Asn
145					150					155				160	
His	Tyr	Gly	Met	Gly	Thr	Ala	Glu	Tyr	Arg	Ala	Ala	Lys	Ser	Pro	Ser
				165					170					175	
Tyr	Tyr	Lys	Arg	Gly	Asp	Tyr	Val	Pro	Gly	Leu	Lys	Val	Asp	Gly	Met

180	185	190
Asp Ala Phe Ala Val Lys Gln Ala Cys Lys Phe Ala Lys Gln His Ala		
195	200	205
Leu Glu Lys Gly Pro Ile Ile Leu Glu Met Asp Thr Tyr Arg Tyr His		
210	215	220
Gly His Ser Met Ser Asp Pro Gly Ser Thr Tyr Arg Thr Arg Asp Glu		
225	230	235
Ile Ser Gly Val Arg Gln Glu Arg Asp Pro Ile Glu Arg Ile Lys Lys		
245	250	255
Leu Val Leu Ser His Asp Leu Ala Thr Glu Lys Glu Leu Lys Asp Met		
260	265	270
Glu Lys Glu Ile Arg Lys Glu Val Asp Asp Ala Ile Ala Lys Ala Lys		
275	280	285
Asp Cys Pro Met Pro Glu Pro Ser Glu Leu Phe Thr Asn Val Tyr Val		
290	295	300
Lys Gly Phe Gly Thr Glu Ser Phe Gly Pro Asp Arg Lys Glu Val Lys		
305	310	315
Ala Ser Leu Pro		320

(2) INFORMATION FOR SEQ ID NO:2607:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..321

(D) OTHER INFORMATION: / Ceres Seq. ID 1573753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2607:

Met Arg Arg Met Glu Ile Xaa Xaa Asp Ser Leu Tyr Lys Ala Lys Leu	
1	5
Ile Xaa Gly Phe Cys His Leu Tyr Asp Gly Gln Glu Ala Val Ala Ile	10
20	25
Gly Xaa Glu Ala Xaa Ile Thr Lys Lys Asp Ala Ile Ile Thr Ala Tyr	30
35	40
Arg Asp His Cys Ile Phe Leu Gly Arg Gly Gly Ser Leu His Glu Val	45
50	55
Phe Ser Glu Leu Met Gly Arg Gln Ala Gly Cys Ser Lys Gly Lys Gly	60
65	70
Gly Ser Met His Phe Tyr Lys Lys Glu Ser Ser Phe Tyr Gly Gly His	75
85	90
Gly Ile Val Gly Ala Gln Val Pro Leu Gly Cys Gly Ile Ala Phe Ala	95
100	105
Gln Lys Tyr Asn Lys Glu Glu Ala Val Thr Phe Ala Leu Tyr Gly Asp	110
115	120
Gly Ala Ala Asn Gln Gly Gln Leu Phe Glu Ala Leu Asn Ile Ser Ala	125
130	135
Leu Trp Asp Leu Pro Ala Ile Leu Val Cys Glu Asn Asn His Tyr Gly	140
145	150
Met Gly Thr Ala Glu Trp Arg Ala Ala Lys Ser Pro Ser Tyr Tyr Lys	155
165	170
Arg Gly Asp Tyr Val Pro Gly Leu Lys Val Asp Gly Met Asp Ala Phe	175
180	185
Ala Val Lys Gln Ala Cys Lys Phe Ala Lys Gln His Ala Leu Glu Lys	190
195	200
Gly Pro Ile Ile Leu Glu Met Asp Thr Tyr Arg Tyr His Gly His Ser	205
210	215
Met Ser Asp Pro Gly Ser Thr Tyr Arg Thr Arg Asp Glu Ile Ser Gly	220
225	230
	235
	240

Val	Arg	Gln	Glu	Arg	Asp	Pro	Ile	Glu	Arg	Ile	Lys	Lys	Leu	Val	Leu
				245						250				255	
Ser	His	Asp	Leu	Ala	Thr	Glu	Lys	Glu	Leu	Lys	Asp	Met	Glu	Lys	Glu
			260					265					270		
Ile	Arg	Lys	Glu	Val	Asp	Asp	Ala	Ile	Ala	Lys	Ala	Lys	Asp	Cys	Pro
		275					280					285			
Met	Pro	Glu	Pro	Ser	Glu	Leu	Phe	Thr	Asn	Val	Tyr	Val	Lys	Gly	Phe
	290					295					300				
Gly	Thr	Glu	Ser	Phe	Gly	Pro	Asp	Arg	Lys	Glu	Val	Lys	Ala	Ser	Leu
305				310						315				320	
Pro															

(2) INFORMATION FOR SEQ ID NO:2608:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..318

(D) OTHER INFORMATION: / Ceres Seq. ID 1573754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2608:

Met	Glu	Ile	Xaa	Xaa	Asp	Ser	Leu	Tyr	Lys	Ala	Lys	Leu	Ile	Xaa	Gly
1			5					10					15		
Phe	Cys	His	Leu	Tyr	Asp	Gly	Gln	Glu	Ala	Val	Ala	Ile	Gly	Xaa	Glu
			20				25					30			
Ala	Xaa	Ile	Thr	Lys	Lys	Asp	Ala	Ile	Ile	Thr	Ala	Tyr	Arg	Asp	His
		35				40					45				
Cys	Ile	Phe	Leu	Gly	Arg	Gly	Gly	Ser	Leu	His	Glu	Val	Phe	Ser	Glu
	50				55						60				
Leu	Met	Gly	Arg	Gln	Ala	Gly	Cys	Ser	Lys	Gly	Lys	Gly	Gly	Ser	Met
65				70					75					80	
His	Phe	Tyr	Lys	Lys	Glu	Ser	Ser	Phe	Tyr	Gly	Gly	His	Gly	Ile	Val
			85						90			95			
Gly	Ala	Gln	Val	Pro	Leu	Gly	Cys	Gly	Ile	Ala	Phe	Ala	Gln	Lys	Tyr
		100						105				110			
Asn	Lys	Glu	Glu	Ala	Val	Thr	Phe	Ala	Leu	Tyr	Gly	Asp	Gly	Ala	Ala
		115				120					125				
Asn	Gln	Gly	Gln	Leu	Phe	Glu	Ala	Leu	Asn	Ile	Ser	Ala	Leu	Trp	Asp
	130				135						140				
Leu	Pro	Ala	Ile	Leu	Val	Cys	Glu	Asn	Asn	His	Tyr	Gly	Met	Gly	Thr
	145			150						155				160	
Ala	Glu	Trp	Arg	Ala	Ala	Lys	Ser	Pro	Ser	Tyr	Tyr	Lys	Arg	Gly	Asp
		165						170					175		
Tyr	Val	Pro	Gly	Leu	Lys	Val	Asp	Gly	Met	Asp	Ala	Phe	Ala	Val	Lys
		180					185					190			
Gln	Ala	Cys	Lys	Phe	Ala	Lys	Gln	His	Ala	Leu	Glu	Lys	Gly	Pro	Ile
	195					200						205			
Ile	Leu	Glu	Met	Asp	Thr	Tyr	Arg	Tyr	His	Gly	His	Ser	Met	Ser	Asp
	210				215						220				
Pro	Gly	Ser	Thr	Tyr	Arg	Thr	Arg	Asp	Glu	Ile	Ser	Gly	Val	Arg	Gln
	225				230					235				240	
Glu	Arg	Asp	Pro	Ile	Glu	Arg	Ile	Lys	Lys	Leu	Val	Leu	Ser	His	Asp
		245						250					255		
Leu	Ala	Thr	Glu	Lys	Glu	Leu	Lys	Asp	Met	Glu	Lys	Glu	Ile	Arg	Lys
		260						265					270		
Glu	Val	Asp	Asp	Ala	Ile	Ala	Lys	Ala	Lys	Asp	Cys	Pro	Met	Pro	Glu
		275						280				285			
Pro	Ser	Glu	Leu	Phe	Thr	Asn	Val	Tyr	Val	Lys	Gly	Phe	Gly	Thr	Glu

290 295 300
Ser Phe Gly Pro Asp Arg Lys Glu Val Lys Ala Ser Leu Pro
305 310 315

(2) INFORMATION FOR SEQ ID NO:2609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1336

(D) OTHER INFORMATION: / Ceres Seq. ID 1573759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2609:

tactttggcg gtgctgagaa gaaagatgag agggttcttg ttcttgattt gggttcctta 60
acaagcatct atgacagggc aagggaattg ttctattatt tgaaggagg ggtagttgat 120
tttgccgaag agcatagcga Nggcttggtg acattctcgg ttggaagaa gatacgaaca 180
agggcaatcac cctgaattgg atgaggatca tctattcat ttgtggggc attcagcggg 240
tgcgcaagtt gtgcgtgtat tgcagcaaat gcttgagat caggcatttg aagggtttga 300
agaaacgaat gagaattggg ttctgagtgt gacatcggtta tccggggcat tcaatggaac 360
taccaggcac tacttagatg gcatgcggac agatgatgga gtgagcatga aaccaataatg 420
ttgtttgcag ctgtgtcgta tagcgctgat aatgacgat tggttggaca ttctatggct 480
aaagacttat tacaatttgc ggttcgatca ctccaacatt ttctggaaga agacgggtgt 540
gagaggtctc gttgattgcc taatgggaaa cacaggctct ttgtctctg gcgatttgat 600
cttacctgat ctcacaatcc aaggctcaac aagtattaac tccaatctcc agacgttccc 660
aaacacttacc tacttcagct acgcgactaa acgcacccgc agagtcatgg gtatgacaa 720
cccttcagggt gtctttggaa tccaccogat gctctctcct ccgctcttc abatagcacNc 780
Aatggaattt cccacaagat gtctctcctc ctataaaagg ctacagggat gaggactggc 840
aagagaacga cggggcattg aacacaatat caatgacaca tccgaggcta cctgttgagc 900
atccgagccg gttcataagg agcgattcgg aatgtcaaac attacaaccc gggatctggt 960
attataagat agtggaaaga gatcacataa tgttcatagt gaacagagag agagctgggt 1020
ttcagtttga tctgatatac gacagcatct tccaacgttg caggaaacat gtttttagaa 1080
agattctcca gactctcccc aatcaatctc ctctctctcc tegtctcatc tcatcaccca 1140
gaataaaca aatttgtacat tgatcacatg caaaaaaaa atgttttagg gttgttaagt 1200
tgaggcgcta agtttttgtt taggctattt actactaata cagattattc attgtctctc 1260
ttgtctctct cctgatttgt tgtactgtaa aatatatac ttccattttg aaaattataa 1320
tatattgttag ttgcgc

(2) INFORMATION FOR SEQ ID NO:2610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 1573760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2610:

Met Leu Ala Asp Gln Ala Phe Glu Gly Phe Glu Glu Thr Asn Glu Asn
1 5 10 15
Trp Val Leu Ser Val Thr Ser Leu Ser Gly Ala Phe Asn Gly Thr Thr
20 25 30
Arg Thr Tyr Leu Asp Gly Met Arg Thr Asp Asp Gly Val Ser Met Lys
35 40 45
Pro Ile Cys Leu Leu Gln Leu Cys Arg Ile Gly Val Ile Met Tyr Asp
50 55 60
Trp Leu Asp Ile Ser Trp Leu Lys Thr Tyr Tyr Asn Phe Gly Phe Asp
65 70 75 80
His Phe Asn Ile Ser Trp Lys Lys Thr Gly Val Arg Gly Leu Val Asp

85 90 95
Cys Leu Met Gly Asn Thr Gly Pro Phe Ala Ser Gly Asp Trp Ile Leu
100 105 110
Pro Asp Leu Thr Ile Gln Gly Ser Thr Ser Ile Asn Ser Asn Leu Gln
115 120 125
Thr Phe Pro Asn Thr Tyr Tyr Phe Ser Tyr Ala Thr Lys Arg Thr Arg
130 135 140
Arg Val Met Gly Met Thr Ile Pro Ser Gly Val Leu Gly Ile His Pro
145 150 155 160
Met Leu Phe Leu Arg Val Phe Xaa Met Ser Xaa Met Glu Ile Pro Thr
165 170 175
Arg Cys Leu Ser Ser Leu
180

(2) INFORMATION FOR SEQ ID NO:2611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1573761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2611:

Met Arg Thr Asp Asp Gly Val Ser Met Lys Pro Ile Cys Leu Leu Gln
1 5 10 15
Leu Cys Arg Ile Gly Val Ile Met Tyr Asp Trp Leu Asp Ile Ser Trp
20 25 30
Leu Lys Thr Tyr Tyr Asn Phe Gly Phe Asp His Phe Asn Ile Ser Trp
35 40 45
Lys Lys Thr Gly Val Arg Gly Leu Val Asp Cys Leu Met Gly Asn Thr
50 55 60
Gly Pro Phe Ala Ser Gly Asp Trp Ile Leu Pro Asp Leu Thr Ile Gln
65 70 75 80
Gly Ser Thr Ser Ile Asn Ser Asn Leu Gln Thr Phe Pro Asn Thr Tyr
85 90 95
Tyr Phe Ser Tyr Ala Thr Lys Arg Thr Arg Arg Val Met Gly Met Thr
100 105 110
Ile Pro Ser Gly Val Leu Gly Ile His Pro Met Leu Phe Leu Arg Val
115 120 125
Phe Xaa Met Ser Xaa Met Glu Ile Pro Thr Arg Cys Leu Ser Ser Leu
130 135 140

(2) INFORMATION FOR SEQ ID NO:2612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1573762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2612:

Met Lys Pro Ile Cys Leu Leu Gln Leu Cys Arg Ile Gly Val Ile Met
1 5 10 15
Tyr Asp Trp Leu Asp Ile Ser Trp Leu Lys Thr Tyr Tyr Asn Phe Gly
20 25 30

Phe Asp His Phe Asn Ile Ser Trp Lys Lys Thr Gly Val Arg Gly Leu
35 40 45
Val Asp Cys Leu Met Gly Asn Thr Gly Pro Phe Ala Ser Gly Asp Trp
50 55 60
Ile Leu Pro Asp Leu Thr Ile Gln Gly Ser Thr Ser Ile Asn Ser Asn
65 70 75 80
Leu Gln Thr Phe Pro Asn Thr Tyr Tyr Phe Ser Tyr Ala Thr Lys Arg
85 90 95
Thr Arg Arg Val Met Gly Met Thr Ile Pro Ser Gly Val Leu Gly Ile
100 105 110
His Pro Met Leu Phe Leu Arg Val Phe Xaa Met Ser Xaa Met Glu Ile
115 120 125
Pro Thr Arg Cys Leu Ser Ser Leu
130 135

(2) INFORMATION FOR SEQ ID NO:2613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..590
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2613:

atcacttact	taacatacta	agagagttat	tagaacttgc	aaaaaatggc	ttccaaggct	60
ttgattctgt	taggtctctt	ctcagttctt	ctcgtctgtc	ccgaagtgtc	tgccgcaagg	120
caatcgggca	tggtgaagcc	agagagttag	gaaactgtgc	aacctgaagg	ttatggcggt	180
ggccacggag	gacatggtgg	tcacggaggg	ggaggaggcc	acggacatgg	aggacacaa	240
ggaggagggg	gccacggact	tgacggatac	ggaggacact	acggaggtgg	tgaggaggga	300
tacggaggtg	gaggaggaca	ccacggaggga	ggaggccacg	ggctaaccga	acctgttcag	360
actaagccgg	gtgtttaaaa	ctatataata	ttttcactac	catgcatgat	tgcatatata	420
tatatacgct	tatgtattat	ctatatgcct	ataaataaac	catgggtgag	ttgtaacgca	480
GtgcNcttca	gaaatgttcg	gaataaattt	ccataatatt	agtataatgt	ctctctgttt	540
gaattataaa	ctcgctgttt	tgcataataa	aatctcttgt	agctaggctg		

(2) INFORMATION FOR SEQ ID NO:2614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2614:

Met	Ala	Ser	Lys	Ala	Leu	Ile	Leu	Leu	Gly	Leu	Phe	Ser	Val	Leu	Leu
1				5					10				15		
Val	Val	Ser	Glu	Val	Ser	Ala	Ala	Arg	Gln	Ser	Gly	Met	Val	Lys	Pro
				20				25					30		
Glu	Ser	Glu	Glu	Thr	Val	Gln	Pro	Glu	Gly	Tyr	Gly	Gly	Gly	His	Gly
				35				40				45			
Gly	His	Gly	Gly	His	Gly	Gly	Gly	Gly	Gly	His	Gly	His	Gly	Gly	His
				50				55				60			
Asn	Gly	Gly	Gly	Gly	His	Gly	Leu	Asp	Gly	Tyr	Gly	Gly	His	Tyr	Gly
				65				70				75		80	
Gly	Gly	Gly	Gly	Gly	Tyr	Gly	Gly	Gly	Gly	Gly	His	His	Gly	Gly	Gly
				85				90				95			
Gly	His	Gly	Leu	Asn	Glu	Pro	Val	Gln	Thr	Lys	Pro	Gly	Val		

100 105 110

(2) INFORMATION FOR SEQ ID NO:2615:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..82
(D) OTHER INFORMATION: / Ceres Seq. ID 1573792
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2615:

Met	Val	Lys	Pro	Glu	Ser	Glu	Glu	Thr	Val	Gln	Pro	Glu	Gly	Tyr	Gly
1		5						10					15		
Gly	Gly	His	Gly	Gly	His	Gly	Gly	Gly	Gly	Gly	Gly	Gly	His	Gly	
		20					25						30		
His	Gly	Gly	His	Asn	Gly	Gly	Gly	Gly	His	Gly	Leu	Asp	Gly	Tyr	Gly
		35					40					45			
Gly	His	Tyr	Gly	Gly	Gly	Gly	Gly	Gly	Tyr	Gly	Gly	Gly	Gly	Gly	His
		50					55					60			
His	Gly	Gly	Gly	Gly	His	Gly	Leu	Asn	Glu	Pro	Val	Gln	Thr	Lys	Pro
65					70					75					80
Gly	Val														

(2) INFORMATION FOR SEQ ID NO:2616:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..57
(D) OTHER INFORMATION: / Ceres Seq. ID 1573793
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2616:

Met	Ala	Val	Ala	Thr	Glu	Asp	Met	Val	Val	Thr	Glu	Gly	Glu	Ala	
1		5						10					15		
Thr	Asp	Met	Glu	Asp	Thr	Thr	Glu	Glu	Gly	Ala	Thr	Asp	Leu	Thr	Asp
		20						25					30		
Thr	Glu	Asp	Thr	Thr	Glu	Val	Val	Glu	Glu	Asp	Thr	Glu	Val	Glu	Glu
		35					40					45			
Asp	Thr	Thr	Glu	Glu	Glu	Ala	Thr	Gly							
		50					55								

(2) INFORMATION FOR SEQ ID NO:2617:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 461 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..461
(D) OTHER INFORMATION: / Ceres Seq. ID 1573798
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2617:

atcacttact	taacatacta	agagagttat	tagaacttgc	aaaaaatggc	ttccaaggct	60
ttgattctgt	taggtctctt	ctcagttctt	ctcgtctgtc	ccgaagtgtc	tgccgcaagg	120
aatcgggcat	ggtgaagcca	gagagtggag	aaactgtgca	acctgaaggt	tatggcgggt	180
gccacggagg	acatggtggt	cacggagggg	gaggaggcca	cggacatgga	ggacacaacg	240

gaggtggagg aggacacacc ggaggaggag gccacggcgt aaacgaacct gttcagacta 300
agccgggtgt ttaaaactat ataatatctt cactaccatg catgattgca tatatatata 360
tacgcttatg tattatctat atgcctataa ataaaccatg gtgagttgtg aacgcagtcg 420
Tcttcagaaa tgttcggaat aaatttccat aatattagta t

(2) INFORMATION FOR SEQ ID NO:2618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2618:

His	Leu	Leu	Asn	Ile	Leu	Arg	Glu	Leu	Glu	Leu	Ala	Lys	Asn	Gly
1			5				10						15	
Phe	Gln	Gly	Phe	Asp	Ser	Val	Arg	Ser	Leu	Ser	Ser	Ser	Arg	Arg
			20				25					30		
Leu	Arg	Ser	Val	Cys	Arg	Lys	Glu	Ser	Gly	Met	Val	Lys	Pro	Glu
			35				40					45		
Glu	Glu	Thr	Val	Gln	Pro	Glu	Gly	Tyr	Gly	Gly	Gly	His	Gly	Gly
			50			55					60			
Gly	Gly	His	Gly	Gly	Gly	Gly	Gly	His	Gly	His	Gly	Gly	His	Asn
			65			70			75				80	
Gly	Gly	Gly	Gly	His	His	Gly	Gly	Gly	Gly	His	Gly	Leu	Asn	Glu
			85				90					95		
Val	Gln	Thr	Lys	Pro	Gly	Val								
			100											

(2) INFORMATION FOR SEQ ID NO:2619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2619:

Met	Val	Lys	Pro	Glu	Ser	Glu	Glu	Thr	Val	Gln	Pro	Glu	Gly	Tyr	Gly
1			5				10						15		
Gly	Gly	His	Gly	Gly	His	Gly	Gly	His	Gly	Gly	Gly	Gly	Gly	His	Gly
			20				25					30			
His	Gly	Gly	His	Asn	Gly	Gly	Gly	Gly	His	His	Gly	Gly	Gly	Gly	Gly
			35				40					45			
His	Gly	Leu	Asn	Glu	Pro	Val	Gln	Thr	Lys	Pro	Gly	Val			
			50			55					60				

(2) INFORMATION FOR SEQ ID NO:2620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..596
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2620:

```
actcatcact tacttaacat actaagagag ttattagatc ttgaaaaaca tggcttccaa 60
ggctttgatt ctgttgggtc tcttcgcaat tctctgggtg gtctccgaag tttctggcgc 120
aaggcaKctg ggcattgtga agccagagag gaaactgtgc aacctgaagg ttatcacgga 180
ggacatgggt gtacaggagg gggaggccac tacggaggag gaggccacgg gcatggaggga 240
cacaacggag gagggggcca cggacttgac ggatacggag gaggacatgg aggacactac 300
ggaggaggag gaggacacta cggaggagga ggaggccacg gtggtgtggtg acactatgga 360
ggtggaggac accatggagg agggaggtcac gggctgaacg aacctgttca gacgaagccg 420
ggtgtttaaa agttataact atcaataaaa ttaccatcgc ataattgcat ctctatatac 480
acttatgtct tatatgtatc catcaaaata aacctgggtg agtttgaat gcagttccctt 540
cagaaatgtg tggaaataatg ttccacaata ataatagaat atctctgttg attctg
```

(2) INFORMATION FOR SEQ ID NO:2621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2621:

```
Thr His His Leu Leu Asn Ile Leu Arg Glu Leu Leu Asp Leu Glu Lys
1 5 10 15
His Gly Phe Gln Gly Phe Asp Ser Val Gly Ser Leu Arg Asn Ser Ser
20 25 30
Gly Gly Leu Arg Ser Phe Cys Arg Lys Ala Xaa Gly His Gly Glu Ala
35 40 45
Arg Glu Glu Thr Val Gln Pro Glu Gly Tyr His Gly Gly His Gly Gly
50 55 60
His Gly Gly Gly Gly His Tyr Gly Gly Gly His Gly His Gly Gly
65 70 75 80
His Asn Gly Gly Gly His Gly Leu Asp Gly Tyr Gly Gly His
85 90 95
Gly Gly His Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly
100 105 110
His Gly Gly Gly Gly His Tyr Gly Gly Gly His His Gly Gly Gly
115 120 125
Gly His Gly Leu Asn Glu Pro Val Gln Thr Lys Pro Gly Val
130 135 140
```

(2) INFORMATION FOR SEQ ID NO:2622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2622:

```
Met Ala Ser Lys Ala Leu Ile Leu Leu Gly Leu Phe Ala Ile Leu Leu
1 5 10 15
Val Val Ser Glu Val Ser Ala Ala Arg Xaa Ser Gly Met Val Lys Pro
20 25 30
Glu Arg Lys Leu Cys Asn Leu Lys Val Ile Thr Glu Asp Met Val Val
35 40 45
Thr Gly Gly Glu Ala Thr Thr Glu Glu Ala Thr Gly Met Glu Asp
50 55 60
```

Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu Glu Asp Met
65 70 75 80
Glu Asp Thr Thr Glu Glu Glu Asp Thr Thr Glu Glu Glu Ala
85 90 95
Thr Val Val Val Asp Thr Met Glu Val Glu Asp Thr Met Glu Glu Glu
100 105 110
Val Thr Gly
115

(2) INFORMATION FOR SEQ ID NO:2623:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1573804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2623:

Met	Val	Lys	Pro	Glu	Arg	Lys	Leu	Cys	Asn	Leu	Lys	Val	Ile	Thr	Glu	
1			5					10					15			
Asp	Met	Val	Val	Thr	Glu	Gly	Glu	Ala	Thr	Thr	Glu	Glu	Glu	Ala	Thr	
			20				25					30				
Gly	Met	Glu	Asp	Thr	Thr	Glu	Glu	Gly	Ala	Thr	Asp	Leu	Thr	Asp	Thr	
			35				40					45				
Glu	Glu	Asp	Met	Glu	Asp	Thr	Thr	Glu	Glu	Glu	Ala	Asp	Thr	Thr	Glu	
			50			55				60						
Glu	Glu	Glu	Ala	Thr	Val	Val	Val	Asp	Thr	Met	Glu	Val	Glu	Asp	Thr	
65			70					75						80		
Met	Glu	Glu	Glu	Val	Thr	Gly										
			85													

(2) INFORMATION FOR SEQ ID NO:2624:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 587 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..587

(D) OTHER INFORMATION: / Ceres Seq. ID 1573809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2624:

actcatcaact	tacttaacat	actaagagag	ttattagatc	ttgaaaaaca	tggcttccaa	60
ggcttttgatt	ctgttgggtc	tcttcgcaat	tcttctgggt	gtctccgaag	ttctgcccgc	120
aaggCaGtNc	Ngggcatggt	gaagccagag	agtgaggaaa	ctgtgcaacc	tgaagggtat	180
cacggaggac	atggtgggtca	cggaggggga	ggccactacg	gaggaggagg	ccacgggcat	240
ggaggacaca	acggaggagg	gggccacgga	cttgacggat	acggaggagg	acatggagga	300
cactacggag	gaggaggagg	acactacgga	ggaggatcac	gtgggtggtg	aggaggaggt	360
tacggaggaa	gcgggtggtg	tggaggatgg	taattccttt	aattagggtt	aggattacca	420
atgaatgttc	tctctctcgc	ttgttatgct	tctacttggt	tttgtgtgtt	ctctattttg	480
ttctggtttc	gctttagatt	tgatgtaaca	gttcgtgatt	aggtattttg	gtatctggaa	540
acgtaatggt	aagtcacttg	tcattttcta	aataacaaat	ttcttcg		

(2) INFORMATION FOR SEQ ID NO:2625:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1573810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2625:

Thr His His Leu Leu Asn Ile Leu Arg Glu Leu Leu Asp Leu Glu Lys
1 5 10 15
His Gly Phe Gln Gly Phe Asp Ser Val Gly Ser Leu Arg Asn Ser Ser
20 25 30
Gly Gly Leu Arg Ser Phe Cys Arg Lys Ala Xaa Xaa Gly Met Val Lys
35 40 45
Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr His Gly Gly His
50 55 60
Gly Gly His Gly Gly Gly Gly His Tyr Gly Gly Gly His Gly His
65 70 75 80
Gly Gly His Asn Gly Gly Gly Gly His Gly Leu Asp Gly Tyr Gly Gly
85 90 95
Gly His Gly Gly His Tyr Gly Gly Gly Gly His Tyr Gly Gly Gly
100 105 110
Tyr Gly Gly Gly Glu Gly Gly Tyr Gly Gly Ser Gly Gly Gly Gly
115 120 125
Gly Trp
130

(2) INFORMATION FOR SEQ ID NO:2626:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1573811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2626:

Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr His
1 5 10 15
Gly Gly His Gly Gly His Gly Gly Gly Gly His Tyr Gly Gly Gly Gly
20 25 30
His Gly His Gly Gly His Asn Gly Gly Gly Gly His Gly Leu Asp Gly
35 40 45
Tyr Gly Gly Gly His Gly Gly His Tyr Gly Gly Gly Gly His Tyr
50 55 60
Gly Gly Gly Tyr Gly Gly Gly Glu Gly Gly Tyr Gly Gly Ser Gly
65 70 75 80
Gly Gly Gly Gly Trp
85

(2) INFORMATION FOR SEQ ID NO:2627:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1573812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2627:

Met Val Val Thr Glu Gly Glu Ala Thr Thr Glu Glu Glu Ala Thr Gly
1 5 10 15

Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu
20 25 30
Glu Asp Met Glu Asp Thr Thr Glu Glu Glu Asp Thr Thr Glu Glu
35 40 45
Asp Thr Val Val Val Lys Glu Glu Val Thr Glu Glu Ala Val Val Val
50 55 60
Glu Asp Gly Asn Ser Phe Asn
65 70

(2) INFORMATION FOR SEQ ID NO:2628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..550
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2628:

atcacttact	taacatacta	agagagttat	tagaacttgc	aaaaaatggc	ttccaaggct	60
ttgattctgt	taggtctctt	ctcagttctt	ctcgtcgtct	ccgaagtgtc	tgccgcaagg	120
CaaNtcgggc	atggtgaagc	cagagagtga	ggaaactgtg	caacctgaag	gttatrgcgg	180
tggccacgga	ggacatgggt	gtcacggarg	gggaggaggc	cacggacatg	gaggacacaa	240
cggaggaggg	ggccacggac	ttgacggata	cggaggagggt	ggaggacact	atggaggarg	300
tggaggacac	tgccaggagg	gtggaggaca	ctacggaggga	ggtggaggac	actacggagg	360
aggtggccac	gggctaaacg	aacctgttca	gactaagccg	ggtgtttaaa	actatataat	420
atcttcacta	ccatgcatag	ttgcatatat	atatatacgc	ttatgtatta	tctatatgcc	480
tataaataaa	ccatgggtgag	tttgtaacgc	agtgccctca	gaaatgttcg	gaataaaatt	540
ccataaatatt						

(2) INFORMATION FOR SEQ ID NO:2629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2629:

Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr Xaa	
1 5 10 15	
Gly Gly His Gly Gly His Gly Gly His Gly Xaa Gly Gly Gly His Gly	
20 25 30	
His Gly Gly His Asn Gly Gly Gly Gly His Gly Leu Asp Gly Tyr Gly	
35 40 45	
Gly Gly Gly Gly His Tyr Gly Gly Xaa Gly Gly His Tyr Gly Gly Gly	
50 55 60	
Gly Gly His Tyr Gly Gly Gly Gly His Tyr Gly Gly Gly Gly His	
65 70 75 80	
Gly Leu Asn Glu Pro Val Gln Thr Lys Pro Gly Val	
85 90	

(2) INFORMATION FOR SEQ ID NO:2630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..60

(D) OTHER INFORMATION: / Ceres Seq. ID 1573815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2630:

```
Met Val Val Thr Xaa Gly Glu Glu Ala Thr Asp Met Glu Asp Thr Thr
1          5          10          15
Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu Glu Val Glu Asp Thr
20          25          30
Met Glu Xaa Val Glu Asp Thr Thr Glu Glu Val Glu Asp Thr Thr Glu
35          40          45
Glu Val Glu Asp Thr Thr Glu Glu Val Ala Thr Gly
50          55          60
```

(2) INFORMATION FOR SEQ ID NO:2631:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..49

(D) OTHER INFORMATION: / Ceres Seq. ID 1573816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2631:

```
Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu
1          5          10          15
Glu Val Glu Asp Thr Thr Met Glu Xaa Val Glu Asp Thr Thr Glu Val
20          25          30
Glu Asp Thr Thr Glu Glu Val Glu Asp Thr Thr Glu Glu Val Ala Thr
35          40          45
Gly
```

(2) INFORMATION FOR SEQ ID NO:2632:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 597 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..597

(D) OTHER INFORMATION: / Ceres Seq. ID 1573817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2632:

```
atcaacttact taacatacta agagagtatt tagactcttga aaaacatggc ttccaagggt 60
ttgattctctg ttgggtctctt cgcaattctt ctgggtggtc cgaagatttc tgccgcaagg 120
CaTgTcgggc atggtgaagc cagagagtga ggaactgtg caacctgaag gttatcacgg 180
aggacatggt ggtcacggag ggggaggcca ctacggagga ggaggccacg ggcattggag 240
acacaacgga ggaggggggc acggacttaa cggatacgga ggaggacatg gaggacata 300
cggaggagga ggaggacact acggaggarg agggagccac ggtggtggtg gacactatgg 360
agggtggagga caccatggag gavgagotca cgggctgaac gaacctgttc agacgaagcc 420
gggtgtttaa aagttataac tatcaataa attocaccat cataattgca tctctatata 480
cacttatgtc ttatatgtat ccatcaaaat aaaccatggt gagtttgtaa tgcagtttct 540
tcagaaatgt gtggaaataa ttttcacaat aataatagaa tatctctgtt gattctg
```

(2) INFORMATION FOR SEQ ID NO:2633:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1573818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2633:

Met Ser Gly Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu
1 5 10 15
Gly Tyr His Gly Gly His Gly Gly His Gly Gly Gly Gly His Tyr Gly
20 25 30
Gly Gly Gly His Gly His Gly Gly His Asn Gly Gly Gly Gly His Gly
35 40 45
Leu Asn Gly Tyr Gly Gly Gly His Gly Gly His Tyr Gly Gly Gly Gly
50 55 60
Gly His Tyr Gly Gly Xaa Gly Gly His Gly Gly Gly Gly His Tyr Gly
65 70 75 80
Gly Gly Gly His His Gly Gly Xaa Gly His Gly Leu Asn Glu Pro Val
85 90 95
Gln Thr Lys Pro Gly Val
100

(2) INFORMATION FOR SEQ ID NO:2634:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1573819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2634:

Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr His
1 5 10 15
Gly Gly His Gly Gly His Gly Gly Gly Gly His Tyr Gly Gly Gly Gly
20 25 30
His Gly His Gly Gly His Asn Gly Gly Gly Gly His Gly Leu Asn Gly
35 40 45
Tyr Gly Gly Gly His Gly Gly His Tyr Gly Gly Gly Gly His Tyr
50 55 60
Gly Gly Xaa Gly Gly His Gly Gly Gly Gly His Tyr Gly Gly Gly Gly
65 70 75 80
His His Gly Gly Xaa Gly His Gly Leu Asn Glu Pro Val Gln Thr Lys
85 90 95
Pro Gly Val

(2) INFORMATION FOR SEQ ID NO:2635:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1573820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2635:

Met Val Val Thr Glu Gly Glu Ala Thr Thr Glu Glu Glu Ala Thr Gly
1 5 10 15
Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu

20 25 30
Glu Asp Met Glu Asp Thr Thr Glu Glu Glu Asp Thr Thr Glu Xaa
35 40 45
Glu Glu Ala Thr Val Val Val Asp Thr Met Glu Val Glu Asp Thr Met
50 55 60
Glu Xaa Glu Val Thr Gly
65 70

(2) INFORMATION FOR SEQ ID NO:2636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..537
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2636:

atcaccttact taacatacta agagagttat tagatcttga aaaacatggc ttccaaggct	60
ttgattctgt tgggtctctt cgcaattctt ctgggtgtct ccgaagtctc tgcgcgaagg	120
CaKtGcgggc atgggtgaagc cagagagtga ggaaactgtg caacctgaag gttatcacgg	180
aggacatggt ggtcacggar ggggaggcca ctacggagga ggaggccaag gccatggagg	240
acacaacgga ggagggggcc acggacttga cggatacggga ggaggacatg gaggacacta	300
cggargagga ggaggacact acggargagg aggaggccac ggtgtgtgtg gacactatgg	360
aggtggagga caccatggag gaggaggcca cgggctgaac gaacctgttc agacgaaggg	420
tgaggacaa gaggcaggga agaaggattt cattcagata ctcaagactc ttgaatctga	480
gcttggagac aaaccttact ttagtggcga tgactttggc tatgtagaca ttaaggg	

(2) INFORMATION FOR SEQ ID NO:2637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2637:

Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr His	
1 5 10 15	
Gly Gly His Gly Gly His Gly Xaa Gly Gly His Tyr Gly Gly Gly Gly	
20 25 30	
His Gly His Gly Gly His Asn Gly Gly Gly Gly His Gly Leu Asp Gly	
35 40 45	
Tyr Gly Gly Gly His Gly Gly His Tyr Gly Xaa Gly Gly His Tyr	
50 55 60	
Gly Xaa Gly Gly His Gly Gly Gly His Tyr Gly Gly Gly Gly	
65 70 75 80	
His His Gly Gly Gly His Gly Leu Asn Glu Pro Val Gln Thr Lys	
85 90 95	
Gly Glu Glu Gln Glu Ala Gly Lys Lys Asp Phe Ile Gln Ile Leu Lys	
100 105 110	
Thr Leu Glu Ser Glu Leu Gly Asp Lys Pro Tyr Phe Ser Gly Asp Asp	
115 120 125	
Phe Gly Tyr Val Asp Ile Lys	
130 135	

(2) INFORMATION FOR SEQ ID NO:2638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..70
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1573823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2638:
Met Val Val Thr Xaa Gly Glu Ala Thr Thr Glu Glu Glu Ala Thr Gly
1 5 10 15
Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu
20 25 30
Glu Asp Met Glu Asp Thr Thr Xaa Glu Glu Glu Asp Thr Thr Xaa Glu
35 40 45
Glu Glu Ala Thr Val Val Val Asp Thr Met Glu Val Glu Asp Thr Met
50 55 60
Glu Glu Glu Val Thr Gly
65 70

- (2) INFORMATION FOR SEQ ID NO:2639:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1021 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:

- (i) NAME/KEY: -
- (B) LOCATION: 1..1021
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573832
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2639:

aataaaaaatt tgtttctttc ttctctgttt ttttttgott tgcgtttcaa gagagagaga 60
gagagagata caaagagaga aatttgggtt ttgtttgaac gaagcttctt cggtctctct 120
tctccgtctt acgattgtca acgcgtgtgtt ccattcttcaa tttgtttctt attttagcac 180
aagtttctcg agcttcaaat actgtttcag atcaatcaat cagtcaatca tggcgtagctc 240
tggaaaacaa aacatcaacg ccaaatgtgt attactagga gatgttgagg ctggaaaatc 300
aagtcttggt ctacggtttg tgaagatca gttttgtgaa ttccaggaat caaccatttg 360
tgcagctttt ttctctcaaa cattggctgt gaatgatgag actgtgaagt ttgagatag 420
ggatacagct ggtcaggaac gataccacag ttggctcca atgtactaca ggggtgcagc 480
tgctgtctatt attgtctttg acattactaa tcaagcctca tttagagagg cgaaraaatg 540
ggttcaggaa ctgcaggcac aaggtaaacc taatatggtg atggctcttg ctggaaaacaa 600
agctgattta tttagcgcaa ggaaggtgtc tgcagaggag gcagagatat atgctcaaga 660
gaacagcctt ttctttatg aaacctcagc gaagaccgca acaaatgtca aagacatatt 720
ctacgaaata cgcgaaaagg taccacgtat acagccagct gaaaaccgca caggaattgt 780
tctcccaaac gggccagggt ctacggcagt gaggttcatg tgttgtgctt agattcgtac 840
ctgaagagag atctcatttg gttagtcaca tagtagagaa catctggact ttcattgttt 900
tgcttctctt tgcgtttgtg tactttactt tgcttgcaat gacaacaaca acagtgtata 960
tcatgatgat acctattctg cctttgtgaa atcttgaaga tatttgtatt tggagagatt 1020
t

- (2) INFORMATION FOR SEQ ID NO:2640:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..276
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1573833
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2640:

```

Ile Lys Ile Cys Phe Phe Leu Leu Cys Phe Phe Leu Leu Ser Ser Ser
1      5      10      15
Arg Glu Arg Glu Arg Glu Ile Gln Arg Glu Lys Phe Gly Cys Leu Leu
20      25      30
Thr Glu Ala Ser Ser Val Ser Leu Leu Arg Leu Thr Ile Val Asn Ala
35      40      45
Trp Phe His Leu Gln Phe Cys Phe Tyr Phe Ser Arg Ser Phe Ser Ser
50      55      60
Phe Lys Tyr Cys Phe Arg Ser Ile Asn Gln Ser Ile Met Ala Ser Ser
65      70      75
Gly Asn Lys Asn Ile Asn Ala Lys Leu Val Leu Leu Gly Asp Val Gly
85      90      95
Ala Gly Lys Ser Ser Leu Val Leu Arg Phe Val Lys Asp Gln Phe Val
100     105     110
Glu Phe Gln Glu Ser Thr Ile Gly Ala Ala Phe Phe Ser Gln Thr Leu
115     120     125
Ala Val Asn Asp Ala Thr Val Lys Phe Glu Ile Trp Asp Thr Ala Gly
130     135     140
Gln Glu Arg Tyr His Ser Ser Leu Ala Pro Met Tyr Tyr Arg Gly Ala Ala
145     150     155
Ala Ala Ile Ile Val Phe Asp Ile Thr Asn Gln Ala Ser Phe Glu Arg
165     170     175
Ala Xaa Lys Trp Val Gln Glu Leu Gln Ala Gln Gly Asn Pro Asn Met
180     185     190
Val Met Ala Leu Ala Gly Asn Lys Ala Asp Leu Leu Asp Ala Arg Lys
195     200     205
Val Ser Ala Glu Glu Ala Glu Ile Tyr Ala Gln Glu Asn Ser Leu Phe
210     215     220
Phe Met Glu Thr Ser Ala Lys Thr Ala Thr Asn Val Lys Asp Ile Phe
225     230     235
Tyr Glu Ile Ala Lys Arg Leu Pro Arg Ile Gln Pro Ala Glu Asn Pro
245     250     255
Thr Gly Met Val Leu Pro Asn Gly Pro Gly Ala Thr Ala Val Ser Ser
260     265     270
Ser Cys Cys Ala
275

```

(2) INFORMATION FOR SEQ ID NO:2641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..200
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2641:

```

Met Ala Ser Ser Gly Asn Lys Asn Ile Asn Ala Lys Leu Val Leu Leu
1      5      10      15
Gly Asp Val Gly Ala Gly Lys Ser Ser Leu Val Leu Arg Phe Val Lys
20      25      30
Asp Gln Phe Val Glu Phe Gln Glu Ser Thr Ile Gly Ala Ala Phe Phe
35      40      45
Ser Gln Thr Leu Ala Val Asn Asp Ala Thr Val Lys Phe Glu Ile Trp
50      55      60
Asp Thr Ala Gly Gln Glu Arg Tyr His Ser Leu Ala Pro Met Tyr Tyr
65      70      75
Arg Gly Ala Ala Ala Ala Ile Ile Val Phe Asp Ile Thr Asn Gln Ala
85      90      95
Ser Phe Glu Arg Ala Xaa Lys Trp Val Gln Glu Leu Gln Ala Gln Gly

```

100	105	110
Asn Pro Asn Met Val Met	Ala Leu Ala Gly Asn Lys Ala Asp Leu Leu	
115	120	125
Asp Ala Arg Lys Val Ser	Ala Glu Glu Ala Glu Ile Tyr Ala Gln Glu	
130	135	140
Asn Ser Leu Phe Phe Met	Glu Thr Ser Ala Lys Thr Ala Thr Asn Val	
145	150	155
Lys Asp Ile Phe Tyr Glu	Ile Ala Lys Arg Leu Pro Arg Ile Gln Pro	
165	170	175
Ala Glu Asn Pro Thr Gly Met Val	Leu Pro Asn Gly Pro Gly Ala Thr	
180	185	190
Ala Val Ser Ser Ser Cys Cys Ala		
195	200	

(2) INFORMATION FOR SEQ ID NO:2642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2642:

gagcgggact	tactttgtgg	ttgctgatca	cactccattt	ggaatggaga	acgatgttgc	60
tttctgtgag	tatcttattg	aagaagtgtg	ggtcgttgcg	atcccaacga	gcgtctttta	120
tctgaatcca	gaagaaggga	agaatttgg	taggtttgcg	ttctgtaaag	acgaagagac	180
ggttcgttgt	gcaattgaga	ggaatgaagca	gaagcttaag	agaaaagtct	gaagtgttgaa	240
ttagaaagat	accttatttt	tatctagtgt	tgtaacttct	tcttcggttc	catttcggga	300
gagactttga	tttagcaaa	caaatacata	aagtaaaagt	tacgtGtate	aaatgcaata	360
atagtcttta	gagtc					

(2) INFORMATION FOR SEQ ID NO:2643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2643:

Ser Gly Thr Tyr Phe Val Val Ala Asp His Thr Pro Phe Gly Met Glu	
1	5
Asn Asp Val Ala Phe Cys Glu Tyr Leu Ile Glu Glu Val Gly Val Val	
20	25
Ala Ile Pro Thr Ser Val Phe Tyr Leu Asn Pro Glu Glu Gly Lys Asn	
35	40
Leu Val Arg Phe Ala Phe Cys Lys Asp Glu Glu Thr Leu Arg Gly Ala	
50	55
Ile Glu Arg Met Lys Glu Lys Leu Lys Arg Lys Val	
65	70
	75

(2) INFORMATION FOR SEQ ID NO:2644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..40
(D) OTHER INFORMATION: / Ceres Seq. ID 1573859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2644:

Ala Gly Leu Thr Leu Trp Leu Leu Ile Thr Leu His Leu Glu Trp Arg
1 5 10 15
Thr Met Leu Leu Ser Val Ser Ile Leu Lys Lys Leu Gly Ser Leu
20 25 30
Arg Ser Gln Arg Ala Ser Phe Ile
35 40

(2) INFORMATION FOR SEQ ID NO:2645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..62
(D) OTHER INFORMATION: / Ceres Seq. ID 1573860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2645:

Met Glu Asn Asp Val Ala Phe Cys Glu Tyr Leu Ile Glu Glu Val Gly
1 5 10 15
Val Val Ala Ile Pro Thr Ser Val Phe Tyr Leu Asn Pro Glu Glu Gly
20 25 30
Lys Asn Leu Val Arg Phe Ala Phe Cys Lys Asp Glu Glu Thr Leu Arg
35 40 45
Gly Ala Ile Glu Arg Met Lys Gln Lys Leu Lys Arg Lys Val
50 55 60

(2) INFORMATION FOR SEQ ID NO:2646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1076 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1076
(D) OTHER INFORMATION: / Ceres Seq. ID 1573864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2646:

atttttgatt ggcgtcatctt ctctcttggga aatgtctttg atttagcatt tcagttcgct 60
caaaaacatca aatcttacct tcttttagctt tcacattaga ttctggtaat tattaacaca 120
aaaaaaagat aagccagaat acgaacaacac caaaaaaaga ggattttttt tttttttttt 180
ttcttttcga tgcttccgac caataattac cgaatctccg gcgaaccacc gtctactacg 240
cgcgtctctc caccgcacaa accgaaaaca aggattctct ctctattcct cgttggtgta 300
atcattgttt caatcttctt tctcttctct gtcttctatg gtatcgccct tgtctctatc 360
ctccctctcc tctctctctc tctccatcgt caccaccgac gtctgtctcg taatcgccga 420
caagaatcct cagatgggtt atcttcaaga ttctgtaaaa agcttctctc attcaaatc 480
tccgaacctc gcacatacac acggtacgag agcgattgtg tggtttcttt tgatggattc 540
agacaaggac aatggtgtcg gaattctcct ggttggtggac acgtgtttca tcgaagtgt 600
gtggagacct ggttgctcaa agcctcgacg tctctattK tgcagagcta gggttagatt 660
gtggaggagg gatccacaag aaggagaatt aaggagatgt ttgggtcata qaagaatga 720
tttgctagat ttgtaatat gtgtggttat gttagacgtgg actcagtcta atggatgata 780
agaatctcca aaactgaagc tacgaagagg tacaatacaa gcccaaggact cttctccca 840
tagagaagta gcgggtcgat cttatggtaa tatataagca ctaagcagat gggcggttga 900
tcataataac cctcactacc attaccaaaa agcaatagcc aagagctttt tttttcattt 960
tctttttgaa agccatggat cggttttcgt tcttgaatgt tataatggag gttcgcggtta 1020
ttctaaatga atcccgcaaa ctcttctca agaacaacaaa gttgatgttc tcagcc

(2) INFORMATION FOR SEQ ID NO:2647:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1573865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2647:

Met	Pro	Pro	Thr	Asn	Asn	Tyr	Arg	Ile	Ser	Gly	Glu	Pro	Pro	Ser	Thr	
1			5						10					15		
Thr	Pro	Ser	Pro	Pro	Pro	Pro	Lys	Pro	Lys	Thr	Arg	Ile	Leu	Ser	Leu	
			20					25					30			
Phe	Leu	Val	Gly	Val	Ile	Met	Phe	Ser	Ile	Phe	Phe	Leu	Phe	Leu	Val	
		35					40					45				
Leu	Ile	Gly	Ile	Ala	Ser	Val	Leu	Ile	Leu	Pro	Leu	Leu	Leu	Ser	Ser	
		50				55					60					
Leu	His	Arg	His	His	Arg	Arg	Arg	Arg	Arg	Asn	Arg	Arg	Gln	Glu	Ser	
65				70					75				80			
Ser	Asp	Gly	Leu	Ser	Ser	Arg	Phe	Val	Lys	Lys	Leu	Pro	Gln	Phe	Lys	
			85					90					95			
Phe	Ser	Glu	Pro	Ser	Thr	Tyr	Thr	Arg	Tyr	Glu	Ser	Asp	Cys	Val	Val	
			100					105					110			
Cys	Phe	Asp	Gly	Phe	Arg	Gln	Gly	Gln	Trp	Cys	Arg	Asn	Leu	Pro	Gly	
		115				120						125				
Cys	Gly	His	Val	Phe	His	Arg	Lys	Cys	Val	Asp	Thr	Trp	Leu	Leu	Lys	
		130				135						140				
Ala	Ser	Thr	Cys	Pro	Ile	Xaa	Gln	Ser								
145					150											

(2) INFORMATION FOR SEQ ID NO:2648:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1573866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2648:

Met	Phe	Ser	Ile	Phe	Phe	Leu	Phe	Leu	Val	Leu	Ile	Gly	Ile	Ala	Ser	
1			5						10					15		
Val	Leu	Ile	Leu	Pro	Leu	Leu	Leu	Ser	Ser	Leu	His	Arg	His	His	Arg	
			20					25					30			
Arg	Arg	Arg	Arg	Asn	Arg	Arg	Gln	Glu	Ser	Ser	Asp	Gly	Leu	Ser	Ser	
			35				40					45				
Arg	Phe	Val	Lys	Lys	Leu	Pro	Gln	Phe	Lys	Phe	Ser	Glu	Pro	Ser	Thr	
		50				55				60						
Tyr	Thr	Arg	Tyr	Glu	Ser	Asp	Cys	Val	Val	Cys	Phe	Asp	Gly	Phe	Arg	
65				70					75				80			
Gln	Gly	Gln	Trp	Cys	Arg	Asn	Leu	Pro	Gly	Cys	Gly	His	Val	Phe	His	
			85					90				95				
Arg	Lys	Cys	Val	Asp	Thr	Trp	Leu	Leu	Lys	Ala	Ser	Thr	Cys	Pro	Ile	
			100					105				110				
Xaa	Gln	Ser														
		115														

(2) INFORMATION FOR SEQ ID NO:2649:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 505 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..505
(D) OTHER INFORMATION: / Ceres Seq. ID 1573867

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2649:

atcaatcgga	ttatctgcac	ttgtttcaat	gggtcatcta	atatctctca	agctggtgct	60
cttgcttgcc	ttacaccgga	aggacttgag	gcaatgcata	aggtgattgg	attctataaa	120
gaaaacacaa	acataatcat	tgacacattc	acatctctcg	ggatgatgt	atatggagga	180
aatgcgcctt	acgtatgggt	tcacttcccg	aaccaaaagt	catgggatgt	gtttgctgag	240
attctggaga	agactcatgt	ggttacaact	ccaggaagt	ggttggacc	agggggtgaa	300
gggttctgtc	gtgtcagtc	ctttggtcac	agagagaaca	tcttagaggc	atgtcgaaga	360
ttcaagcagc	tttacaatat	aagaaccttg	tttgtaatcg	ttcctcatca	tcataccctt	420
ctttaatgac	atgatttgag	ttaaaataat	gtcgtttcca	Tgtgkktstg	gaattttag	480
aagacacttt	tgacaccagt	gttttc				

- (2) INFORMATION FOR SEQ ID NO:2650:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..126
(D) OTHER INFORMATION: / Ceres Seq. ID 1573868

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2650:

Ile	Asn	Arg	Ile	Ile	Cys	Thr	Cys	Phe	Asn	Gly	Ala	Ser	Asn	Ile	Ser
1		5						10						15	
Gln	Ala	Gly	Ala	Leu	Ala	Cys	Leu	Thr	Pro	Glu	Gly	Leu	Glu	Ala	Met
		20						25						30	
His	Lys	Val	Ile	Gly	Phe	Tyr	Lys	Glu	Asn	Thr	Asn	Ile	Ile	Ile	Asp
		35						40						45	
Thr	Phe	Thr	Ser	Leu	Gly	Tyr	Asp	Val	Tyr	Gly	Gly	Asn	Ala	Pro	Tyr
		50						55						60	
Val	Trp	Val	His	Phe	Pro	Asn	Gln	Ser	Ser	Trp	Asp	Val	Phe	Ala	Glu
		65						70						75	
Ile	Leu	Glu	Lys	Thr	His	Val	Val	Thr	Thr	Pro	Gly	Ser	Gly	Phe	Gly
		85						90						95	
Pro	Gly	Gly	Glu	Gly	Phe	Val	Arg	Val	Ser	Ala	Phe	Gly	His	Arg	Glu
		100						105						110	
Asn	Ile	Leu	Glu	Ala	Cys	Arg	Arg	Phe	Lys	Gln	Leu	Tyr	Lys		
		115						120						125	

- (2) INFORMATION FOR SEQ ID NO:2651:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..95
(D) OTHER INFORMATION: / Ceres Seq. ID 1573869

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2651:

Met His Lys Val Ile Gly Phe Tyr Lys Glu Asn Thr Asn Ile Ile Ile

1	5	10	15
Asp Thr Phe Thr Ser Leu Gly Tyr Asp Val Tyr Gly Asn Ala Pro			
	20	25	30
Tyr Val Trp Val His Phe Pro Asn Gln Ser Ser Trp Asp Val Phe Ala			
	35	40	45
Glu Ile Leu Glu Lys Thr His Val Val Thr Thr Pro Gly Ser Gly Phe			
	50	55	60
Gly Pro Gly Gly Glu Gly Phe Val Arg Val Ser Ala Phe Gly His Arg			
	65	70	75
Glu Asn Ile Leu Glu Ala Cys Arg Arg Phe Lys Gln Leu Tyr Lys			
	85	90	95

(2) INFORMATION FOR SEQ ID NO:2652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1687 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1687
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2652:

aattctcttgc	tctatttttc	gtcaccctag	ccgctttact	ctcttgcgat	atctctgaga	60
tttggtttgac	agtcctctaac	catggggttaa	gagaagtttc	acatcaacat	ttgtggctatt	120
ggccacgtgc	attctctgaaa	gtcgaccacc	actggacact	tgatctacaa	gttgggtgggt	180
attgacaagc	gtgtcattga	gaggttcgag	aaggaggctg	ctgagatgaa	caagaggttcc	240
ttcaagtacg	catgggtttt	ggacaaactt	aaggctgagc	gtgagcgtgg	tatcacattct	300
gacattgtcc	tctggaaagt	cgagaccacc	aagtactact	gcactgtcat	tgatgtctct	360
ggccatcgtg	atttcatcaa	gaacatgac	actggtacct	cccaggctga	ttgtgtctgc	420
cttatcatgc	actccaccac	tggtgtgttt	gaggctggta	tctccaagga	tggtcagacc	480
cgtgagcagc	ctctcctctg	tttcacctt	gggttcaaac	agatgatctg	ctgttgttaac	540
aagatggatg	ccactaccct	caagtactcc	aaggccaggt	acgatgaat	tatcaaggag	600
gtgtcttctt	acttgaagaa	ggttggttac	aaccocgaca	aaatccctt	tggtcccatc	660
tctggattcg	aggggtgaca	catgattgag	aggtccacca	acctagactg	gtacaaaggga	720
ccaactcttc	ttgaggctct	tgaccagatc	aacgagccca	agaggccact	agacaaagcc	780
cttcgtctcc	cacttcaggga	tgctacaag	attggtggta	ttgaaacggt	gccagtgagg	840
cgtgttgaga	ctgttatgat	caagcctggt	atggttttga	cctttgtctc	cacagggttg	900
accactgagg	tcaagtctgt	tgagatgcac	cacgagcttc	tcttggaggc	acttcagggt	960
gacacagctg	ggttcaatgt	taagaatgtt	gctgtcaagg	atcttaagag	aggggtacgtc	1020
gcactcaact	ccaagatga	ccctgcgaag	gggtgtccta	acttcacctc	ccaggtctatc	1080
atcatgaacc	accctgggtc	gattgtgaac	ggttacgccc	cagtcctgtc	ttgccaaccc	1140
tctcacattg	cagtcgaagt	ctctgagatc	ttgaccaaga	ttgacaggcg	ctgttcttaag	1200
gagatgtaga	agagagccaa	gttcttgaag	aatggtgatg	ctggtatggt	gaagatgaat	1260
ccaaccaagg	ccatgggtgt	ggagaccctt	tctgagtacc	caccacttgg	acgttttcgt	1320
gtgaggggaca	tgaggcgagc	tggttcagtc	ggtgttatca	agagtgttga	caagaaggag	1380
ccaaccggag	ccaagggttac	caaggctgcc	gtcaagaagg	gtgcgaagtg	aacctatctc	1440
aaaactctat	ctgcgcaggg	tgaatcaaa	gacagtgtta	gtttttattc	aatagtttgg	1500
tatttctgtc	cgtgtctctg	ttcttgtttc	gtttttctcc	cgtcagagcg	ttgttctcgt	1560
atttgggttc	ttgatcggag	gtggcggatc	tacacacaca	ttcttctcgt	tttttctgtt	1620
ttatttgttt	tctcattttg	aactgtttaa	aatttctggt	atatgaatga	atgtttttccc	1680
tgcggtc						

(2) INFORMATION FOR SEQ ID NO:2653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1573900

[illegible]

Lys

(2) INFORMATION FOR SEQ ID NO:2654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..401

(D) OTHER INFORMATION: / Ceres Seq. ID 1573901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2654:

```

Met Asn Lys Arg Ser Phe Lys Tyr Ala Trp Val Leu Asp Lys Leu Lys
1      5      10      15
Ala Glu Arg Glu Arg Gly Ile Thr Ile Asp Ile Ala Leu Trp Lys Phe
20      25      30
Glu Thr Thr Lys Tyr Tyr Cys Thr Val Ile Asp Ala Pro Gly His Arg
35      40      45
Asp Phe Ile Lys Asn Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala
50      55      60
Xaa Leu Ile Ile Asp Ser Thr Thr Gly Gly Phe Glu Ala Gly Ile Ser
65      70      75      80
Lys Asp Gly Gln Thr Arg Glu His Ala Leu Ala Phe Thr Leu Gly
85      90      95
Val Lys Gln Met Ile Cys Cys Cys Asn Lys Met Asp Ala Thr Thr Pro
100      105      110
Lys Tyr Ser Lys Ala Arg Tyr Asp Glu Ile Ile Lys Glu Val Ser Ser
115      120      125
Tyr Leu Lys Lys Val Gly Tyr Asn Pro Asp Lys Ile Pro Phe Val Pro
130      135      140
Ile Ser Gly Phe Glu Gly Asp Asn Met Ile Glu Arg Ser Thr Asn Leu
145      150      155      160
Asp Trp Tyr Lys Gly Pro Thr Leu Leu Glu Ala Leu Asp Gln Ile Asn
165      170      175
Glu Pro Lys Arg Pro Ser Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp
180      185      190
Val Tyr Lys Ile Gly Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu
195      200      205
Thr Gly Met Ile Lys Pro Gly Met Val Val Thr Phe Ala Pro Thr Gly
210      215      220
Leu Thr Thr Glu Val Lys Ser Val Glu Met His His Glu Ser Leu Leu
225      230      235      240
Glu Ala Leu Pro Gly Asp Asn Val Gly Phe Asn Val Lys Asn Val Ala
245      250      255
Val Lys Asp Leu Lys Arg Gly Tyr Val Ala Ser Asn Ser Lys Asp Asp
260      265      270
Pro Ala Lys Gly Ala Ala Asn Phe Thr Ser Gln Val Ile Ile Met Asn
275      280      285
His Pro Gly Gln Ile Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His
290      295      300
Thr Ser His Ile Ala Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp
305      310      315      320
Arg Arg Ser Gly Lys Glu Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn
325      330      335
Gly Asp Ala Gly Met Val Lys Met Thr Pro Thr Lys Pro Met Val Val
340      345      350
Glu Thr Phe Ser Glu Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp
355      360      365
Met Arg Gln Thr Val Ala Val Gly Val Ile Lys Ser Val Asp Lys Lys
370      375      380
Asp Pro Thr Gly Ala Lys Val Thr Lys Ala Ala Val Lys Lys Gly Ala

```

385 390 395 400
Lys

(2) INFORMATION FOR SEQ ID NO:2655:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1573902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2655:

Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala Xaa Leu Ile Asp
1 5 10 15
Ser Thr Thr Gly Gly Phe Glu Ala Gly Ile Ser Lys Asp Gly Gln Thr
20 25 30
Arg Glu His Ala Leu Leu Ala Phe Thr Leu Gly Val Lys Gln Met Ile
35 40 45
Cys Cys Cys Asn Lys Met Asp Ala Thr Thr Pro Lys Tyr Ser Lys Ala
50 55 60
Arg Tyr Asp Glu Ile Ile Lys Glu Val Ser Ser Tyr Leu Lys Lys Val
65 70 75 80
Gly Tyr Asn Pro Asp Lys Ile Pro Phe Val Pro Ile Ser Gly Phe Glu
85 90 95
Gly Asp Asn Met Ile Glu Arg Ser Thr Asn Leu Asp Trp Tyr Lys Gly
100 105 110
Pro Thr Leu Leu Glu Ala Leu Asp Gln Ile Asn Glu Pro Lys Arg Pro
115 120 125
Ser Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp Val Tyr Lys Ile Gly
130 135 140
Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu Thr Gly Met Ile Lys
145 150 155 160
Pro Gly Met Val Val Thr Phe Ala Pro Thr Gly Leu Thr Thr Glu Val
165 170 175
Lys Ser Val Glu Met His His Glu Ser Leu Leu Glu Ala Leu Pro Gly
180 185 190
Asp Asn Val Gly Phe Asn Val Lys Asn Val Ala Val Lys Asp Leu Lys
195 200 205
Arg Gly Tyr Val Ala Ser Asn Ser Lys Asp Asp Pro Ala Lys Gly Ala
210 215 220
Ala Asn Phe Thr Ser Gln Val Ile Ile Met Asn His Pro Gly Gln Ile
225 230 235 240
Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His Thr Ser His Ile Ala
245 250 255
Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp Arg Arg Ser Gly Lys
260 265 270
Glu Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn Gly Asp Ala Gly Met
275 280 285
Val Lys Met Thr Thr Pro Thr Lys Pro Met Val Val Glu Thr Phe Ser Glu
290 295 300
Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr Val
305 310 315 320
Ala Val Gly Val Ile Lys Ser Val Asp Lys Lys Asp Pro Thr Gly Ala
325 330 335
Lys Val Thr Lys Ala Ala Val Lys Lys Gly Ala Lys
340 345

(2) INFORMATION FOR SEQ ID NO:2656:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 660 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..660
(D) OTHER INFORMATION: / Ceres Seq. ID 1573909
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2656:
agggtttctg tttgcgcgt caggtttcgt gaaaagaatc tatcttgagc aatgtctcca 60
gctaaagtgt atgtcaccac gaaagccgac cctaaggcta aggccttgaa agctgcgaaa 120
gcagtgaaat ctggccaaat ctgtaaaagc cctgcgaaga agatcaggac aaaggttact 180
ttccacaggc cMaaGacat tgaccgttcc tagaaagcct aagtacccaa agatcagtcg 240
tactccaagg aacaaaattg atcattacca gatcctcaag taccctetca ctactgaatc 300
tgccatgaaa aagattgaag acaacaacac cttagtcttc attggtgaca tccgtgctga 360
caagaaaaag atcaaatgat ctgtcaagaa gatgtatgac attcagacca agaaagtcaa 420
cacctcatt aggcccgatg gaacaaagaa ggcgtatgtg aggttgactc ctgattatga 480
tgctttggat gtggctaaca aaatcgggat catctaactc gatcattgtc gctctgtgat 540
tttacttttt ctggtttttc tcttccatag tctcagtttt gctagagaag ttaagatatt 600
actatcacca tctctttgtt atgcttttat ctttggtatt aaaaagatta tatgtttggc 660

(2) INFORMATION FOR SEQ ID NO:2657:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..53
(D) OTHER INFORMATION: / Ceres Seq. ID 1573910
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2657:
Met Ser Pro Ala Lys Val Asp Val Thr Lys Lys Ala Asp Pro Lys Ala
1 5 10 15
Lys Ala Leu Lys Ala Ala Lys Ala Val Lys Ser Gly Gln Ile Val Lys
20 25 30
Lys Pro Ala Lys Lys Ile Arg Thr Lys Val Thr Phe His Arg Xaa Lys
35 40 45
Asp Ile Asp Arg Ser
50

(2) INFORMATION FOR SEQ ID NO:2658:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..70
(D) OTHER INFORMATION: / Ceres Seq. ID 1573911
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2658:
Met Lys Lys Ile Glu Asp Asn Asn Thr Leu Val Phe Ile Val Asp Ile
1 5 10 15
Arg Ala Asp Lys Lys Lys Ile Lys Asp Ala Val Lys Lys Met Tyr Asp
20 25 30
Ile Gln Thr Lys Lys Val Asn Thr Leu Ile Arg Pro Asp Gly Thr Lys
35 40 45
Lys Ala Tyr Val Arg Leu Thr Pro Asp Tyr Asp Ala Leu Asp Val Ala

50 55 60
Asn Lys Ile Gly Ile Ile
65 70
(2) INFORMATION FOR SEQ ID NO:2659:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..41
(D) OTHER INFORMATION: / Ceres Seq. ID 1573912
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2659:
Met Tyr Asp Ile Gln Thr Lys Lys Val Asn Thr Leu Ile Arg Pro Asp
1 5 10 15
Gly Thr Lys Lys Ala Tyr Val Arg Leu Thr Pro Asp Tyr Asp Ala Leu
20 25 30
Asp Val Ala Asn Lys Ile Gly Ile Ile
35 40

(2) INFORMATION FOR SEQ ID NO:2660:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 559 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..559
(D) OTHER INFORMATION: / Ceres Seq. ID 1573920
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2660:
aattcaactga ttattgtttt aaggcaaat aagatcatct tcaaaatctt ctcatgctc 60
ttccaatttt ctagaataaa catgtcttgc tgtggtggaa gctgtggttg tggatctgcc 120
tgcaagtgcg gcaattggtg cggagggtgc aaaaggtacc ctgacttgga gaacaccgcc 180
accgagactc ttgtctctcg ttgtgctcgc gcgataaact ctcatgacga ggcttccggT 240
cgSagacttt cgttgccgag aatgatgcct gcaaatgcgg atctgactgc aagtgcaccc 300
cttgtaactg caaatgaaga acttcataaa ccctaagtct gtaataaccc taatgttatg 360
ttaggtttgc ttatatgtaa taattggctg atttttccgg tagttttgcc ggcgacgttg 420
gtctttctct tcttcttctt cttctgtgtg tgtttttatg gtttggtcac taagatatct 480
ctgcaaatgt ttatctttgt gactttatta atcctaagac tattatgggt ttgtattaaa 540
gtttgcttct tcttgcctc

(2) INFORMATION FOR SEQ ID NO:2661:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..111
(D) OTHER INFORMATION: / Ceres Seq. ID 1573921
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2661:
Asn Ser Leu Ile Ile Val Leu Arg Gln Ile Lys Ile Ile Phe Lys Ile
1 5 10 15
Phe Ser Asp Leu Phe Gln Phe Ser Arg Lys Asn Met Ser Cys Cys Gly
20 25 30
Gly Ser Cys Gly Cys Gly Ser Ala Cys Lys Cys Gly Asn Gly Cys Gly
35 40 45

Gly Cys Lys Arg Tyr Pro Asp Leu Glu Asn Thr Ala Thr Glu Thr Leu
50 55 60
Val Leu Gly Val Ala Pro Ala Met Asn Ser Gln Tyr Glu Ala Ser Gly
65 70 75 80
Xaa Arg Leu Ser Leu Pro Arg Met Met Pro Ala Asn Ala Asp Leu Thr
85 90 95
Ala Ser Ala Thr Leu Val Pro Ala Asn Glu Glu Leu His Lys Pro
100 105 110

(2) INFORMATION FOR SEQ ID NO:2662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2662:

Met Ser Cys Cys Gly Gly Ser Cys Gly Cys Gly Ser Ala Cys Lys Cys
1 5 10 15
Gly Asn Gly Cys Gly Gly Cys Lys Arg Tyr Pro Asp Leu Glu Asn Thr
20 25 30
Ala Thr Glu Thr Leu Val Leu Gly Val Ala Pro Ala Met Asn Ser Gln
35 40 45
Tyr Glu Ala Ser Gly Xaa Arg Leu Ser Leu Pro Arg Met Met Pro Ala
50 55 60
Asn Ala Asp Leu Thr Ala Ser Ala Thr Leu Val Pro Ala Asn Glu Glu
65 70 75 80
Leu His Lys Pro

(2) INFORMATION FOR SEQ ID NO:2663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2663:

Met Leu Gly Leu Leu Ile Cys Asn Asn Trp Leu Ile Phe Pro Val Val
1 5 10 15
Leu Pro Ala Thr Leu Val Phe Leu Phe Phe Phe Phe Cys Val Cys
20 25 30
Phe Tyr Gly Leu Val Ile Lys Ile Ser Leu Gln Ser Phe Ile Phe Val
35 40 45
Thr Leu Leu Ile Leu Arg Leu Leu Trp Val Cys Ile Lys Val Cys Phe
50 55 60
Phe Leu Ala
65

(2) INFORMATION FOR SEQ ID NO:2664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1211
(D) OTHER INFORMATION: / Ceres Seq. ID 1573941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2664:

aaaagcaaca	tgaagacaaa	ttaagctggt	tcttcttctt	gttcttgggtc	ttcgtggaaa	60
atatgtttgt	tgctctgtct	ctttctcacc	gagacgatca	ccgcgcgtgaa	gctgccgcca	120
aaattgtatta	tccgcgtgtg	aatcgctttc	ggagactcca	ctgtcgacac	aggaatgaac	180
aacaatgtca	aaaccggtgt	taagtgtgat	tttcttctct	atgggtatcaa	tttccaaagc	240
ggagttgcc	cggggagatt	ctgcgatgga	cgagtcctcg	ccgattttgct	agccgaagaa	300
ctgggaataa	aatcaattgt	accagcatca	ctagatccga	atctaaaatc	gaaagatctt	360
ttaacgggtg	tatgttttgc	gtccggaggt	tctggttatg	atcctataac	accgaaactt	420
gtggcgagta	tatcattaga	agatcaattg	agttatttgc	aggagtagat	agagaaagtg	480
aagaatatag	ttggggaagc	aagaaaagac	ttcatagtag	ccaacagctt	attcttatgt	540
gtcgcaggca	gcgacgacat	agccaataca	tactatactc	tacgtgcaag	acctgaatac	600
gacgtcgatt	catacactac	tcttatgtct	gactctgcct	cagaatttgt	gactaaacta	660
tatggatatg	gagtgagaag	agtagctgtg	tttgggtcac	caccaattgg	gtgtgtacca	720
tccagagaa	cgttaggagg	aggtatcttg	agagattgtg	ctgataatta	caacgaagca	780
gcaaaacttt	ttaattcaaa	gcctctccca	aaattggatt	cgttgcgtta	aacctaccgc	840
ggcatcaaac	cgatctacat	taatatctat	gatcctcttt	tgcacatcat	ccagaatcct	900
gcaaatatgt	ggtttgaagt	gtctaataaa	ggatgctgtg	gaacaggagc	catagaagtt	960
gctgtgttgt	gcaataaaaa	cacatctctt	gtatgtcccg	acgtgtctac	ctatgtgttt	1020
tgggacagnt	tatcatctca	cagagaaaac	ttacaaaagta	ttagtctcac	tggtgattaa	1080
caaatattgt	aaatcagttg	tctgaattaa	aaactatttt	cacggcataa	tgattgatta	1140
tattttatct	catcttgttt	gtattatttg	ataattgtat	tcgatttaaa	taaaaatta	1200
attttcttgt	t					

(2) INFORMATION FOR SEQ ID NO:2665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..359
(D) OTHER INFORMATION: / Ceres Seq. ID 1573942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2665:

Lys	Ser	Asn	Met	Lys	Asp	Asn	Ser	Ser	Trp	Ser	Cys	Ser	Cys	Ser	Trp
1				5					10					15	
Ser	Ser	Trp		Lys	Ile	Cys	Leu	Leu	Ser	Val	Leu	Thr	Glu	Thr	
				20					25				30		
Ile	Thr	Ala	Val	Lys	Leu	Pro	Pro	Lys	Leu	Ile	Ile	Pro	Ala	Val	Ile
				35					40				45		
Ala	Phe	Gly	Asp	Ser	Ile	Val	Asp	Thr	Gly	Met	Asn	Asn	Val	Lys	
				50					55				60		
Thr	Val	Val	Lys	Cys	Asp	Phe	Leu	Pro	Tyr	Gly	Ile	Asn	Phe	Gln	Ser
				65					70				75		80
Gly	Val	Ala	Thr	Gly	Arg	Phe	Cys	Asp	Gly	Arg	Val	Pro	Ala	Asp	Leu
				85					90				95		
Leu	Ala	Glu	Glu	Leu	Gly	Ile	Lys	Ser	Ile	Val	Pro	Ala	Tyr	Leu	Asp
				100					105				110		
Pro	Asn	Leu	Lys	Ser	Lys	Asp	Leu	Leu	Thr	Gly	Val	Ser	Phe	Ala	Ser
				115					120				125		
Gly	Gly	Ser	Gly	Tyr	Asp	Pro	Ile	Thr	Pro	Lys	Leu	Val	Ala	Val	Ile
				130					135				140		
Ser	Leu	Glu	Asp	Gln	Leu	Ser	Tyr	Phe	Glu	Glu	Tyr	Ile	Glu	Lys	Val
				145					150				155		160
Lys	Asn	Ile	Val	Gly	Glu	Ala	Arg	Lys	Asp	Phe	Ile	Val	Ala	Asn	Ser
				165					170				175		
Leu	Phe	Leu	Leu	Val	Ala	Gly	Ser	Asp	Asp	Ile	Ala	Asn	Thr	Tyr	Tyr

180 185 190
Thr Leu Arg Ala Arg Pro Glu Tyr Asp Val Asp Ser Tyr Thr Thr Leu
195 200 205
Met Ser Asp Ser Ala Ser Glu Phe Val Thr Lys Leu Tyr Gly Tyr Gly
210 215 220
Val Arg Arg Val Ala Val Phe Gly Ala Pro Pro Ile Gly Cys Val Pro
225 230 235
Ser Gln Arg Thr Leu Gly Gly Ile Leu Arg Asp Cys Ala Asp Asn
245 250 255
Tyr Asn Glu Ala Ala Lys Leu Phe Asn Ser Lys Leu Ser Pro Lys Leu
260 265 270
Asp Ser Leu Arg Lys Thr Leu Pro Gly Ile Lys Pro Ile Tyr Ile Asn
275 280 285
Ile Tyr Asp Pro Leu Phe Asp Ile Ile Gln Asn Pro Ala Asn Tyr Gly
290 295 300
Phe Glu Val Ser Asn Lys Gly Cys Cys Gly Thr Gly Ala Ile Glu Val
305 310 315
Ala Val Leu Cys Asn Lys Ile Thr Ser Ser Val Cys Pro Asp Val Ser
325 330 335
Thr His Val Phe Trp Asp Xaa Leu Ser Ser Tyr Arg Glu Asn Leu Gln
340 345 350
Ser Ile Ser Leu Thr Val Asp
355

(2) INFORMATION FOR SEQ ID NO:2666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..356
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2666:

Met Lys Asp Asn Ser Ser Trp Ser Cys Ser Cys Ser Trp Ser Ser Trp
1 5 10 15
Lys Ile Cys Leu Leu Ser Val Leu Phe Leu Thr Glu Thr Ile Thr Ala
20 25 30
Val Lys Leu Pro Pro Lys Leu Ile Ile Pro Ala Val Ile Ala Phe Gly
35 40 45
Asp Ser Ile Val Asp Thr Gly Met Asn Asn Asn Val Lys Thr Val Val
50 55 60
Lys Cys Asp Phe Leu Pro Tyr Gly Ile Asn Phe Gln Ser Gly Val Ala
65 70 75 80
Thr Gly Arg Phe Cys Asp Gly Arg Val Pro Ala Asp Leu Leu Ala Glu
85 90 95
Glu Leu Gly Ile Lys Ser Ile Val Pro Ala Tyr Leu Asp Pro Asn Leu
100 105 110
Lys Ser Lys Asp Leu Leu Thr Gly Val Ser Phe Ala Ser Gly Gly Ser
115 120 125
Gly Tyr Asp Pro Ile Thr Pro Lys Leu Val Ala Val Ile Ser Leu Glu
130 135 140
Asp Gln Leu Ser Tyr Phe Glu Glu Tyr Ile Glu Lys Val Lys Asn Ile
145 150 155 160
Val Gly Glu Ala Arg Lys Asp Phe Ile Val Ala Asn Ser Leu Phe Leu
165 170 175
Leu Val Ala Gly Ser Asp Asp Ile Ala Asn Thr Tyr Tyr Thr Leu Arg
180 185 190
Ala Arg Pro Glu Tyr Asp Val Asp Ser Tyr Thr Thr Leu Met Ser Asp
195 200 205

Ser Ala Ser Glu Phe Val Thr Lys Leu Tyr Gly Tyr Gly Val Arg Arg
210 215 220
Val Ala Val Phe Gly Ala Pro Pro Ile Gly Cys Val Pro Ser Gln Arg
225 230 235 240
Thr Leu Gly Gly Gly Ile Leu Arg Asp Cys Ala Asp Asn Tyr Asn Glu
245 250 255
Ala Ala Lys Leu Phe Asn Ser Lys Leu Ser Pro Lys Leu Asp Ser Leu
260 265 270
Arg Lys Thr Leu Pro Gly Ile Lys Pro Ile Tyr Ile Asn Ile Tyr Asp
275 280 285
Pro Leu Phe Asp Ile Ile Gln Asn Pro Ala Asn Tyr Gly Phe Glu Val
290 295 300
Ser Asn Lys Gly Cys Cys Gly Thr Gly Ala Ile Glu Val Ala Val Leu
305 310 315 320
Cys Asn Lys Ile Thr Ser Ser Val Cys Pro Asp Val Ser Thr His Val
325 330 335
Phe Trp Asp Xaa Leu Ser Ser Tyr Arg Glu Asn Leu Gln Ser Ile Ser
340 345 350
Leu Thr Val Asp
355

(2) INFORMATION FOR SEQ ID NO:2667:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 301 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..301

(D) OTHER INFORMATION: / Ceres Seq. ID 1573944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2667:

Met Asn Asn Asn Val Lys Thr Val Val Lys Cys Asp Phe Leu Pro Tyr
1 5 10 15
Gly Ile Asn Phe Gln Ser Gly Val Ala Thr Gly Arg Phe Cys Asp Gly
20 25 30
Arg Val Pro Ala Asp Leu Leu Ala Glu Glu Leu Gly Ile Lys Ser Ile
35 40 45
Val Pro Ala Tyr Leu Asp Pro Asn Leu Lys Ser Lys Asp Leu Leu Thr
50 55 60
Gly Val Ser Phe Ala Ser Gly Gly Ser Gly Tyr Asp Pro Ile Thr Pro
65 70 75 80
Lys Leu Val Ala Val Ile Ser Leu Glu Asp Gln Leu Ser Tyr Phe Glu
85 90 95
Glu Tyr Ile Glu Lys Val Lys Asn Ile Val Gly Glu Ala Arg Lys Asp
100 105 110
Phe Ile Val Ala Asn Ser Leu Phe Leu Leu Val Ala Gly Ser Asp Asp
115 120 125
Ile Ala Asn Thr Tyr Tyr Thr Leu Arg Ala Arg Pro Glu Tyr Asp Val
130 135 140
Asp Ser Tyr Thr Thr Leu Met Ser Asp Ser Ala Ser Glu Phe Val Thr
145 150 155 160
Lys Leu Tyr Gly Tyr Gly Val Arg Arg Val Ala Val Phe Gly Ala Pro
165 170 175
Pro Ile Gly Cys Val Pro Ser Gln Arg Thr Leu Gly Gly Gly Ile Leu
180 185 190
Arg Asp Cys Ala Asp Asn Tyr Asn Glu Ala Ala Lys Leu Phe Asn Ser
195 200 205
Lys Leu Ser Pro Lys Leu Asp Ser Leu Arg Lys Thr Leu Pro Gly Ile
210 215 220
Lys Pro Ile Tyr Ile Asn Ile Tyr Asp Pro Leu Phe Asp Ile Ile Gln

225	230	235	240
Asn Pro Ala Asn Tyr Gly Phe Glu Val Ser Asn Lys Gly Cys Cys Gly			
	245	250	255
Thr Gly Ala Ile Glu Val Ala Val Leu Cys Asn Lys Ile Thr Ser Ser			
	260	265	270
Val Cys Pro Asp Val Ser Thr His Val Phe Trp Asp Xaa Leu Ser Ser			
	275	280	285
Tyr Arg Glu Asn Leu Gln Ser Ile Ser Leu Thr Val Asp			
	290	295	300

(2) INFORMATION FOR SEQ ID NO:2668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1257
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2668:

gtaatctcaa	tcacaaacta	tttccccctt	tcgttcatca	aatcctcaag	agaaaaaaaa	60
aatccccaaa	agcttcccta	aaaccctaac	acagatctct	cgatctcttc	cgatctgtct	120
tttctcctaa	tcctggtttag	tttgatttaa	ttggattgaa	gatgtcagac	gctttgaata	180
tgactettga	tgaattgtg	aagaagagta	agagtgaag	gtctgcagct	gcaaggctctg	240
gaggtaaagg	agtttccgt	aagagtggac	gtggacgtgg	tggaacctaat	ggtgtgttag	300
gagctggaag	aggaggtgga	cctgttccta	gaggtcctct	tgtctgtta	actcggccat	360
catcatcctt	ctccataaac	aagcttgccc	gcaGgaagag	gagcttgcca	tggcagaaac	420
agaatgattt	gtatgaagaa	acccttagag	ctgttgggg	gtcaggagtg	gaagtcgga	480
ccacagttta	tattaccaac	cttgatcagg	gagtgacaaa	tgaagatata	agggaaactct	540
atgctgagat	tggagagctG	Raaagatag	caattcacta	tgacaaaaat	gggcgtccaa	600
gtggatcgcg	tgaagtgtg	tatatgagaa	gaagtgatgc	aattcaagct	atgaggaat	660
acaTacaatg	tacttttgg	tggaaagcct	atgaaactgg	agattctggg	tggaaagtact	720
gaatctgtct	ctgtcgcagc	tcgtgtta	gtgactggat	tgaatggaag	gatgaagagg	780
agtgctctca	ttggacaagg	agtttagaggt	gggagagtag	gaagaggaa	aggttcaggt	840
ccttctggaa	gagcgccttc	agtccaacaa	aaccaacaag	gtggtcgagg	tggtcaggcc	900
ggggtccgtg	gtagaggcag	aggtgctggt	ggaggcagag	ggaataaaa	tggtgcgccg	960
ggtggaaga	agccggtgga	gaagtctgct	gcggatctcg	acaaagatct	cgaaagctat	1020
catgctgaag	ctatgaacat	ctcttaaagc	aagacttccg	atcttgtcat	gtacttttgt	1080
gttctttatt	cgtagtctct	gactaaatat	gtgccaaagt	ctggttttgt	ttaatcaagt	1140
ttagagttgc	tctactctgc	tttcgttttc	ctcttttttc	gtttcacact	ttcacagtca	1200
cttttggtta	tgaagttaa	aagagattta	gctgtaaatg	agaaagctgt	tcttgtt	

(2) INFORMATION FOR SEQ ID NO:2669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2669:

Met Ser Asp Ala Leu Asn Met Thr Leu Asp Glu Ile Val Lys Lys Ser	
1	5
Lys Ser Glu Arg Ser Ala Ala Ala Arg Ser Gly Gly Lys Gly Val Ser	
	10
Arg Lys Ser Gly Arg Gly Arg Gly Gly Pro Asn Gly Val Val Gly Ala	
	15
Gly Arg Gly Gly Gly Pro Val Arg Arg Gly Pro Leu Ala Val Asn Thr	
	20
	25
	30
	35
	40
	45

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..118
(D) OTHER INFORMATION: / Ceres Seq. ID 1573952
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2671:
Met Lys Leu Glu Ile Leu Gly Gly Ser Thr Glu Ser Ala Pro Val Ala
1 5 10 15
Ala Arg Val Asn Val Thr Gly Leu Asn Gly Arg Met Lys Arg Ser Val
20 25 30
Phe Ile Gly Gln Gly Val Arg Gly Gly Arg Val Gly Arg Gly Arg Gly
35 40 45
Ser Gly Pro Ser Gly Arg Arg Leu Pro Val Gln Gln Asn Gln Gln Gly
50 55 60
Gly Arg Gly Gly Arg Gly Gly Val Arg Gly Arg Gly Arg Gly Ala Gly
65 70 75 80
Gly Gly Arg Gly Asn Lys Ser Gly Gly Arg Gly Gly Lys Lys Pro Val
85 90 95
Glu Lys Ser Ala Ala Asp Leu Asp Lys Asp Leu Glu Ser Tyr His Ala
100 105 110
Glu Ala Met Asn Ile Ser
115

(2) INFORMATION FOR SEQ ID NO:2672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..600
(D) OTHER INFORMATION: / Ceres Seq. ID 1573953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2672:

ggatcatata ttgtctgtat gagcattgtt tcagcacaa gccaagcaaa gcaggggatg 60
agcagttgaa cttgttcogt ttccctcttc ttgtagctcc catcaagtgc acgggtttcc 120
cgcttgttca gaaccaacaa ttcgaggaag cagccaaagt tatttccaa gaactcgct 180
ctgtcgggat ctcccataag attgacatca ctggtacatc gatagggaag agatatcgga 240
gaaccgatga gcttggagtg ccatttgcaa taacagtgga ctcgatgaca tcagtgacaa 300
tcagagaaaag agacagcaaa gatcaagtc gagtcacatt gaaggaggca gcttccgttg 360
tgagctcagt ctacaggggg aaaatgacgt ggcaagacgt ctggggcaacc ttccctcacc 420
attctctcgc tgctgcagac gagtagctag ctccctgttt ttttccGaa ttaaaaacca 480
aagtgttaaa ttaattgttg ctgaattctac tcatttttaa tgtttgttt cttagtgtca 540
cgtaaaaagt tcgataccag attgttagac gaagyggtcta taaagtataa actctctgtc 600

(2) INFORMATION FOR SEQ ID NO:2673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..147
(D) OTHER INFORMATION: / Ceres Seq. ID 1573954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2673:

Ile Ile Tyr Cys Leu Tyr Glu His Cys Phe Ser Thr Arg Pro Ser Lys
1 5 10 15
Ala Gly Asp Glu Gln Leu Asn Leu Phe Arg Phe Pro Pro Leu Val Ala
20 25 30
Pro Ile Lys Cys Thr Val Phe Pro Leu Val Gln Asn Gln Gln Phe Glu
35 40 45

Glu Ala Ala Lys Val Ile Ser Lys Glu Leu Ala Ser Val Gly Ile Ser
50 55 60
His Lys Ile Asp Ile Thr Gly Thr Ser Ile Gly Lys Arg Tyr Ala Arg
65 70 75 80
Thr Asp Glu Leu Gly Val Pro Phe Ala Ile Thr Val Asp Ser Asp Thr
85 90 95
Ser Val Thr Ile Arg Glu Arg Asp Ser Lys Asp Gln Val Arg Val Thr
100 105 110
Leu Lys Glu Ala Ala Ser Val Val Ser Ser Val Ser Glu Gly Lys Met
115 120 125
Thr Trp Gln Asp Val Trp Ala Thr Phe Pro His His Ser Ser Ala Ala
130 135 140
Ala Asp Glu
145

(2) INFORMATION FOR SEQ ID NO:2674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2674:

aattgcaaat	caaatggatc	gtcttaagct	tattttctcc	gttttcgttt	tgtctttctt	60
tatcgtctcg	gtttcgtcgt	ctgatgtcaa	cgacggcgat	gatctcgtga	tcgcgcaggt	120
ggttgggtga	gccgagccct	aggttttgac	ctcagaggat	cactttttctc	tcttcaagcg	180
gaagttcggg	aaggtctcac	cttccaacga	ggagcatgac	tatagattct	cggtttgagt	240
tcctgaagaa	gcacttgggg	gttagaagtg	gctttaagct	tctttaaagt	gccaaacaag	300
ctccgattct	ccctaccgaa	aattctccctg	aggattttga	ttggagagat	catggcgccg	360
ttaactcccg	caaaaatcac	ggatcttgcg	gctcttgcgt	gagtttccgc	gccactggag	420
ctttggaagg	tgttaacttc	ctcgtctaccg	gcagactcgt	cagcctcagc	gaacaacagc	480
tcgtcgactg	tgatcacgag	tgtgatcccg	aggagcagaa	ttTcctgcga	ctctgttggt	540
aatgggtggc	taatgaacag	cgcttttgaa	tacaccCtca	aaaccggagg	gctcatgaaa	600
gaagaagact	atcctttacac	cggaaaggac	ggcaagacct	gcaagctaga	caagtccaag	660
atcgttgcct	ctgtctccaa	cttcagtggt	atctccattg	atgaagaaca	gattgtgcga	720
aacctgtgca	agaacggacc	tcttgctgtga	gccatcaacg	ctggctatat	gcagacttac	780
attggaggag	tctcatgccc	ttacatatgc	accaggaggc	tcaaccaacg	tgtcttattg	840
gttggtctatg	gagcggcagg	tacgctccg	gctaggttca	aggagaagcc	ttactggatc	900
atcaagaact	cgtggggaga	gaactggggg	gaaaatgggt	tctacaaaat	ctgcaaaagg	960
cgtaacattt	gtggtgttga	cagtatggtc	tccactgttg	cagccaccgt	ctcaaccacc	1020
gccattataa	catctcgtca	ataagtttta	attacttttg	tgatttgat	gagcgcgtc	1080
tctttggcgt	gctgactctc	tctatttate	tctgcttctt	gcttgtaaat	aaaatgcggt	1140
ctattg						

(2) INFORMATION FOR SEQ ID NO:2675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..246
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2675:

Met Pro Thr Arg Leu Arg Phe Ser Leu Pro Lys Ile Ser Leu Arg Ile
1 5 10 15
Leu Ile Gly Glu Ile Met Ala Pro Leu Leu Pro Ser Lys Ile Arg Asp

20	25	30
Leu Ala Ala Leu Ala Gly Val Ser Ala Pro Leu Glu Leu Trp Lys Val		
35	40	45
Leu Thr Ser Ser Leu Pro Ala Asp Ser Ser Ala Ser Ala Asn Asn Ser		
50	55	60
Ser Ser Thr Val Ile Thr Ser Val Ile Pro Arg Arg Gln Ile Ser Cys		
65	70	75
Asp Ser Gly Cys Asn Gly Gly Leu Met Asn Ser Ala Phe Glu Tyr Thr		
85	90	95
Leu Lys Thr Gly Gly Leu Met Lys Glu Glu Asp Tyr Pro Tyr Thr Gly		
100	105	110
Lys Asp Gly Lys Thr Cys Lys Leu Asp Lys Ser Lys Ile Val Ala Ser		
115	120	125
Val Ser Asn Phe Ser Val Ile Ser Ile Asp Glu Glu Gln Ile Ala Ala		
130	135	140
Asn Leu Val Lys Asn Gly Pro Leu Ala Val Ala Ile Asn Ala Gly Tyr		
145	150	155
Met Gln Thr Tyr Ile Gly Gly Val Ser Cys Pro Tyr Ile Cys Thr Arg		
165	170	175
Arg Leu Asn His Gly Val Leu Leu Val Gly Tyr Gly Ala Ala Gly Tyr		
180	185	190
Ala Pro Ala Arg Phe Lys Glu Lys Pro Tyr Trp Ile Ile Lys Asn Ser		
195	200	205
Trp Gly Glu Thr Trp Gly Glu Asn Gly Phe Tyr Lys Ile Cys Lys Gly		
210	215	220
Arg Asn Ile Cys Gly Val Asp Ser Met Val Ser Thr Val Ala Ala Thr		
225	230	235
Val Ser Thr Thr Ala His		
245		

(2) INFORMATION FOR SEQ ID NO:2676:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..225

(D) OTHER INFORMATION: / Ceres Seq. ID 1573957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2676:

Met Ala Pro Leu Leu Pro Ser Lys Ile Arg Asp Leu Ala Ala Leu Ala		
1	5	10
Gly Val Ser Ala Pro Leu Glu Leu Trp Lys Val Leu Thr Ser Ser Leu		
20	25	30
Pro Ala Asp Ser Ser Ala Ser Ala Asn Asn Ser Ser Ser Thr Val Ile		
35	40	45
Thr Ser Val Ile Pro Arg Arg Gln Ile Ser Cys Asp Ser Gly Cys Asn		
50	55	60
Gly Gly Leu Met Asn Ser Ala Phe Glu Tyr Thr Leu Lys Thr Gly Gly		
65	70	75
Leu Met Lys Glu Glu Asp Tyr Pro Tyr Thr Gly Lys Asp Gly Lys Thr		
85	90	95
Cys Lys Leu Asp Lys Ser Lys Ile Val Ala Ser Val Ser Asn Phe Ser		
100	105	110
Val Ile Ser Ile Asp Glu Glu Gln Ile Ala Ala Asn Leu Val Lys Asn		
115	120	125
Gly Pro Leu Ala Val Ala Ile Asn Ala Gly Tyr Met Gln Thr Tyr Ile		
130	135	140
Gly Gly Val Ser Cys Pro Tyr Ile Cys Thr Arg Leu Asn His Gly		
145	150	155
		160

Val Leu Leu Val Gly Tyr Gly Ala Ala Gly Tyr Ala Pro Ala Arg Phe
165 170 175
Lys Glu Lys Pro Tyr Trp Ile Ile Lys Asn Ser Trp Gly Glu Thr Trp
180 185 190
Gly Glu Asn Gly Phe Tyr Lys Ile Cys Lys Gly Arg Asn Ile Cys Gly
195 200 205
Val Asp Ser Met Val Ser Thr Val Ala Ala Thr Val Ser Thr Thr Ala
210 215 220

His
225

(2) INFORMATION FOR SEQ ID NO:2677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573958
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2677:

Met Asn Ser Ala Phe Glu Tyr Thr Leu Lys Thr Gly Gly Leu Met Lys
1 5 10 15
Glu Glu Asp Tyr Pro Tyr Thr Gly Lys Asp Gly Lys Thr Cys Lys Leu
20 25 30
Asp Lys Ser Lys Ile Val Ala Ser Val Ser Asn Phe Ser Val Ile Ser
35 40 45
Ile Asp Glu Glu Gln Ile Ala Ala Asn Leu Val Lys Asn Gly Pro Leu
50 55 60
Ala Val Ala Ile Asn Ala Gly Tyr Met Gln Thr Tyr Ile Gly Gly Val
65 70 75 80
Ser Cys Pro Tyr Ile Cys Thr Arg Arg Leu Asn His Gly Val Leu Leu
85 90 95
Val Gly Tyr Gly Ala Ala Gly Tyr Ala Pro Ala Arg Phe Lys Glu Lys
100 105 110
Pro Tyr Trp Ile Ile Lys Asn Ser Trp Gly Glu Thr Trp Gly Glu Asn
115 120 125
Gly Phe Tyr Lys Ile Cys Lys Gly Arg Asn Ile Cys Gly Val Asp Ser
130 135 140
Met Val Ser Thr Val Ala Ala Thr Val Ser Thr Thr Ala His
145 150 155

(2) INFORMATION FOR SEQ ID NO:2678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..883
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573960
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2678:

aaaaaaaaat	catcgtgAaa	cggtcgaagg	ccattttcct	tggacgacca	tcggcggttaa	60
ggagagagct	tagatctcgt	gcgctcgtgc	gacgttggtt	tccggcgttg	tcaaaatggg	120
gttgctcatt	ggaaagtgtg	tcagcaggct	cttgcgaag	aaagagatgc	gtattctgat	180
ggttggtctc	gatcgtcgtg	gtaagacgac	tatctctcac	aagctcaaac	ttggagagat	240
cgtcaccact	attccaacca	tggggttcaa	cgttgagact	gttgaataca	agaacatcag	300
cttcaccgtg	tgggatgttg	ggggccaaga	caagatccgt	ccattgtgga	gacattactt	360
ccagaacaca	cagggaactta	tctttgttgt	ggacagcaat	gatcgtgacc	gtgtgtgtga	420

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agccagggag  gagcttcaca  ggaatgctgaa  tgaggatgaa  ttgagggatg  cagttctgct  480
tgtatttgcg  aacaagcaag  atcttcccaa  cgcgatgaac  gctgctgaga  taactgacaa  540
gcttggggctt  cattctcttc  gtcaacgaca  ctggtacatt  cagagcacat  gtgccacctc  600
tggagaagga  ctctatgagg  gacttgactg  gctctccaac  aacatcgcaa  gcaaggcata  660
gatggaatgt  tagccaagatt  cctcttctgc  ttgtttgggt  tacaaatcaa  agacagaggt  720
ctgtttctct  agtactaaaa  gatttattat  tatattcttc  ttctgcactt  atctcaaacg  780
cagatcattt  tacactttgt  acttccccct  caataacttg  ttacttctct  cgtttgcttc  840
cgaatttgag  tatatcattt  ttacatctgc  ttttcatcaa  agc

```

(2) INFORMATION FOR SEQ ID NO:2679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..181
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2679:

```

Met Gly Leu Ser Phe Gly Lys Leu Phe Ser Arg Leu Phe Ala Lys Lys
1      5      10      15
Glu Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr
20      25      30
Ile Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr
35      40      45
Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr
50      55      60
Val Trp Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His
65      70      75      80
Tyr Phe Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp
85      90      95
Arg Asp Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn
100      105      110
Glu Asp Glu Leu Arg Asp Ala Val Leu Leu Val Phe Ala Asn Lys Gln
115      120      125
Asp Leu Pro Asn Ala Met Asn Ala Ala Glu Ile Thr Asp Lys Leu Gly
130      135      140
Leu His Ser Leu Arg Gln Arg His Trp Tyr Ile Gln Ser Thr Cys Ala
145      150      155      160
Thr Ser Gly Glu Gly Leu Tyr Glu Gly Leu Asp Trp Leu Ser Asn Asn
165      170      175
Ile Ala Ser Lys Ala
180

```

(2) INFORMATION FOR SEQ ID NO:2680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2680:

```

Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile
1      5      10      15
Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr Ile
20      25      30
Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr Val

```

35	40	45
Trp Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His Tyr		
50	55	60
Phe Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp Arg		
65	70	75
Asp Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn Glu		
85	90	95
Asp Glu Leu Arg Asp Ala Val Leu Leu Val Phe Ala Asn Lys Gln Asp		
100	105	110
Leu Pro Asn Ala Met Asn Ala Ala Glu Ile Thr Asp Lys Leu Gly Leu		
115	120	125
His Ser Leu Arg Gln Arg His Trp Tyr Ile Gln Ser Thr Cys Ala Thr		
130	135	140
Ser Gly Glu Gly Leu Tyr Glu Gly Leu Asp Trp Leu Ser Asn Asn Ile		
145	150	155
Ala Ser Lys Ala		160

(2) INFORMATION FOR SEQ ID NO:2681:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1573963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2681:

Met Val Gly Leu Asp Ala Ala Gly Lys Thr Ile Leu Tyr Lys Leu		
1	5	10
Lys Leu Gly Glu Ile Val Thr Thr Ile Gly Phe Asn Val		15
20	25	30
Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr Val Trp Asp Val Gly		35
35	40	45
Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His Tyr Phe Gln Asn Thr		50
50	55	60
Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp Arg Asp Arg Val Val		65
65	70	75
Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn Glu Asp Glu Leu Arg		80
85	90	95
Asp Ala Val Leu Leu Val Phe Ala Asn Lys Gln Asp Leu Pro Asn Ala		100
100	105	110
Met Asn Ala Ala Glu Ile Thr Asp Lys Leu Gly Leu His Ser Leu Arg		115
115	120	125
Gln Arg His Trp Tyr Ile Gln Ser Thr Cys Ala Thr Ser Gly Glu Gly		130
130	135	140
Leu Tyr Glu Gly Leu Asp Trp Leu Ser Asn Asn Ile Ala Ser Lys Ala		145
145	150	155
		160

(2) INFORMATION FOR SEQ ID NO:2682:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 771 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..771

(D) OTHER INFORMATION: / Ceres Seq. ID 1573964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2682:

acaaatccaaat	caaaacacac	agagagaaga	aaaactcaga	agaaaaagcca	aagagtga	60
caaaaaatggc	gtgcagcact	ctctcaatcg	caacaacaat	cogttcccta	tcttattccta	120
ctctcgtcttc	catcaatcac	ttcccttccc	gaacccamcac	catcgaaatc	ccctctcgct	180
tcgggtggttg	ttcatcatcc	acattgaccc	accgtgcaac	ccatctccgt	ccaatcgccg	240
ccgtcgaaagc	tcggagagaaa	atcgagaaga	toggatccga	aatctcacc	ctaaccctcg	300
aagaagctcg	tatctctgct	gactatctcc	aagacaaat	cggtgtctcc	ccactctctt	360
tagCccccgc	agcagcGgcg	gttgctgctc	cagccgacgg	tggcgcgccg	gctgtagtgg	420
aagagcaaac	agagttcgat	gtggttatca	atgaagttcc	cagcagttcc	cgtattgcaag	480
tgattaaagc	tgttagggct	ttaaactagct	tggcggtgaa	ggaagctaa	gagctaactc	540
aaggattacc	aaagaagttt	aaagaaggtta	tcactaaaga	tgaagctgaa	gaagctaaga	600
agactcttga	agaagctggg	gctaagactct	ccattgctta	aggtttttat	taaaaaaaaa	660
aaagaagttg	ttatcttttc	tggaaattga	ttggtctttt	gtgtgtgtta	gtatagtttg	720
cgtctggaat	tgttgagaaa	ttgttgtaat	ttgaatcaca	tttggtttcc	c	

(2) INFORMATION FOR SEQ ID NO:2683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1573965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2683:

Asn	Pro	Ile	Lys	Thr	His	Arg	Glu	Lys	Lys	Asn	Ser	Glu	Glu	Lys	Pro
1			5							10				15	
Lys	Ser	Glu	Thr	Lys	Met	Ala	Ser	Thr	Thr	Leu	Ser	Ile	Ala	Thr	Thr
			20						25				30		
Ile	Arg	Ser	Ser	Ser	Tyr	Pro	Thr	Leu	Ala	Ser	Ile	Asn	His	Phe	Pro
			35					40				45			
Ser	Arg	Thr	Xaa	Thr	Ile	Glu	Phe	Pro	Ser	Arg	Phe	Gly	Gly	Ser	
			50			55				60					
Ser	Ser	Thr	Leu	Thr	His	Arg	Ala	Thr	His	Leu	Arg	Pro	Ile	Ala	Ala
			65			70				75				80	
Val	Glu	Ala	Pro	Glu	Lys	Ile	Glu	Lys	Ile	Gly	Ser	Glu	Ile	Ser	Ser
			85					90						95	
Leu	Thr	Leu	Glu	Glu	Ala	Arg	Ile	Leu	Val	Asp	Tyr	Leu	Gln	Asp	Lys
			100					105					110		
Phe	Gly	Val	Ser	Pro	Leu	Ser	Leu	Ala	Pro	Ala	Ala	Ala	Ala	Val	Ala
			115					120					125		
Ala	Pro	Ala	Asp	Gly	Gly	Ala	Ala	Ala	Val	Val	Glu	Glu	Gln	Thr	Glu
			130					135					140		
Phe	Asp	Val	Val	Ile	Asn	Glu	Val	Pro	Ser	Ser	Ser	Arg	Ile	Ala	Val
			145			150				155				160	
Ile	Lys	Ala	Val	Arg	Ala	Leu	Thr	Ser	Leu	Ala	Leu	Lys	Glu	Ala	Lys
			165					170					175		
Glu	Leu	Ile	Glu	Gly	Leu	Pro	Lys	Lys	Phe	Lys	Glu	Gly	Ile	Thr	Lys
			180					185					190		
Asp	Glu	Ala	Glu	Glu	Ala	Lys	Lys	Thr	Leu	Glu	Glu	Ala	Gly	Ala	Lys
			195				200					205			
Val	Ser	Ile	Ala												
			210												

(2) INFORMATION FOR SEQ ID NO:2684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..191

SEQUENCE DESCRIPTION: SEQ ID NO:2684:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2684:

Met	Ala	Ser	Thr	Thr	Leu	Ser	Ile	Ala	Thr	Thr	Ile	Arg	Ser	Ser	Ser
1				5					10					15	
Tyr	Pro	Thr	Leu	Ala	Ser	Ile	Asn	His	Phe	Pro	Ser	Arg	Thr	Xaa	Thr
			20					25					30		
Ile	Glu	Phe	Pro	Ser	Arg	Phe	Gly	Gly	Gly	Ser	Ser	Ser	Thr	Leu	Thr
		35					40					45			
His	Arg	Ala	Thr	His	Leu	Arg	Pro	Ile	Ala	Ala	Val	Glu	Ala	Pro	Glu
		50				55					60				
Lys	Ile	Glu	Lys	Ile	Gly	Ser	Glu	Ile	Ser	Ser	Leu	Thr	Leu	Glu	Glu
65					70					75				80	
Ala	Arg	Ile	Leu	Val	Asp	Tyr	Leu	Gln	Asp	Lys	Phe	Gly	Val	Ser	Pro
				85					90					95	
Leu	Ser	Leu	Ala	Pro	Ala	Ala	Ala	Ala	Val	Ala	Ala	Pro	Ala	Asp	Gly
			100					105					110		
Gly	Ala	Ala	Ala	Val	Val	Glu	Glu	Gln	Thr	Glu	Phe	Asp	Val	Val	Ile
			115				120					125			
Asn	Glu	Val	Pro	Ser	Ser	Ser	Arg	Ile	Ala	Val	Ile	Lys	Ala	Val	Arg
		130					135				140				
Ala	Leu	Thr	Ser	Leu	Ala	Leu	Lys	Glu	Ala	Lys	Glu	Leu	Ile	Glu	Glu
145					150					155				160	
Leu	Pro	Lys	Lys	Phe	Lys	Glu	Gly	Ile	Thr	Lys	Asp	Glu	Ala	Glu	Glu
				165					170					175	
Ala	Lys	Lys	Thr	Leu	Glu	Glu	Ala	Gly	Ala	Lys	Val	Ser	Ile	Ala	
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:2685:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 547 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..547

(D) OTHER INFORMATION: / Ceres Seq. ID 1573980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2685:

ttttccagaa	atctctcaact	atcgccatcg	atttttagcac	acatttgaaga	agatggggagt	60
atttcatact	glatgcgaaga	gcggatgcgg	cgcgtggagc	gcGaagCaac	accgaaggaa	120
acttgaactc	tcagctctctt	ctaacctcact	cgctccagcgt	aagTctgtctc	atggttatctc	180
ctccgctgat	tctcccggtg	gggttcacgc	tctggtttct	tctgtctccc	ctacctccgc	240
cgtaattccg	gtaaattgtt	gtgtgtgtgt	tgtgtggaaga	tctctctgtg	gaggagctgc	300
ctcaagtgtg	ggtggtgcgg	gtgaagctgc	cgctgcacct	agaagaagtg	agaagaagtc	360
agaaagaatc	gaagaggaag	aggagacttc	ggattcgatc	tcttggttta	agattgaaat	420
agatttttgt	agggtgttgt	tctgagcttc	catatttgtg	tgggggtgtt	cttcattagt	480
caagtgtgat	atgtcacact	gctttcaata	atatttcgtg	agtaatgaca	agttttctct	540
tcgctgc						

(2) INFORMATION FOR SEQ ID NO:2686:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1573981

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

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(ix) FEATURE:
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(B) LOCATION: 1..727

SEQUENCE DESCRIPTION: SEQ ID NO:2687:

gaataaacgt	cctctctcacc	cgccctctgcc	tgggccacca	atgatgaaga	tcttcaaaag	120
gagtaacgggt	ctgtttctgcg	cggtttctgcg	tcttaagatca	ttaaacgacg	cgagatggatt	180
acgttctctac	agttctgcgga	cgttatctgat	tcttaacgatc	taaacgacg	ggatgcggat	240
gaatacaagg	gtatctggatt	cgtcacctctc	aagacgagca	aagccatgag	ggatgcggat	300
gaagagttagc	acgtgaataag	ctgctgatgta	cgctgaacga	cgttcagtgc	ccgcacgtgc	360
aaagagttagc	gcggtgcggcg	aggagcgcgt	gtgtgaagcg	ctgtgggtta	ggcagcgcga	420
ggcggctgggt	gatactcagg	atgcgctggc	ggcggaatac	caggagggag	cggtgcgtgt	480
ctacagagacg	gtacgcgaag	ttaacgatct	gtgtgagcg	ctggtgcgcg	aggatacgtg	540
ggtgcttgac	gcgcgtgagg	aggtggctac	ggaggcgggt	atgtgtMgaa	gttacgcgcg	600
ctgtgtgtggc	gcttggtaat	caacagatga	gttgtttgat	tgctgcgtgt	ctgtttttgt	660
tttagatttg	gatttgtgtc	accactatga	gtttggttat	cgctcgtgtt	gtttactttt	720
tttagtgaaac	agtttctgtt	aagctcttct	tgtctggatc	gaaatgttaa	ttcgcgtgtt	
gtttacc						

(1) SEQUENCE CHARACTERISTICS

(B) TYPE: amino acid

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(A) NAME

(B) LOCATION: 1..226

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:2688:

Met Ser Glu Val Glu Tyr Arg Cys Phe Val Gly Gly Leu Ala Trp Ala


```

1           5           10           15
Thr Asn Asp Glu Asp Leu Gln Arg Thr Phe Ser Gln Phe Gly Asp Val
20           25           30
Ile Asp Ser Lys Ile Ile Asn Asp Arg Glu Ser Gly Arg Ser Arg Gly
35           40           45
Phe Gly Phe Val Thr Phe Lys Asp Glu Lys Ala Met Arg Asp Ala Ile
50           55           60
Glu Glu Met Asn Gly Lys Glu Leu Asp Gly Arg Val Ile Thr Val Asn
65           70           75           80
Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Gly Arg Gly Gly
85           90           95
Ser Gly Gly Gly Tyr Arg Ser Gly Gly Gly Gly Tyr Ser Gly Gly
100          105          110
Gly Gly Gly Tyr Ser Gly Gly Gly Gly Tyr Glu Arg Arg
115          120          125          130
Ser Gly Gly Tyr Gly Ser Gly Gly Gly Gly Arg Gly Tyr Gly
130          135          140          145
Gly Gly Gly Arg Arg Glu Gly Gly Gly Tyr Gly Gly Asp Gly Xaa
145          150          155          160
Lys Leu Arg Arg Arg Trp Trp Xaa Leu Val Ile Lys Asp Arg Val Val
165          170          175
Cys Val Leu Leu Leu Cys Phe Trp Phe Arg Phe Gly Phe Val Ser Pro
180          185          190
Leu Leu Val Trp Leu Ser Phe Val Trp Phe Thr Phe Leu Met Lys Gln
195          200          205
Phe Arg Leu Ser Leu Leu Cys Leu Asp Arg Asn Val Asn Ser Arg Val
210          215          220
Val Tyr
225

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(2) INFORMATION FOR SEQ ID NO:2689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2689:

```

Met Arg Asp Ala Ile Glu Glu Met Asn Gly Lys Glu Leu Asp Gly Arg
1           5           10           15
Val Ile Thr Val Asn Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Gly
20           25           30
Gly Gly Arg Gly Gly Ser Gly Gly Gly Tyr Arg Ser Gly Gly Gly Gly
35           40           45
Gly Tyr Ser Gly Gly Gly Gly Gly Tyr Ser Gly Gly Gly Gly Gly
50           55           60           65
Gly Tyr Glu Arg Arg Ser Gly Gly Tyr Gly Ser Gly Gly Gly Gly Gly
70           75           80           85
Gly Arg Gly Tyr Gly Gly Gly Arg Arg Glu Gly Gly Gly Tyr Gly
90           95
Gly Gly Asp Gly Xaa Lys Leu Arg Arg Trp Trp Xaa Leu Val Ile
100          105          110
Lys Asp Arg Val Val Cys Val Leu Leu Cys Phe Trp Phe Arg Phe
115          120          125
Gly Phe Val Ser Pro Leu Leu Val Trp Leu Ser Phe Val Trp Phe Thr
130          135          140
Phe Leu Met Lys Gln Phe Arg Leu Ser Leu Leu Cys Leu Asp Arg Asn
145          150          155          160

```

Val Asn Ser Arg Val Val Tyr
165

(2) INFORMATION FOR SEQ ID NO:2690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573985
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2690:

Met	Asn	Gly	Lys	Glu	Leu	Asp	Gly	Arg	Val	Ile	Thr	Val	Asn	Glu	Ala
1			5						10					15	
Gln	Ser	Arg	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Arg	Gly	Gly	Ser	Gly	
			20					25				30			
Gly	Gly	Tyr	Arg	Ser	Gly	Gly	Gly	Gly	Tyr	Ser	Gly	Gly	Gly	Gly	
		35					40				45				
Gly	Gly	Tyr	Ser	Gly	Gly	Gly	Gly	Gly	Tyr	Glu	Arg	Arg	Ser	Gly	
		50				55				60					
Gly	Tyr	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Arg	Gly	Tyr	Gly	Gly	Gly	
		65			70				75					80	
Gly	Arg	Arg	Glu	Gly	Gly	Gly	Tyr	Gly	Gly	Asp	Gly	Xaa	Lys	Leu	
			85					90					95		
Arg	Arg	Arg	Trp	Trp	Xaa	Leu	Val	Ile	Lys	Asp	Arg	Val	Val	Cys	Val
			100					105					110		
Leu	Leu	Leu	Cys	Phe	Trp	Phe	Arg	Phe	Gly	Phe	Val	Ser	Pro	Leu	Leu
			115				120					125			
Val	Trp	Leu	Ser	Phe	Val	Trp	Phe	Thr	Phe	Leu	Met	Lys	Gln	Phe	Arg
		130				135					140				
Leu	Ser	Leu	Leu	Cys	Leu	Asp	Arg	Asn	Val	Asn	Ser	Arg	Val	Val	Tyr
			145		150					155					160

(2) INFORMATION FOR SEQ ID NO:2691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..954
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573986
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2691:

aacaaaaaga	ttaaacaaga	agagaagaat	atggcgagag	ggaagatcca	gatcaagagg	60
atagagaacc	agacaaaacag	acaagtgcag	tattcaaaga	gaagaaatgg	tttattcaag	120
aaagcacatg	agctcacggt	tttgtgtgat	gctagggttt	cgattatcat	gttctctagc	180
tccaacaagc	ttcatgagta	tatcagccct	aacaccacaa	cgaaggagat	cgtagatctg	240
taccaaaacta	tttctgatgt	cgatgttttg	gccactcaat	atgagcgaat	gcaagaaacc	300
aagaggaaac	tggttgagag	aaatagaat	ctccgactc	agatcaagca	gaggctaggt	360
gagtgttttg	acaagcttga	cattcaggag	ctcgctgcgt	ttgaggatga	aatggaaaac	420
actttcaaac	tcgttcgcga	gcgcaagttc	aaatctcttg	ggaatcagat	cgagaccacc	480
aagaaaaaga	acaaaagtca	acaagacata	caaaaagaatc	tcatacatga	gctaactaag	540
agctgaagat	ccctcactat	gactagtaga	caatggagga	gattacgact	caagttcttg	600
ataccaaatc	gaagggtcac	gtGcttacgc	tcttctgttc	caccagaacc	atcaccacta	660
ttaccocaaac	catggccttc	atgcaccctc	tgcctctgac	atcattacct	tcattctctc	720
tgaaataatta	aaggctaaaa	ggtttgcttg	tgccatcatt	gtctatctaa	tttattagta	780

actacttataa acataaggca tgggtgttgc taaacaccttaa actgtcatgt tctttagtta 840
tgtatttttaa agcctaaga aatatggatt gtgtgatcag tagtgcttag gctttattgtg 900
tgtggaatgt ttcaagact ttatcatgt atcgtattat tatattgacc accc

(2) INFORMATION FOR SEQ ID NO:2692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..181
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2692:

Asn Lys Lys Ile Lys Gln Arg Glu Lys Asn Met Ala Arg Gly Lys Ile
1 5 10 15
Gln Ile Lys Arg Ile Glu Asn Gln Thr Asn Arg Gln Val Thr Tyr Ser
20 25 30
Lys Arg Arg Asn Gly Leu Phe Lys Lys Ala His Glu Leu Thr Val Leu
35 40 45
Cys Asp Ala Arg Val Ser Ile Ile Met Phe Ser Ser Ser Asn Lys Leu
50 55 60
His Glu Tyr Ile Ser Pro Asn Thr Thr Thr Lys Glu Ile Val Asp Leu
65 70 75 80
Tyr Gln Thr Ile Ser Asp Val Asp Val Trp Ala Thr Gln Tyr Glu Arg
85 90 95
Met Gln Glu Thr Lys Arg Lys Leu Leu Glu Thr Asn Arg Asn Leu Arg
100 105 110
Thr Gln Ile Lys Gln Arg Leu Gly Glu Cys Leu Asp Lys Leu Asp Ile
115 120 125
Gln Glu Leu Arg Arg Leu Glu Asp Glu Met Glu Asn Thr Phe Lys Leu
130 135 140
Val Arg Glu Arg Lys Phe Lys Ser Leu Gly Asn Gln Ile Glu Thr Thr
145 150 155 160
Lys Lys Lys Asn Lys Ser Gln Gln Asp Ile Gln Lys Asn Leu Ile His
165 170 175
Glu Leu Thr Lys Ser
180

(2) INFORMATION FOR SEQ ID NO:2693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2693:

Met Ala Arg Gly Lys Lys Ile Gln Ile Lys Arg Ile Glu Asn Gln Thr Asn
1 5 10 15
Arg Gln Val Thr Tyr Ser Lys Arg Arg Asn Gly Leu Phe Lys Lys Ala
20 25 30
His Glu Leu Thr Val Leu Cys Asp Ala Arg Val Ser Ile Ile Met Phe
35 40 45
Ser Ser Ser Asn Lys Leu His Glu Tyr Ile Ser Pro Asn Thr Thr Thr
50 55 60
Lys Glu Ile Val Asp Leu Tyr Gln Thr Ile Ser Asp Val Asp Val Tyr
65 70 75 80

Ala Thr Gln Tyr Glu Arg Met Gln Glu Thr Lys Arg Lys Leu Leu Glu
85 90 95
Thr Asn Arg Asn Leu Arg Thr Gln Ile Lys Gln Arg Leu Gly Glu Cys
100 105 110
Leu Asp Lys Leu Asp Ile Gln Glu Leu Arg Arg Leu Glu Asp Glu Met
115 120 125
Glu Asn Thr Phe Lys Leu Val Arg Glu Arg Lys Phe Lys Ser Leu Gly
130 135 140
Asn Gln Ile Glu Thr Thr Lys Lys Lys Asn Lys Ser Gln Gln Asp Ile
145 150 155 160
Gln Lys Asn Leu Ile His Glu Leu Thr Lys Ser
165 170

(2) INFORMATION FOR SEQ ID NO:2694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1573989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2694:

Met Phe Ser Ser Ser Asn Lys Leu His Glu Tyr Ile Ser Pro Asn Thr
1 5 10 15
Thr Thr Lys Glu Ile Val Asp Leu Tyr Gln Thr Ile Ser Asp Val Asp
20 25 30
Val Trp Ala Thr Gln Tyr Glu Arg Met Gln Glu Thr Lys Arg Lys Leu
35 40 45
Leu Glu Thr Asn Arg Asn Leu Arg Thr Gln Ile Lys Gln Arg Leu Gly
50 55 60
Glu Cys Leu Asp Lys Leu Asp Ile Gln Glu Leu Arg Arg Leu Glu Asp
65 70 75 80
Glu Met Glu Asn Thr Phe Lys Leu Val Arg Glu Arg Lys Phe Lys Ser
85 90 95
Leu Gly Asn Gln Ile Glu Thr Thr Lys Lys Lys Asn Lys Ser Gln Gln
100 105 110
Asp Ile Gln Lys Asn Leu Ile His Glu Leu Thr Lys Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:2695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..767
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2695:

ataccaataa gcaatttgct cattagagaa cacagaaaaa aaaaaaacaa tggcaactca 60
agccgcggg atcttcaact ccgcataaac aaccgcgcga acctcggcg tcaagaaact 120
ccactttttc tcaacaaccc accgtcccaa atccctctcc ttcacaaaaa ccgcaatccg 180
cgccgagaaa acagatttct ccgcgcgcgc tgctgcagcc ccgcaccaaa aagaagctcc 240
cgtgggattc acgccaccgc agctagaccc aaacacacgc tctccgatct tcgctggaag 300
cacccggtgg tttctacgta aagcgcaagt ggaagagttc tacgttatca tcgtggaact 360
accgaagaaa cagatctttg agatgcccag aggaggagca cgcgatcatg gagaaggtcc 420
gaatctctc aagctagcga ggaaaagaga gtgtttagct ttggggacaa ggcttagatc 480
caagtacaag atcacttacc agttttacag agtggttctt aacggtgagg ttcaatatct 540

tcacctaataa gatgtgtgttt atccagagaa ggcgaatcca ggaagagaag gtgttggtct 600
caacatgaga tctattggga aaaatgttag tcccatgtaa gtaagttaa ctggcaacaa 660
aagttagat ttgtaagatc tgtaaaactaa aaaaaAccaa aaactatgtg catgtgtgtga 720
tgattatgac tatgtttcat gtTaattttt aatggatttt gKttttg

(2) INFORMATION FOR SEQ ID NO:2696:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1573991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2696:

Ile Pro Ile Ser Asn Leu Leu Ile Arg Glu Gln Arg Lys Lys Lys Asn
1 5 10 15
Asn Gly Asn Ser Ser Arg Arg Asp Leu Gln Leu Arg His Asn Asn Arg
20 25 30
Arg Asn Leu Arg Arg Gln Glu Thr Pro Leu Phe Leu Asn Asn Pro Pro
35 40 45
Ser Gln Ile Pro Leu Leu His Gln Asn Arg Asn Pro Arg Arg Glu Asn
50 55 60
Arg Phe Leu Arg Arg Arg Cys Cys Ser Pro Arg His Glu Arg Ser Ser
65 70 75 80
Arg Gly Ile His Ala Thr Ala Ala Arg Pro Lys His Thr Val Ser Asp
85 90 95
Leu Arg Trp Lys His Arg Trp Ser Ser Thr
100 105

(2) INFORMATION FOR SEQ ID NO:2697:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 1573992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2697:

Met Ala Thr Gln Ala Ala Gly Ile Phe Asn Ser Ala Ile Thr Thr Ala
1 5 10 15
Ala Thr Ser Gly Val Lys Lys Leu His Phe Phe Ser Thr Thr His Arg
20 25 30
Pro Lys Ser Leu Ser Phe Thr Lys Thr Ala Ile Arg Ala Glu Lys Thr
35 40 45
Asp Ser Ser Ala Ala Ala Ala Ala Pro Ala Thr Lys Glu Ala Pro
50 55 60
Val Gly Phe Thr Pro Pro Gln Leu Asp Pro Asn Thr Pro Ser Pro Ile
65 70 75 80
Phe Ala Gly Ser Thr Gly Gly Leu Leu Arg Lys Ala Gln Val Glu Glu
85 90 95
Phe Tyr Val Ile Thr Trp Asn Ser Pro Lys Glu Gln Ile Phe Glu Met
100 105 110
Pro Thr Gly Gly Ala Ala Ile Met Arg Glu Gly Pro Asn Leu Leu Lys
115 120 125
Leu Ala Arg Lys Glu Gln Cys Leu Ala Leu Gly Thr Arg Leu Arg Ser
130 135 140
Lys Tyr Lys Ile Thr Tyr Gln Phe Tyr Arg Val Phe Pro Asn Gly Glu

145	150	155	160
Val Gln Tyr Leu His Pro Lys Asp Gly Val Tyr Pro Glu Lys Ala Asn			
	165	170	175
Pro Gly Arg Glu Gly Val Gly Leu Asn Met Arg Ser Ile Gly Lys Asn			
	180	185	190
Val Ser Pro Ile Glu Val Lys Phe Thr Gly Lys Gln Ser Tyr Asp Leu			
	195	200	205

(2) INFORMATION FOR SEQ ID NO:2698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..800
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2698:

taatttttagga	gaagagcaac	cgttgaaacg	tacggcgagt	gggtggtggt	gtgtctcgac	60
tggcttgat	atgattcccg	gaagtcac	gggatctgac	gtcagcgagc	aattctagtgg	120
tgggtgcacac	gtgttttaaac	caacggttag	atctgaggtt	acagcgctcat	cgtctggtga	180
agatccctcca	acttatctta	gtttgtctct	tccttggaact	gacgagacgg	ttcgagctcaa	240
cgagccgggt	caacttaacc	agaatacgg	tatggacgg	gggtatacgg	cggaGctgtt	300
tccggttaga	aaggaagagc	aagtggaggt	agaagaagaa	gaagcgaaag	ggatatctgg	360
tggattcgg	ggtgagttca	tgacggtggt	tcaggagatg	ataaggacgg	aggtcgaggag	420
ttacatggcg	gatttacagc	gaggaacgt	cgggtgtagt	agttctggcg	gcggaggtgg	480
cggttcgtgt	atgccacaaa	gtgtaaacag	ccgtcgtgtt	gggtttagag	agtttatagt	540
gaaccagatc	ggaattggga	agatggagta	gagtgataag	aacaagtttt	ccctctgttt	600
ctcgggaaaa	taaaagtttc	aggcttttca	tgtatagagc	cagtagtaga	gacgacgaaa	660
ggaggaagcg	aaatcaaaaa	atgttttgtt	atcatcatca	tatgatcttc	tttcgtgatt	720
caattaaaag	caaagcaaga	tcatttatta	acaatttaca	caaacttgaa	gaagaaaagt	780
caaaaacact	tctcaaaact					

(2) INFORMATION FOR SEQ ID NO:2699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..189
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2699:

Asn Leu Gly Glu Glu Gln Pro Leu Lys Arg Thr Ala Ser Gly Gly Gly							
1	5	10	15				
Gly Val Ser Thr Gly Leu Tyr Met Ser Pro Gly Ser Pro Ser Gly Ser							
	20	25	30				
Asp Val Ser Glu Gln Ser Ser Gly Gly Ala His Val Phe Lys Pro Thr							
	35	40	45				
Val Arg Ser Glu Val Thr Ala Ser Ser Ser Gly Glu Asp Pro Pro Thr							
	50	55	60				
Tyr Leu Ser Leu Ser Leu Pro Trp Thr Asp Glu Thr Val Arg Val Asn							
	65	70	75				
Glu Pro Val Gln Leu Asn Gln Asn Thr Val Met Asp Gly Gly Tyr Thr							
	85	90	95				
Ala Glu Leu Phe Pro Val Arg Lys Glu Glu Gln Val Glu Val Glu Glu							
	100	105	110				

Glu Glu Ala Lys Gly Ile Ser Gly Gly Phe Gly Gly Glu Phe Met Thr
115 120 125
Val Val Gln Glu Met Ile Arg Thr Glu Val Arg Ser Tyr Met Ala Asp
130 135 140
Leu Gln Arg Gly Asn Val Gly Gly Ser Ser Ser Gly Gly Gly Gly
145 150 155 160
Gly Ser Cys Met Pro Gln Ser Val Asn Ser Arg Arg Val Gly Phe Arg
165 170 175
Glu Phe Ile Val Asn Gln Ile Gly Ile Gly Lys Met Glu
180 185

(2) INFORMATION FOR SEQ ID NO:2700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1573997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2700:

Met Ser Pro Gly Ser Pro Ser Gly Ser Asp Val Ser Glu Gln Ser Ser
1 5 10 15
Gly Gly Ala His Val Phe Lys Pro Thr Val Arg Ser Glu Val Thr Ala
20 25 30
Ser Ser Ser Gly Glu Asp Pro Pro Thr Tyr Leu Ser Leu Ser Leu Pro
35 40 45
Trp Thr Asp Glu Thr Val Arg Val Asn Glu Pro Val Gln Leu Asn Gln
50 55 60
Asn Thr Val Met Asp Gly Gly Tyr Thr Ala Glu Leu Phe Pro Val Arg
65 70 75 80
Lys Glu Glu Gln Val Glu Val Glu Glu Glu Glu Ala Lys Gly Ile Ser
85 90 95
Gly Gly Phe Gly Gly Glu Phe Met Thr Val Val Gln Glu Met Ile Arg
100 105 110
Thr Glu Val Arg Ser Tyr Met Ala Asp Leu Gln Arg Gly Asn Val Gly
115 120 125
Gly Ser Ser Ser Gly Gly Gly Gly Gly Ser Cys Met Pro Gln Ser
130 135 140
Val Asn Ser Arg Arg Val Gly Phe Arg Glu Phe Ile Val Asn Gln Ile
145 150 155 160
Gly Ile Gly Lys Met Glu
165

(2) INFORMATION FOR SEQ ID NO:2701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1573998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2701:

Met Asp Gly Gly Tyr Thr Ala Glu Leu Phe Pro Val Arg Lys Glu Glu
1 5 10 15
Gln Val Glu Val Glu Glu Glu Glu Ala Lys Gly Ile Ser Gly Gly Phe
20 25 30
Gly Gly Glu Phe Met Thr Val Val Gln Glu Met Ile Arg Thr Glu Val

(2) INFORMATION FOR SEQ ID NO:2702:

(A) LENGTH: 1114 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..1114

(D) OTHER INFORMATION: / Ceres Seq. ID 1573999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2702:

aaaaaagaaa	aaaaaactca	gagcagagga	gatcgagaga	gacaaagaga	gacaaagaga	60
gagagagaga	gagagagaga	gagcagagga	gagagatctt	gacaaagcaa	tgcttatcat	120
catggcgcta	ttctcttcgc	cgatctcttc	ctcactctca	aacctataat	tcatacccac	180
gatctcaacc	ttctctctct	ccacacaaag	ttctctctca	atctcogtct	ctagagcttc	240
ctcgacaact	ggtagcaact	ccccgcgttc	gaaaattctcg	agacctgcgt	ctgtagctgt	300
agagaaagtt	cgcggttaaa	ctccgcgtcc	aagctctctcc	gactctgaaa	acggcgagct	360
tgagggtgaa	gcgcactgatt	cgagtactga	gcaggtaatc	aaattatgaa	atcgcaagtg	420
ggttaataagg	acttgggata	tgaacacgct	cgagaaagat	ggcaaaaactg	attgggattc	480
tggttaactgt	tctgaggcaa	agagagagaaa	attgcttgaa	gataaacctg	aaacacacag	540
taacgacgag	cttgttgctc	ctgataactc	gattattcca	tgttgggcat	ggatgaagag	600
ataccatcta	ctcgaagctg	taactctcaa	tggtgcgtgt	gcgtgataag	ggttcttcac	660
ggcttacttt	gttgtagatc	tacccggagt	aggactctgt	gtacaaatgt	ggaattttct	720
ctgcacaaaca	ctcttctgtg	tggtctgaac	tgaggtcttc	tatctcogta	agaaatgaag	780
tttagacaaa	cttaaggatt	tgtctgatga	gactacgtta	tatgacaaac	aattggcaacg	840
tctagagagaa	gagccagatt	catcagacag	ttttctcaaa	gaatgagaca	aatcttcata	900
atctttactt	ttcctttttt	tgttatcgaa	taactctgtg	atacgtgaaa	gtttattctc	960
actgaactac	tgatctccag	attttgtaat	ctttctgctt	taaaaattct	tatgaagtac	1020
tctcaagaat	aattgatcga	aggctcttga	cttgttaagc	agacctattt	cgttttgacg	1080
cttgataatt	taatacaata	gagatttttt	tttt			

(2) INFORMATION FOR SEQ ID NO:2703:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 312 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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(A) NAME/KEY: peptide

(B) LOCATION: 1..312

(D) OTHER INFORMATION: / Ceres Seq. ID 1574000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2703:

Lys	Lys	Lys	Lys	Lys	Leu	Arg	Ala	Glu	Glu	Ile	Glu	Arg	Asp	Lys	Glu
1				5					10					15	
Arg	Gln	Arg	Glu	Arg	Glu	Arg	Glu	Arg	Glu	Arg	Glu	Arg	Glu	Arg	Asp
			20					25					30		
Leu	Gln	Gln	Ala	Met	Ser	Ile	Ser	Met	Ala	Leu	Phe	Ser	Pro	Pro	Ile
		35				40						45			
Ser	Ser	Ser	Leu	Gln	Asn	Pro	Asn	Leu	Ile	Pro	Lys	Ile	Ser	Thr	Ser
	50				55						60				
Leu	Leu	Ser	Thr	Lys	Arg	Phe	Ser	Leu	Ile	Ser	Val	Pro	Arg	Ala	Ser

65					70					75					80
Ser	Asp	Asn	Gly	Thr	Thr	Ser	Pro	Val	Val	Lys	Ile	Pro	Lys	Pro	Ala
					85					90					95
Ser	Val	Ala	Val	Glu	Glu	Val	Pro	Val	Lys	Ser	Pro	Ala	Glu	Ser	Ser
					100					105					110
Ser	Ala	Ser	Glu	Asn	Gly	Ala	Val	Gly	Gly	Glu	Ala	Thr	Asp	Ser	Ser
					115					120					125
Thr	Glu	Thr	Val	Ile	Lys	Tyr	Gln	Asn	Ala	Lys	Trp	Val	Asn	Gly	Thr
										135					140
Trp	Asp	Leu	Lys	Gln	Phe	Glu	Lys	Asp	Gly	Lys	Thr	Asp	Trp	Asp	Ser
					150					155					160
Val	Ile	Val	Ser	Glu	Ala	Lys	Arg	Arg	Lys	Trp	Leu	Glu	Asp	Asn	Pro
					165					170					175
Glu	Thr	Thr	Ser	Asn	Asp	Glu	Leu	Val	Phe	Asp	Thr	Ser	Ile	Ile	
					180					185					190
Pro	Trp	Trp	Ala	Trp	Met	Lys	Arg	Tyr	His	Leu	Pro	Glu	Ala	Glu	Leu
					195					200					205
Leu	Asn	Gly	Arg	Ala	Ala	Met	Ile	Gly	Phe	Phe	Met	Ala	Tyr	Phe	Val
					210					215					220
Asp	Ser	Leu	Thr	Gly	Val	Gly	Leu	Val	Asp	Gln	Met	Gly	Asn	Phe	Phe
					225					230					235
Cys	Lys	Thr	Leu	Leu	Phe	Val	Ala	Val	Ala	Gly	Val	Leu	Phe	Ile	Arg
					245					250					255
Lys	Asn	Glu	Asp	Leu	Asp	Lys	Leu	Lys	Asp	Leu	Phe	Asp	Glu	Thr	Thr
					260					265					270
Leu	Tyr	Asp	Lys	Gln	Trp	Gln	Ala	Ala	Trp	Lys	Glu	Pro	Asp	Ser	Ser
					275					280					285
Asp	Ser	Phe	Phe	Lys	Glu	Val	Asn	Lys	Phe	Leu	Gln	Ser	Phe	Ile	Phe
					290					295					300
Leu	Phe	Leu	Leu	Cys	Asn	Asn	Leu								
					305										310

(2) INFORMATION FOR SEQ ID NO:2704:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..276
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574001
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2704:

Met	Ser	Ile	Ser	Met	Ala	Leu	Phe	Ser	Pro	Pro	Ile	Ser	Ser	Ser	Leu
1									5	10					15
Gln	Asn	Pro	Asn	Leu	Ile	Pro	Lys	Ile	Ser	Thr	Ser	Leu	Leu	Ser	Thr
									20	25					30
Lys	Arg	Phe	Ser	Leu	Ile	Ser	Val	Pro	Arg	Ala	Ser	Ser	Asp	Asn	Gly
									35	40					45
Thr	Thr	Ser	Pro	Val	Val	Lys	Ile	Pro	Lys	Pro	Ala	Ser	Val	Ala	Val
									50	55					60
Glu	Glu	Val	Pro	Val	Lys	Ser	Pro	Ala	Glu	Ser	Ser	Ser	Ala	Ser	Glu
									65	70					75
Asn	Gly	Ala	Val	Gly	Gly	Glu	Ala	Thr	Asp	Ser	Ser	Thr	Glu	Thr	Val
									85	90					95
Ile	Lys	Tyr	Gln	Asn	Ala	Lys	Trp	Val	Asn	Gly	Thr	Trp	Asp	Leu	Lys
									100	105					110
Gln	Phe	Glu	Lys	Asp	Gly	Lys	Thr	Asp	Trp	Asp	Ser	Thr	Ile	Val	Ser
									115	120					125
Glu	Ala	Lys	Arg	Arg	Lys	Trp	Leu	Glu	Asp	Asn	Pro	Glu	Thr	Thr	Ser
									130	135					140

Asn Asp Glu Leu Val Val Phe Asp Thr Ser Ile Ile Pro Trp Trp Ala
145 150 155 160
Trp Met Lys Arg Tyr His Leu Pro Glu Ala Glu Leu Leu Asn Gly Arg
165 170 175
Ala Ala Met Ile Gly Phe Phe Met Ala Tyr Phe Val Asp Ser Leu Thr
180 185 190
Gly Val Gly Leu Val Asp Gln Met Gly Asn Phe Phe Cys Lys Thr Leu
195 200 205
Leu Phe Val Ala Val Ala Gly Val Leu Phe Ile Arg Lys Asn Glu Asp
210 215 220
Leu Asp Lys Leu Lys Asp Leu Phe Asp Glu Thr Thr Leu Tyr Asp Lys
225 230 235 240
Gln Trp Gln Ala Ala Trp Lys Glu Pro Asp Ser Ser Asp Ser Phe Phe
245 250 255
Lys Glu Val Asn Lys Phe Leu Gln Ser Phe Ile Phe Leu Phe Leu Leu
260 265 270
Cys Asn Asn Leu
275

(2) INFORMATION FOR SEQ ID NO:2705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..272
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2705:

Met Ala Leu Phe Ser Pro Pro Ile Ser Ser Ser Leu Gln Asn Pro Asn
1 5 10 15
Leu Ile Pro Lys Ile Ser Thr Ser Leu Leu Ser Thr Lys Arg Phe Ser
20 25 30
Leu Ile Ser Val Pro Arg Ala Ser Asp Asn Gly Thr Thr Ser Pro
35 40 45
Val Val Lys Ile Pro Lys Pro Ala Ser Val Ala Val Glu Glu Val Pro
50 55 60
Val Lys Ser Pro Ala Glu Ser Ser Ser Ala Ser Glu Asn Gly Ala Val
65 70 75 80
Gly Gly Glu Ala Thr Asp Ser Ser Thr Glu Thr Val Ile Lys Tyr Gln
85 90 95
Asn Ala Lys Trp Val Asn Gly Thr Trp Asp Leu Lys Gln Phe Glu Lys
100 105 110
Asp Gly Lys Thr Asp Trp Asp Ser Val Ile Val Ser Glu Ala Lys Arg
115 120 125
Arg Lys Trp Leu Glu Asp Asn Pro Glu Thr Thr Ser Asn Asp Glu Leu
130 135 140
Val Val Phe Asp Thr Ser Ile Ile Pro Trp Trp Ala Trp Met Lys Arg
145 150 155 160
Tyr His Leu Pro Glu Ala Glu Leu Leu Asn Gly Arg Ala Ala Met Ile
165 170 175
Gly Phe Phe Met Ala Tyr Phe Val Asp Ser Leu Thr Gly Val Gly Leu
180 185 190
Val Asp Gln Met Gly Asn Phe Phe Cys Lys Thr Leu Leu Phe Val Ala
195 200 205
Val Ala Gly Val Leu Phe Ile Arg Lys Asn Glu Asp Leu Asp Lys Leu
210 215 220
Lys Asp Leu Phe Asp Glu Thr Thr Leu Tyr Asp Lys Gln Trp Gln Ala
225 230 235 240
Ala Trp Lys Glu Pro Asp Ser Ser Asp Ser Phe Phe Lys Glu Val Asn

	245		250		255										
Lys	Phe	Leu	Gln	Ser	Phe	Ile	Phe	Leu	Phe	Leu	Leu	Cys	Asn	Asn	Leu
	260							265						270	

(2) INFORMATION FOR SEQ ID NO:2706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..551
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2706:

ataaacaaaa	agaatttgaa	ccaacaaagc	aaaacatgaa	aggcacattc	actaacttgc	60
ttgtgtcctc	cctcattgca	cttgtttgtg	ccaatgtcgg	tgctaggaaa	gttatctccg	120
aagataccca	attcaaggat	gaaaaatctt	tcctcggagg	cagtggcagc	ggtgatggct	180
tagggcttgg	ccttggtgga	ggagctggtc	ttggtgggct	tgggattggg	gctgggactg	240
gcgcgggagc	cggaactagg	ttaggtggag	gcggtggggg	aggagccggt	ggcggactcg	300
ttggccttcc	ttgaacgtat	tgacaagtgt	gcgtgtgaga	gctgattctc	agcttattac	360
taattaatta	agttactttc	attctcttaa	taaaatctag	agggtttgaa	tttcggattt	420
cttcagcttt	aatttaaac	tcaatatttg	aacaaaaaaa	ggctttagct	actagaggtt	480
atgctcgtaa	tcgtattatg	tgtaAcgcgc	gttctgatat	tcttatgtgc	aAgtgtggaa	540
cgtttctctt	t					

(2) INFORMATION FOR SEQ ID NO:2707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2707:

Lys	Gln	Lys	Glu	Phe	Glu	Pro	Thr	Lys	Gln	Asn	Met	Lys	Gly	Thr	Phe
1			5						10					15	
Thr	Asn	Leu	Leu	Val	Leu	Leu	Leu	Ile	Ala	Leu	Val	Cys	Ala	Asn	Val
			20					25					30		
Gly	Ala	Arg	Lys	Val	Ile	Ser	Glu	Asp	Thr	Gln	Phe	Lys	Asp	Glu	Lys
		35					40					45			
Ser	Phe	Leu	Gly	Gly	Ser	Gly	Ser	Gly	Asp	Gly	Leu	Gly	Leu	Gly	Leu
	50						55				60				
Gly	Gly	Gly	Ala	Gly	Leu	Gly	Gly	Leu	Gly	Ile	Gly	Ala	Gly	Ile	Gly
	65				70				75					80	
Ala	Gly	Ala	Gly	Leu	Gly	Leu	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Gly
			85					90					95		
Gly	Gly	Leu	Val	Gly	Leu	Pro									
			100												

(2) INFORMATION FOR SEQ ID NO:2708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..92
(D) OTHER INFORMATION: / Ceres Seq. ID 1574008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2708:

Met Lys Gly Thr Phe Thr Asn Leu Leu Val Leu Leu Ile Ala Leu
1 5 10 15
Val Cys Ala Asn Val Gly Ala Arg Lys Val Ile Ser Glu Asp Thr Gln
20 25 30
Phe Lys Asp Glu Lys Ser Phe Leu Gly Gly Ser Gly Ser Gly Asp Gly
35 40 45
Leu Gly Leu Gly Leu Gly Gly Ala Gly Leu Gly Gly Leu Gly Ile
50 55 60
Gly Ala Gly Ile Gly Ala Gly Ala Gly Leu Gly Leu Gly Gly Gly Gly
65 70 75 80
Gly Gly Gly Ala Gly Gly Gly Leu Val Gly Leu Pro
85 90

(2) INFORMATION FOR SEQ ID NO:2709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1005 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1005
(D) OTHER INFORMATION: / Ceres Seq. ID 1574009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2709:

aaaaacaaac aaaaaaatca gtgttcgacct ctaacacagct cgaacacatc ggcggtctcg 60
tttaatacaa cgtttcacca gcctttctctg agtcccagct gtacatcaaa gctttattct 120
gggttaaaag ctcaatctcg aagctttttg gcaagtgggt atcagaattt gaataaaggag 180
ttctatggaa gagttcataa gactctgcaa tctgggactg gcaaagcgag caggtcacgg 240
gtaaaagtga tgccaatagg aacaccgaga gtgccttaca gaaaccgtga agaaggcact 300
tggcaakggg ttgatatacg gaatgcccct tatcgagagc gtgtaattct cattggacaa 360
aacattgatg aagagttttag caaccagata ttagcaacca tgttgtacct tgataactct 420
gatgactcga ggaggattta tatgtacct aatggtcocg gtgggtgatct tactccaagt 480
ctagccatct atgatacaat gaagagcttg aaaaagtcgg ttgggacaca ttgcgttggg 540
cttgcttaca accttgacgg tttttctctt gcggtctggg aaaaagggtca ccgatttgcg 600
atgcatttgt caagaatcgc cctccaatca ccagctgggt cagcccggtg ccaggctgat 660
gatatccaaa atgaagcaaa agagctttca aggataagag actacctctt caatgaacta 720
gccaagaata caggccagcc tcgggaaaag gtcttcaaa acttgagcgc ggtgaaaagg 780
ttcaatgcag aggaagcaat cgaagtatga cttattgata agattgttag accacgcgac 840
atcaaaagaag acgctctctg ccaagacgaa agcgacgggc taggctagtc tttttgttt 900
gtttgttatg tcaaaaagtt taattcttat gttatttgta ttgtgattg tacctaaaaa 960
aatcaactgat tattgttttt tcattccacc gattttctga ttctt

(2) INFORMATION FOR SEQ ID NO:2710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..295
(D) OTHER INFORMATION: / Ceres Seq. ID 1574010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2710:

Lys Asn Lys Gln Lys Asn Gln Cys Ser Ala Leu Thr Arg Ser Thr Thr
1 5 10 15
Met Ala Val Ser Phe Asn Thr Thr Leu His Gln Pro Ser Leu Ser Pro
20 25 30

Ser Cys Ser Ile Lys Leu Tyr Ser Gly Leu Lys Pro Gln Ser Ala Ser
35 40 45
Phe Leu Ala Ser Gly Tyr Gln Asn Leu Asn Lys Glu Phe Tyr Gly Arg
50 55 60
Val His Lys Ser Leu Gln Ser Gly Thr Gly Lys Ala Ser Arg Ser Arg
65 70 75 80
Val Lys Met Met Pro Ile Gly Thr Pro Arg Val Pro Tyr Arg Asn Arg
85 90 95
Glu Glu Gly Thr Trp Gln Xaa Val Asp Ile Trp Asn Ala Leu Tyr Arg
100 105 110
Glu Arg Val Ile Phe Ile Gly Gln Asn Ile Asp Glu Glu Phe Ser Asn
115 120 125
Gln Ile Leu Ala Thr Met Leu Tyr Leu Asp Thr Leu Asp Asp Ser Arg
130 135 140
Arg Ile Tyr Met Tyr Leu Asn Gly Pro Gly Gly Asp Leu Thr Pro Ser
145 150 155 160
Leu Ala Ile Tyr Asp Thr Met Lys Ser Leu Lys Ser Pro Val Gly Thr
165 170 175
His Cys Val Gly Leu Ala Tyr Asn Leu Ala Gly Phe Leu Leu Ala Ala
180 185 190
Gly Glu Lys Gly His Arg Phe Ala Met Pro Leu Ser Arg Ile Ala Leu
195 200 205
Gln Ser Pro Ala Gly Ala Ala Arg Gly Gln Ala Asp Asp Ile Gln Asn
210 215 220
Glu Ala Lys Glu Leu Ser Arg Ile Arg Asp Tyr Leu Phe Asn Glu Leu
225 230 235 240
Ala Lys Asn Thr Gly Gln Pro Ala Glu Arg Val Phe Lys Asp Leu Ser
245 250 255
Arg Val Lys Arg Phe Asn Ala Glu Glu Ala Ile Glu Tyr Gly Leu Ile
260 265 270
Asp Lys Ile Val Arg Pro Pro Arg Ile Lys Glu Asp Ala Pro Arg Gln
275 280 285
Asp Glu Ser Ala Gly Leu Gly
290 295

(2) INFORMATION FOR SEQ ID NO:2711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..279
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2711:

Met Ala Val Ser Phe Asn Thr Thr Leu His Gln Pro Ser Leu Ser Pro
1 5 10 15
Ser Cys Ser Ile Lys Leu Tyr Ser Gly Leu Lys Pro Gln Ser Ala Ser
20 25 30
Phe Leu Ala Ser Gly Tyr Gln Asn Leu Asn Lys Glu Phe Tyr Gly Arg
35 40 45
Val His Lys Ser Leu Gln Ser Gly Thr Gly Lys Ala Ser Arg Ser Arg
50 55 60
Val Lys Met Met Pro Ile Gly Thr Pro Arg Val Pro Tyr Arg Asn Arg
65 70 75 80
Glu Glu Gly Thr Trp Gln Xaa Val Asp Ile Trp Asn Ala Leu Tyr Arg
85 90 95
Glu Arg Val Ile Phe Ile Gly Gln Asn Ile Asp Glu Glu Phe Ser Asn
100 105 110
Gln Ile Leu Ala Thr Met Leu Tyr Leu Asp Thr Leu Asp Asp Ser Arg

(2) INFORMATION FOR SEO ID NO:2712:

(A) LENGTH: 213 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(A) NAME/KEY: peptide

(B) LOCATION: 1..213

(D) OTHER INFORMATION: / Ceres Seq. ID 1574012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2712:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..597
(D) OTHER INFORMATION: / Ceres Seq. ID 1574013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2713:

tctcKSGatt	aaagaggttg	atctagcgat	tgttcgcat	cttggtacgc	tocagcgatt	60
accgagtatc	gttgggtatg	ctaacgccat	ggaattagct	ttaactgctc	ggagattctc	120
tgagagtgaa	gcaaaggatc	ttggtttggt	ttctaaagtt	ttcggatcta	aatcggaagt	180
tgacaacggc	gtcagtacaa	tcgctgaagg	aataggaggc	aagtcctcct	tagctgtgac	240
agggacaaag	gcagtgttat	taagaagcag	agaggtgagt	gtagaacaag	gacttgacta	300
tgtagcaact	tggaactcgg	ctatgcttat	atcagatgat	ctcaacgaag	ctgtttctgc	360
tcagatgatg	aaaacaaaaa	ctcggtttgc	taaaactgtga	tacagctctc	gtgttgcttc	420
tttgtcttcc	aaagctcttc	tggtactaaa	agtaataaga	tattacttca	aataagttta	480
gttattgata	gttccttaat	tacggattag	ggctatagat	aaaatggctt	tctacacatg	540
agaatatgat	taatactctg	cacaatgcac	attggtaaat	gctatacctc	aatgttt	

(2) INFORMATION FOR SEQ ID NO:2714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..132
(D) OTHER INFORMATION: / Ceres Seq. ID 1574014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2714:

Leu	Xaa	Ile	Lys	Glu	Val	Asp	Leu	Ala	Ile	Val	Ala	Asp	Leu	Gly	Thr
1				5					10					15	
Leu	Gln	Arg	Leu	Pro	Ser	Ile	Val	Gly	Tyr	Ala	Asn	Ala	Met	Glu	Leu
				20					25					30	
Ala	Leu	Thr	Ala	Arg	Arg	Phe	Ser	Gly	Gly	Glu	Ala	Lys	Asp	Leu	Gly
				35					40					45	
Leu	Val	Ser	Lys	Val	Phe	Gly	Ser	Lys	Ser	Glu	Leu	Asp	Asn	Gly	Val
				50					55					60	
Ser	Thr	Ile	Ala	Glu	Gly	Ile	Gly	Gly	Lys	Ser	Pro	Leu	Ala	Val	Thr
				65					70					75	
Gly	Thr	Lys	Ala	Val	Leu	Leu	Arg	Ser	Arg	Glu	Val	Ser	Val	Glu	Gln
				85					90					95	
Gly	Leu	Asp	Tyr	Val	Ala	Thr	Trp	Asn	Ser	Ala	Met	Leu	Ile	Ser	Asp
				100					105					110	
Asp	Leu	Asn	Glu	Ala	Val	Ser	Ala	Gln	Met	Met	Lys	Thr	Lys	Pro	Arg
				115					120					125	
Phe	Ala	Lys	Leu												
				130											

(2) INFORMATION FOR SEQ ID NO:2715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1574015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2715:

Met Glu Leu Ala Leu Thr Ala Arg Arg Phe Ser Gly Gly Glu Ala Lys
1 5 10 15
Asp Leu Gly Leu Val Ser Lys Val Phe Gly Ser Lys Ser Glu Leu Asp
20 25 30
Asn Gly Val Ser Thr Ile Ala Glu Gly Ile Gly Lys Ser Pro Leu
35 40 45
Ala Val Thr Gly Thr Lys Ala Val Leu Leu Arg Ser Arg Glu Val Ser
50 55 60
Val Glu Gln Gly Leu Asp Tyr Val Ala Thr Trp Asn Ser Ala Met Leu
65 70 75 80
Ile Ser Asp Asp Leu Asn Glu Ala Val Ser Ala Gln Met Met Lys Thr
85 90 95
Lys Pro Arg Phe Ala Lys Leu
100

(2) INFORMATION FOR SEQ ID NO:2716:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2259 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2259

(D) OTHER INFORMATION: / Ceres Seq. ID 1574021

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2716:

gctcgcgctc	cgccgctgctg	ccacaacaa	tctccgactt	cgtttctctc	atctatcatc	60
gtcgtgtctca	acccttattta	tctcttaatt	tatcattaaa	acaaaaaaac	caaaaaaaac	120
ctctagactt	tcgtttcttc	aatcccagca	aaaaaaatgg	ctcaggttca	agctctctct	180
tcacattctc	ctctctctcc	tgctgttggt	aacgacgggg	ctgcgacggc	ttctgttacc	240
cctggaatgc	gcgtcgggcg	cggtggagac	ggagtcaact	acggtgctct	ttgttctctc	300
tatgtcggag	atctggattt	caatgtcacc	gattctcagc	tttatgacta	tttcaccagag	360
gtgtgtcagg	ttgtatctgt	tcgtgtttgt	cgtgatgctg	ctaccaatca	ttctcttggt	420
tatggttatg	tcaactacag	caacaccgac	gatgcggaga	aggccaatga	gaagtgtgaac	480
tcagttatct	tcaattggaa	gatgattcgg	attacttact	cttctcgtga	ctcttctgcc	540
cgtagaatgc	gggttgggaa	tttgtttgta	aagaattttg	ataagtcagt	tgacaacaaa	600
acccctcacg	aggcgttttc	cggtgtgtgg	actattgtgt	cctgtaaggt	tgctactgat	660
cacatgggtc	agctacagag	atattgggtt	gtgcagtttg	acactaagga	ttcacagtaag	720
aagtctattg	agaaagctga	cgggaaagtg	ttgaatgaca	aacagatttt	tggtggacct	780
tttcttcgta	aggaggaagc	agagtctgct	gctgataaga	tgaagttttac	taattgtttat	840
gtgaagaatc	tttcggagtc	gactactgac	gatgagttga	agactacttt	tggtcagtat	900
ggtagtatct	cgagcgctgt	agttatgagg	gatggagatg	ggaaatccag	gtgttttggga	960
ttgttcaact	ttgagaatcc	tgaagatgca	gctcgtgctg	ttgaagctct	caatggaagc	1020
aaagtgtgat	ataaggatgt	gtatgtgggt	aaagctcagS	aagaaatctc	agagggaaact	1080
tgagtgtagc	cggagatatg	aacaaggctc	aaagtgatgt	ggaaaacaat	ttgatggggt	1140
gaatttttat	gttaagaatcc	ttgatgatac	cgctcacggt	gagaagttgc	gcgagtgtgt	1200
tgccgaattt	tgtaacaatca	ctctcttgca	ggttatcgcg	gacctcagtg	gtactacgaa	1260
aggatcagga	tttgtttgct	tctctgctgc	cagtgaagct	tcaagatgag	tgaaatgaaat	1320
gaatgtgtaa	atggtttggtg	gcaaaacggt	gtatgttgct	cttgacacag	ggaaaagaaga	1380
aaggagggct	aagctgcagc	cacagttttc	tcaaatgaga	cttgcttttta	tcctccggtgt	1440
gggtctctga	atgccaatat	tcaacaggtg	tgctccaggt	cttgacacaa	agcttttttta	1500
cggtcaagga	ctctccaccaa	tcattcctca	ccagcctgga	tttgatatac	agcctcagct	1560
gggtctcggga	atgaggccgg	cccttttttg	tggaacgatg	atgcagccag	gtcagcaagg	1620
tcacacccag	gtggcagacg	gttcagtgat	ggacccatgc	gccatcagca	tcagcagcca	1680
atgctcttaca	tgacgacaca	gatgatgcca	agaggacgag	ggatccggta	cccttctggc	1740
gttagaatac	tgctctcagc	tccaatgcca	ggaggaatgg	ttccagttgt	tatgacacat	1800
aatgtaatgc	cgatatagtca	gcctatgtcc	gctgtgcaat	tggtactctc	ccctgtcaat	1860
gctacacctg	ctcaacagag	aacacttctt	ggtagagatc	tattaccatt	agtggaacag	1920

atagagagtg agcagcgtgc gaaagtgc ggtatgcttc tggaaatgga tcagaccgag 1980
gttttgcac tcgtcgagtc accagaggtc ctaaatgcc aagtttcaga ggcattagat 2040
gtgttgagaa acgtgaaatca gccatottca caggggaagt aaggcaacaa aagtgggaagt 2100
ccaagtgtac ttttggcttc actttccatc aatgatcaat tatgagaagc ttttgttcga 2160
gttttttttt ttttactttg actctctctc tctctatctc tctctctgat tgacaaattt 2220
ttgcgggaat ctatttgctg ttttagactt ttttgcctc

(2) INFORMATION FOR SEQ ID NO:2717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..304
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2717:

Met	Ala	Gln	Val	Gln	Ala	Pro	Ser	Ser	His	Ser	Pro	Pro	Pro	Ala
1		5						10				15		
Val	Val	Asn	Asp	Gly	Ala	Ala	Thr	Ala	Ser	Ala	Thr	Pro	Gly	Ile
		20						25				30		Gly
Val	Gly	Gly	Gly	Gly	Asp	Gly	Val	Thr	His	Gly	Ala	Leu	Cys	Ser
		35					40					45		Leu
Tyr	Val	Gly	Asp	Leu	Asp	Phe	Asn	Val	Thr	Asp	Ser	Gln	Leu	Tyr
		50				55				60				Asp
Tyr	Phe	Thr	Glu	Val	Cys	Gln	Val	Val	Ser	Val	Arg	Val	Cys	Arg
65			70						75					80
Ala	Ala	Thr	Asn	Thr	Ser	Leu	Gly	Tyr	Gly	Tyr	Val	Asn	Tyr	Ser
			85					90					95	Asn
Thr	Asp	Asp	Ala	Glu	Lys	Ala	Met	Gln	Lys	Leu	Asn	Tyr	Ser	Tyr
			100					105				110		Leu
Asn	Gly	Lys	Met	Ile	Arg	Ile	Thr	Tyr	Ser	Ser	Arg	Asp	Ser	Ser
			115				120					125		Ala
Arg	Arg	Ser	Gly	Val	Gly	Asn	Leu	Phe	Val	Lys	Asn	Leu	Asp	Lys
			130			135				140				Ser
Val	Asp	Asn	Lys	Thr	Leu	His	Glu	Ala	Phe	Ser	Gly	Cys	Gly	Thr
145			150						155					160
Val	Ser	Cys	Lys	Val	Ala	Thr	Asp	His	Met	Gly	Gln	Ser	Arg	Gly
			165					170						175
Gly	Phe	Val	Gln	Phe	Asp	Thr	Lys	Asp	Ser	Ala	Lys	Asn	Ala	Ile
			180					185				190		Glu
Lys	Leu	Asn	Gly	Lys	Val	Leu	Asn	Asp	Lys	Gln	Ile	Phe	Val	Gly
			195				200					205		Pro
Phe	Leu	Arg	Lys	Glu	Glu	Arg	Glu	Ser	Ala	Ala	Asp	Lys	Met	Lys
			210				215				220			Phe
Thr	Asn	Val	Tyr	Val	Lys	Asn	Leu	Ser	Glu	Ala	Thr	Thr	Asp	Asp
225			230						235					Glu
Leu	Lys	Thr	Thr	Phe	Gly	Gln	Tyr	Gly	Ser	Ile	Ser	Ser	Ala	Val
			245					250						255
Met	Arg	Asp	Gly	Asp	Gly	Lys	Ser	Arg	Cys	Phe	Gly	Phe	Val	Asn
			260					265				270		Phe
Glu	Asn	Pro	Glu	Asp	Ala	Ala	Arg	Ala	Val	Glu	Ala	Leu	Asn	Gly
			275				280					285		Lys
Lys	Phe	Asp	Asp	Lys	Glu	Trp	Tyr	Val	Gly	Lys	Ala	Gln	Xaa	Glu
			290			295					300			Ile

(2) INFORMATION FOR SEQ ID NO:2718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..257
(D) OTHER INFORMATION: / Ceres Seq. ID 1574023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2718:

```
Met Glu Met Gly Asn Pro Gly Val Leu Asp Leu Ser Thr Leu Arg Ile
1      5      10      15
Leu Lys Met Gln Leu Val Leu Leu Lys Leu Ser Met Glu Arg Ser Leu
20      25      30
Met Ile Arg Ser Gly Met Trp Val Lys Leu Xaa Lys Lys Ser Glu Arg
35      40      45
Glu Leu Glu Leu Ser Arg Arg Tyr Glu Gln Gly Ser Ser Asp Gly Gly
50      55      60
Asn Lys Phe Asp Gly Leu Asn Leu Tyr Val Lys Asn Leu Asp Asp Thr
65      70      75      80
Val Thr Asp Glu Lys Leu Arg Glu Leu Phe Ala Glu Phe Gly Thr Ile
85      90      95
Thr Ser Cys Lys Val Met Arg Asp Pro Ser Gly Thr Ser Lys Gly Ser
100      105      110
Gly Phe Val Ala Phe Ser Ala Ala Ser Glu Ala Ser Arg Val Leu Asn
115      120      125
Glu Met Asn Gly Lys Met Val Gly Gly Lys Pro Leu Tyr Val Ala Leu
130      135      140
Ala Gln Arg Lys Glu Glu Arg Arg Ala Lys Leu Gln Ala Gln Phe Ser
145      150      155      160
Gln Met Arg Pro Ala Phe Ile Pro Gly Val Gly Pro Arg Met Pro Ile
165      170      175
Phe Thr Gly Gly Ala Pro Gly Leu Gly Gln Gln Ile Phe Tyr Gly Gln
180      185      190
Gly Pro Pro Pro Ile Ile Pro His Gln Pro Gly Phe Gly Tyr Gln Pro
195      200      205
Gln Leu Val Pro Gly Met Arg Pro Ala Phe Phe Gly Gly Pro Met Met
210      215      220
Gln Pro Gly Gln Gln Gly Pro His Gln Val Ala Asp Gly Gln Val Met
225      230      235      240
Asp Pro Cys Ala Ile Ser Ile Ser Ser Gln Cys Leu Thr Cys Ser His
245      250      255
Arg
```

(2) INFORMATION FOR SEQ ID NO:2719:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..255

(D) OTHER INFORMATION: / Ceres Seq. ID 1574024

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2719:

```
Met Gly Asn Pro Gly Val Leu Asp Leu Ser Thr Leu Arg Ile Leu Lys
1      5      10      15
Met Gln Leu Val Leu Leu Lys Leu Ser Met Glu Arg Ser Leu Met Ile
20      25      30
Arg Ser Gly Met Trp Val Lys Leu Xaa Lys Lys Ser Glu Arg Glu Leu
35      40      45
```

Glu	Leu	Ser	Arg	Arg	Tyr	Glu	Gln	Gly	Ser	Ser	Asp	Gly	Gly	Asn	Lys		
50						55					60						
Phe	Asp	Gly	Leu	Asn	Leu	Tyr	Val	Lys	Asn	Leu	Asp	Asp	Thr	Val	Thr		
65				70					75					80			
Asp	Glu	Lys	Leu	Arg	Glu	Leu	Phe	Ala	Glu	Phe	Gly	Thr	Ile	Thr	Ser		
			85						90					95			
Cys	Lys	Val	Met	Arg	Asp	Pro	Ser	Gly	Thr	Ser	Lys	Gly	Ser	Gly	Phe		
			100						105					110			
Val	Ala	Phe	Ser	Ala	Ala	Ser	Glu	Ala	Ser	Arg	Val	Leu	Asn	Glu	Met		
			115						120					125			
Asn	Gly	Lys	Met	Val	Gly	Gly	Lys	Pro	Leu	Tyr	Val	Ala	Leu	Ala	Gln		
			130				135					140					
Arg	Lys	Glu	Glu	Arg	Arg	Ala	Lys	Leu	Gln	Ala	Gln	Phe	Ser	Gln	Met		
			145				150				155				160		
Arg	Pro	Ala	Phe	Ile	Pro	Gly	Val	Gly	Pro	Arg	Met	Pro	Ile	Phe	Thr		
			165						170					175			
Gly	Gly	Ala	Pro	Gly	Leu	Gly	Gln	Gln	Ile	Phe	Tyr	Gly	Gln	Gly	Pro		
			180						185					190			
Pro	Pro	Ile	Ile	Pro	His	Gln	Pro	Gly	Phe	Gly	Tyr	Gln	Pro	Gln	Leu		
			195				200						205				
Val	Pro	Gly	Met	Arg	Pro	Ala	Phe	Phe	Gly	Gly	Pro	Met	Met	Gln	Pro		
			210				215					220					
Gly	Gln	Gln	Gly	Pro	His	Gln	Val	Ala	Asp	Gly	Gln	Val	Met	Asp	Pro		
			225			230					235				240		
Cys	Ala	Ile	Ser	Ile	Ser	Ser	Gln	Cys	Leu	Thr	Cys	Ser	His	Arg			
			245						250					255			

(2) INFORMATION FOR SEQ ID NO:2720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..927
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2720:

atttttcatt	cttctaagcc	ctagctcaaa	gctttctctc	tcaaatccgc	catgactaaa	60
cagcacgcga	actggtctcc	ttacgataac	aatggaggaa	catgtgtggc	catcgctgga	120
tcggattact	gtgttatcgc	cgccgatact	cggatgtcta	ctggttacag	tattcttagt	180
cgcgattact	ccaaaatcca	taaaactagcg	gacagacctg	ttttgtcttc	ctctggtctc	240
caggctgatg	tgaaagcttt	cgagaaggtt	ctcaaatcca	gacacttgat	ctatcaacat	300
cagcataaca	agcagatgag	ctgtctctgca	atggcccagc	ttctctccaa	cacgctttat	360
ttcaagcggt	ttttccctta	ctatgccttt	aatgttctag	gagggcttga	cgaggaagga	420
aaagggtgtg	tctttactta	cgacgctgtt	ggctcatacg	agagagttgg	atacgggtgct	480
caagggtctg	gtttccacat	catcatgcct	ttccttgaca	atcagctcaa	gtctccaagt	540
ctctcttttg	tacctaaaca	ggattcaaac	acgCcccttt	cogaagctga	agcagttgac	600
ttggttAaaa	ctgttttcgc	atctgcacca	Tgagagggat	atctacactg	gagacaagct	660
tgagattatg	atacttaagc	cgcagcgtat	caagaccgaa	ctcatggacc	tgaggaaaga	720
ctaagctcct	ttagtgcatt	tagccaacct	tatcggtttg	ttatttcact	tcaacatcga	780
gcttctcgag	ttgtagaact	cgtatgaact	gtactgggtt	ttgatatttt	acagttaaaa	840
tcatgactcg	tgtttgaagt	ttctccaaaa	ctgtttccct	atgtatgaga	atcactcgaa	900
tcttgtcttt	aatcaatgt	ttctccc				

(2) INFORMATION FOR SEQ ID NO:2721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1574026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2721:

```
Met Thr Lys Gln His Ala Asn Trp Ser Pro Tyr Asp Asn Asn Gly Gly
1      5      10      15
Thr Cys Val Ala Ile Ala Gly Ser Asp Tyr Cys Val Ile Ala Ala Asp
      20      25      30
Thr Arg Met Ser Thr Gly Tyr Ser Ile Leu Ser Arg Asp Tyr Ser Lys
      35      40      45
Ile His Lys Leu Ala Asp Arg Pro Val Leu Ser Ser Ser Gly Phe Gln
      50      55      60
Ala Asp Val Lys Ala Leu Gln Lys Val Leu Lys Ser Arg His Leu Ile
65      70      75      80
Tyr Gln His Gln His Asn Lys Gln Met Ser Cys Pro Ala Met Ala Gln
      85      90      95
Leu Leu Ser Asn Thr Leu Tyr Phe Lys Arg Phe Phe Pro Tyr Tyr Ala
      100      105      110
Phe Asn Val Leu Gly Gly Leu Asp Glu Glu Gly Lys Gly Cys Val Phe
      115      120      125
Thr Tyr Asp Ala Val Gly Ser Tyr Glu Arg Val Gly Tyr Gly Ala Gln
      130      135      140
Gly Ser Gly Ser Thr Leu Ile Met Pro Phe Leu Asp Asn Gln Leu Lys
145      150      155      160
Ser Pro Ser Pro Leu Leu Leu Pro Lys Gln Asp Ser Asn Thr Pro Leu
      165      170      175
Ser Glu Ala Glu Ala Val Asp Leu Val Lys Thr Val Phe Ala Ser Ala
      180      185      190
Thr
```

(2) INFORMATION FOR SEQ ID NO:2722:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1574027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2722:

```
Met Ser Thr Gly Tyr Ser Ile Leu Ser Arg Asp Tyr Ser Lys Ile His
1      5      10      15
Lys Leu Ala Asp Arg Pro Val Leu Ser Ser Ser Gly Phe Gln Ala Asp
      20      25      30
Val Lys Ala Leu Gln Lys Val Leu Lys Ser Arg His Leu Ile Tyr Gln
      35      40      45
His Gln His Asn Lys Gln Met Ser Cys Pro Ala Met Ala Gln Leu Leu
      50      55      60
Ser Asn Thr Leu Tyr Phe Lys Arg Phe Phe Pro Tyr Tyr Ala Phe Asn
65      70      75      80
Val Leu Gly Gly Leu Asp Glu Glu Gly Lys Gly Cys Val Phe Thr Tyr
      85      90      95
Asp Ala Val Gly Ser Tyr Glu Arg Val Gly Tyr Gly Ala Gln Gly Ser
      100      105      110
Gly Ser Thr Leu Ile Met Pro Phe Leu Asp Asn Gln Leu Lys Ser Pro
      115      120      125
Ser Pro Leu Leu Leu Pro Lys Gln Asp Ser Asn Thr Pro Leu Ser Glu
      130      135      140
```

Ala Glu Ala Val Asp Leu Val Lys Thr Val Phe Ala Ser Ala Thr
145 150 155

(2) INFORMATION FOR SEQ ID NO:2723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2723:

Met Ser Cys Pro Ala Met Ala Gln Leu Leu Ser Asn Thr Leu Tyr Phe
1 5 10 15
Lys Arg Phe Phe Pro Tyr Tyr Ala Phe Asn Val Leu Gly Gly Leu Asp
20 25 30
Glu Glu Gly Lys Gly Cys Val Phe Thr Tyr Asp Ala Val Gly Ser Tyr
35 40 45
Glu Arg Val Gly Tyr Gly Ala Gln Gly Ser Gly Ser Thr Leu Ile Met
50 55 60
Pro Phe Leu Asp Asn Gln Leu Lys Ser Pro Ser Pro Leu Leu Leu Pro
65 70 75 80
Lys Gln Asp Ser Asn Thr Pro Leu Ser Glu Ala Glu Ala Val Asp Leu
85 90 95
Val Lys Thr Val Phe Ala Ser Ala Thr
100 105

(2) INFORMATION FOR SEQ ID NO:2724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2724:

tttgatgact gttcagcagc caatgtcact atccatcgaa atccctggaag ttgagttcgg 60
tgaagctcgcg gatattggcg aagaagcaat ctattataga catttcaaac cggtgatctt 120
gtggagcctt caaaactgga ttggtattgg gcttgagagg aagatgagaa cagctttggc 180
cactgtcaat cgtatgtttg cgaagatcat atcttcaaga agaaaaggagg agataagtcg 240
cgccaaaaac gagccatatt ccaaggacgc gttgacgtat tatatgaatg tggacacgag 300
caaatataag ctcttgaaac ctaataaaga taagtttata agagatgtta tttttagtct 360
agtgttagca ggaaggagaca ccacaagctc agttctcact tggttctttt ggcttctttc 420
taagcatcct caagttatgg ccaagctcag acatgagatc aacacaaagt ttgataatga 480
agatctagag aagctcgtgt atctgcatcg tgcattgtcc gaatcaatga gactctaccc 540
gccactctcc ttcaaccaca agtctCctgc gaaGccagat gtaacttccaa gcgggcacaa 600
agttgatgca aattcaaaga tcgtgatatg tatctatgca ttgggggagga tgagatctgt 660
atggggagaa gacgcattgg atttcaaacc agagagatgg atttcagaca atggaggtct 720
aagacatgaa ccttcaatca agttcatggc tttaaattct ggctcgagaa cttgcttggt 780
taaaaaacta gctctcttgc agatgaagat ggtagctctg gagatcatac gaaactatga 840
ctttaaggtc attgaaggtc acaaggctga accaattcct tctatctctc tccgtatgaa 900
acatggctct taacttcacg tcacaaagaa gatatgatta ttatgcttcg ttgcttctta 960
cggaacctat taacttttcc ttattttaa atgtgttact ctatgtttgt cccacgttat 1020
aactactgtt attacgtact aagtacggtg ttgtgcccaac gtcatgtctca taaataaatt 1080
aatatcgtca aataaagtatt agacatcct cgctcat

(2) INFORMATION FOR SEQ ID NO:2725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..311
(D) OTHER INFORMATION: / Ceres Seq. ID 1574030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2725:

Leu Met Thr Gly Tyr Asp Pro Met Ser Leu Ser Ile Glu Ile Leu Glu
1 5 10 15
Val Glu Phe Gly Glu Ala Ala Asp Ile Gly Glu Glu Ala Ile Tyr Tyr
20 25 30
Arg His Phe Lys Pro Val Ile Leu Trp Arg Leu Gln Asn Trp Ile Gly
35 40 45
Ile Gly Leu Glu Arg Lys Met Arg Thr Ala Leu Ala Thr Val Asn Arg
50 55 60
Met Phe Ala Lys Ile Ile Ser Ser Arg Arg Lys Glu Glu Ile Ser Arg
65 70 75 80
Ala Lys Thr Glu Pro Tyr Ser Lys Asp Ala Leu Thr Tyr Tyr Met Asn
85 90 95
Val Asp Thr Ser Ser Lys Tyr Lys Leu Leu Lys Pro Asn Lys Asp Lys Phe
100 105 110
Ile Arg Asp Val Ile Phe Ser Leu Val Leu Ala Gly Arg Asp Thr Thr
115 120 125
Ser Ser Val Leu Thr Trp Phe Phe Trp Leu Leu Ser Lys His Pro Gln
130 135 140
Val Met Ala Lys Leu Arg His Glu Ile Asn Thr Lys Phe Asp Asn Glu
145 150 155 160
Asp Leu Glu Lys Leu Val Tyr Leu His Ala Ala Leu Ser Glu Ser Met
165 170 175
Arg Leu Tyr Pro Pro Leu Pro Phe Asn His Lys Ser Pro Ala Lys Pro
180 185 190
Asp Val Leu Pro Ser Gly His Lys Val Asp Ala Asn Ser Lys Ile Val
195 200 205
Ile Cys Ile Tyr Ala Leu Gly Arg Met Arg Ser Val Trp Gly Glu Asp
210 215 220
Ala Leu Asp Phe Lys Pro Glu Arg Trp Ile Ser Asp Asn Gly Gly Leu
225 230 235 240
Arg His Glu Pro Ser Tyr Lys Phe Met Ala Phe Asn Ser Gly Pro Arg
245 250 255
Thr Cys Leu Gly Lys Asn Leu Ala Leu Leu Gln Met Lys Met Val Ala
260 265 270
Leu Glu Ile Ile Arg Asn Tyr Asp Phe Lys Val Ile Glu Gly His Lys
275 280 285
Val Glu Pro Ile Pro Ser Ile Leu Leu Arg Met Lys His Gly Leu Lys
290 295 300
Val Thr Val Thr Lys Lys Ile
305 310

(2) INFORMATION FOR SEQ ID NO:2726:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..310
(D) OTHER INFORMATION: / Ceres Seq. ID 1574031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2726:

Met Thr Gly Tyr Asp Pro Met Ser Leu Ser Ile Glu Ile Leu Glu Val
1 5 10 15
Glu Phe Gly Glu Ala Ala Asp Ile Gly Glu Glu Ala Ile Tyr Tyr Arg
20 30
His Phe Lys Pro Val Ile Leu Trp Arg Leu Gln Asn Trp Ile Gly Ile
35 40 45
Gly Leu Glu Arg Lys Met Arg Thr Ala Leu Ala Thr Val Asn Arg Met
50 55 60
Phe Ala Lys Ile Ile Ser Ser Arg Arg Lys Glu Glu Ile Ser Arg Ala
65 70 75 80
Lys Thr Glu Pro Tyr Ser Lys Asp Ala Leu Thr Tyr Tyr Met Asn Val
85 90 95
Asp Thr Ser Lys Tyr Lys Leu Leu Lys Pro Asn Lys Asp Lys Phe Ile
100 105 110
Arg Asp Val Ile Phe Ser Leu Val Leu Ala Gly Arg Asp Thr Thr Ser
115 120 125
Ser Val Leu Thr Trp Phe Phe Trp Leu Leu Ser Lys His Pro Gln Val
130 135 140
Met Ala Lys Leu Arg His Glu Ile Asn Thr Lys Phe Asp Asn Glu Asp
145 150 155 160
Leu Glu Lys Leu Val Tyr Leu His Ala Ala Leu Ser Glu Ser Met Arg
165 170 175
Leu Tyr Pro Pro Leu Pro Phe Asn His Lys Ser Pro Ala Lys Pro Asp
180 185 190
Val Leu Pro Ser Gly His Lys Val Asp Ala Asn Ser Lys Ile Val Ile
195 200 205
Cys Ile Tyr Ala Leu Gly Arg Met Arg Ser Val Trp Gly Glu Asp Ala
210 215 220
Leu Asp Phe Lys Pro Glu Arg Trp Ile Ser Asp Asn Gly Gly Leu Arg
225 230 235 240
His Glu Pro Ser Tyr Lys Phe Met Ala Phe Asn Ser Gly Pro Arg Thr
245 250 255
Cys Leu Gly Lys Asn Leu Ala Leu Leu Gln Met Lys Met Val Ala Leu
260 265 270
Glu Ile Ile Arg Asn Tyr Asp Phe Lys Val Ile Glu Gly His Lys Val
275 280 285
Glu Pro Ile Pro Ser Ile Leu Leu Arg Met Lys His Gly Leu Lys Val
290 295 300
Thr Val Thr Lys Lys Ile
305 310

(2) INFORMATION FOR SEQ ID NO:2727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..304
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2727:

Met Ser Leu Ser Ile Glu Ile Leu Glu Val Glu Phe Gly Glu Ala Ala
1 5 10 15
Asp Ile Gly Glu Glu Ala Ile Tyr Tyr Arg His Phe Lys Pro Val Ile
20 25 30
Leu Trp Arg Leu Gln Asn Trp Ile Gly Ile Gly Leu Glu Arg Lys Met
35 40 45
Arg Thr Ala Leu Ala Thr Val Asn Arg Met Phe Ala Lys Ile Ile Ser
50 55 60

Ser Arg Arg Lys Glu Glu Ile Ser Arg Ala Lys Thr Glu Pro Tyr Ser
65 70 75 80
Lys Asp Ala Leu Thr Tyr Tyr Met Asn Val Asp Thr Ser Lys Tyr Lys
85 90 95
Leu Leu Lys Pro Asn Lys Asp Lys Phe Ile Arg Asp Val Ile Phe Ser
100 105 110
Leu Val Leu Ala Gly Arg Asp Thr Thr Ser Ser Val Leu Thr Trp Phe
115 120 125
Phe Trp Leu Leu Ser Lys His Pro Gln Val Met Ala Lys Leu Arg His
130 135 140
Glu Ile Asn Thr Lys Phe Asp Asn Glu Asp Leu Glu Lys Leu Val Tyr
145 150 155 160
Leu His Ala Ala Leu Ser Glu Ser Met Arg Leu Tyr Pro Pro Leu Pro
165 170 175
Phe Asn His Lys Ser Pro Ala Lys Pro Asp Val Leu Pro Ser Gly His
180 185 190
Lys Val Asp Ala Asn Ser Lys Ile Val Ile Cys Ile Tyr Ala Leu Gly
195 200 205
Arg Met Arg Ser Val Trp Gly Glu Asp Ala Leu Asp Phe Lys Pro Glu
210 215 220
Arg Trp Ile Ser Asp Asn Gly Gly Leu Arg His Glu Pro Ser Tyr Lys
225 230 235 240
Phe Met Ala Phe Asn Ser Gly Pro Arg Thr Cys Leu Gly Lys Asn Leu
245 250 255
Ala Leu Leu Gln Met Lys Met Val Ala Leu Glu Ile Ile Arg Asn Tyr
260 265 270
Asp Phe Lys Val Ile Glu Gly His Lys Val Glu Pro Ile Pro Ser Ile
275 280 285
Leu Leu Arg Met Lys His Gly Leu Lys Val Thr Val Thr Lys Lys Ile
290 295 300

(2) INFORMATION FOR SEQ ID NO:2728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..923
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2728:

agtgcgagaga	aagataaaca	aaatggcggc	aatcagaacg	atgacgaaca	tgattctacg	60
cgagttcatc	catcatccac	ttctcttcca	ctcttcatcg	aaatcgtgtc	aatctctttt	120
taccatgtct	ccgtctcact	cccctaattt	ctccaaattca	ccctaattcc	cgggtctgat	180
ccgtccgatg	tgccggcatcg	acctccgggtg	gaagcgggtgg	tgatcggaaa	gtctcttcac	240
ggtttgtcgca	ggtgcaaacg	atgcttcatg	aagccgaaga	gagagctagt	tcgcgtggca	300
atgagcctac	tcctcaaatc	actctagaca	atgttacact	taactttgct	agaagtgggtg	360
gtcctgtagg	ccagaatgtg	aacaaattga	ataccaaaagt	agatatgcgc	ttcaatgtta	420
agaacgcgta	ttgctgagtg	gacaggatca	gagagaaaaat	cttactgacg	gagaagaatc	480
ggatcaacaa	ggatgggtgaa	cttgtgatat	cttcaaccaa	aaccagaacg	cagaagaagca	540
acatcgacga	tgccacttgaa	aaactacagg	cgatcattga	tgccgctctt	tatgttccac	600
ctccaccatc	agaagaacag	aagaagaaaa	tagtaaaagt	ggctgcgaaa	gctgacataa	660
aacgacttaa	aagcaaaaaa	gttctgtcag	acaagaaaat	tgccgagaaga	agcccgcgta	720
gtttacgatga	ttaaaactta	aaccatacaa	tggagttccg	gtgtattcta	aagcttttaa	780
cttaaaatga	ttgttatatt	cttggaaatt	aatgtaaacac	aaacaacaaa	tcatccaata	840
aaaattgcag	tatatggagt	tttatgtaca	aaccactctt	atacaaaata	tgaacaaaaa	900
aagtatcaaa	cataaacattc	ctc				

(2) INFORMATION FOR SEQ ID NO:2729:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..157
(D) OTHER INFORMATION: / Ceres Seq. ID 1574039
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2729:
Met Leu His Glu Ala Glu Glu Arg Ala Ser Ser Ala Gly Asn Glu Pro
1 5 10 15
Thr Pro Gln Ile Thr Leu Asp Asn Val Thr Leu Asn Phe Ala Arg Ser
20 25 30
Gly Gly Pro Gly Gly Gln Asn Val Asn Lys Leu Asn Thr Lys Val Asp
35 40 45
Met Arg Phe Asn Val Lys Asn Ala Tyr Trp Leu Ser Asp Arg Ile Arg
50 55 60
Glu Lys Ile Leu Leu Thr Glu Lys Asn Arg Ile Asn Lys Asp Gly Glu
65 70 75 80
Leu Val Ile Ser Ser Thr Lys Thr Arg Thr Gln Lys Gly Asn Ile Asp
85 90 95
Asp Ala Leu Glu Lys Leu Gln Ala Ile Ile Asp Ala Ala Ser Tyr Val
100 105 110
Pro Pro Pro Pro Ser Glu Glu Gln Lys Lys Lys Ile Val Lys Leu Ala
115 120 125
Ala Lys Ala Asp Asn Lys Arg Leu Lys Ser Lys Lys Val Leu Ser Asp
130 135 140
Lys Lys Ser Ala Arg Arg Ser Arg Gly Ser Tyr Asp Asp
145 150 155
(2) INFORMATION FOR SEQ ID NO:2730:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..109
(D) OTHER INFORMATION: / Ceres Seq. ID 1574040
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2730:
Met Arg Phe Asn Val Lys Asn Ala Tyr Trp Leu Ser Asp Arg Ile Arg
1 5 10 15
Glu Lys Ile Leu Leu Thr Glu Lys Asn Arg Ile Asn Lys Asp Gly Glu
20 25 30
Leu Val Ile Ser Ser Thr Lys Thr Arg Thr Gln Lys Gly Asn Ile Asp
35 40 45
Asp Ala Leu Glu Lys Leu Gln Ala Ile Ile Asp Ala Ala Ser Tyr Val
50 55 60
Pro Pro Pro Pro Ser Glu Glu Gln Lys Lys Lys Ile Val Lys Leu Ala
65 70 75 80
Ala Lys Ala Asp Asn Lys Arg Leu Lys Ser Lys Lys Val Leu Ser Asp
85 90 95
Lys Lys Ser Ala Arg Arg Ser Arg Gly Ser Tyr Asp Asp
100 105
(2) INFORMATION FOR SEQ ID NO:2731:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 506 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..506
(D) OTHER INFORMATION: / Ceres Seq. ID 1574041
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2731:
ggactatctta ttacttggtc cacaataat gtacttagta cgcgcccaaca agtatatctg 60
cgtaaaactag gtggtgcgaa gccaaatatg gatgaaaacg caagcaaaaat aataagtgcg 120
ggacgagcaaa agagatctat tgctcagcct gacgatgctg gcgaacatt tagacaatta 180
aaagagcaag agaagcgag Caagaagaac aaggcggttg cgaagatac agttgaattg 240
gtagaagaat ctcagtctga atcagaagaa gggtctgatg atgagggaaga agaggctcgt 300
gaaggagcgt tagCttcgag cacaacaagc aagccgcttc ctgaggttgg ccaacgaaga 360
agcaaaaagat cgaagcgga acgcactgta tagaaccaaa gcaaacgaaa ttgcaagtaa 420
ggaagagaaa agagagagat ttgaatcttg ttccttagtt tgatcttttg atatattatt 480
gcatacacca tgtccggtaa ttatcc

(2) INFORMATION FOR SEQ ID NO:2732:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..130
(D) OTHER INFORMATION: / Ceres Seq. ID 1574042
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2732:
Gly Leu Ser Ile Tyr Trp Leu Thr Asn Asn Val Leu Ser Thr Ala Gln
1 5 10 15
Gln Val Tyr Leu Arg Lys Leu Gly Gly Ala Lys Pro Asn Met Asp Glu
20 25 30
Asn Ala Ser Lys Ile Ile Ser Ala Gly Arg Ala Lys Arg Ser Ile Ala
35 40 45
Gln Pro Asp Asp Ala Gly Glu Thr Phe Arg Gln Leu Lys Glu Gln Glu
50 55 60
Lys Arg Ser Lys Lys Asn Lys Ala Val Ala Lys Asp Thr Val Glu Leu
65 70 75 80
Val Glu Glu Ser Gln Ser Glu Ser Glu Glu Gly Ser Asp Asp Glu Glu
85 90 95
Glu Glu Ala Arg Glu Gly Ala Leu Ala Ser Ser Thr Thr Ser Lys Pro
100 105 110
Leu Pro Glu Val Gly Gln Arg Arg Ser Lys Arg Ser Lys Arg Lys Arg
115 120 125
Thr Val
130

(2) INFORMATION FOR SEQ ID NO:2733:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..101
(D) OTHER INFORMATION: / Ceres Seq. ID 1574043
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2733:
Met Asp Glu Asn Ala Ser Lys Ile Ile Ser Ala Gly Arg Ala Lys Arg
1 5 10 15

Ser Ile Ala Gln Pro Asp Asp Ala Gly Glu Thr Phe Arg Gln Leu Lys
20 25 30
Glu Gln Glu Lys Arg Ser Lys Lys Asn Lys Ala Val Ala Lys Asp Thr
35 40 45
Val Glu Leu Val Glu Glu Ser Gln Ser Glu Ser Glu Glu Gly Ser Asp
50 55 60
Asp Glu Glu Glu Glu Ala Arg Glu Gly Ala Leu Ala Ser Ser Thr Thr
65 70 75 80
Ser Lys Pro Leu Pro Glu Val Gly Gln Arg Arg Ser Lys Arg Ser Lys
85 90 95
Arg Lys Arg Thr Val
100

(2) INFORMATION FOR SEQ ID NO:2734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1496
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2734:

acggaccgac gcttgctctg tgctcatcgt tctcttcttc accttattcca tgggtggttta 60
gttcatgatt ttggagtttt taagaacttt ttctactaga actcgaatc ttccaagtttc 120
tggtttttat tcgataagta ctagtataat gcgagatatac aaagtcacaa ctgattcttaa 180
ggagttttcta acatcatctg atgaagaaga agaatacagtt tccattagag tgcgtcttcc 240
ttcttctctg agtagtggtta aatcgacgcc tgagattgag aaaaagtatg ttcacagagt 300
ttacgatacgc attgctcttc attttagctc tactaggttt gctaagtggc ctaaaagttgc 360
tgcttctctc gaatcgttac cgtctggatc ggtgattctc gatgccggtt gcggtaacgg 420
gaagtatttg ggggtgaatc ctagtgtgtt ctctaatggt tgtgataaa gtcactcttt 480
gattaaaaatc tgtctcgata aagggaaga ggttttgggt gcagatgctg ttaatctKbc 540
ttatagagag gagtttggcg atcgacgatc ttcatagagc gttttgcatc atttgagtagc 600
agagaataga aggaagaaga ctattgaaga gcttgctcgt gttgttaagc ctgggtgatt 660
tgtttctcatt actgtctcggg ctgctgaaca ggagatatac tcgttgctta cgaataggac 720
acctttgtct gctaagtatg ttgaggaatg ggttggtcca ggtagtcga tgaatagtc 780
tcgtgtgagg aacaatccgt tcttttagtct tgagagtatc ccagagactg aggtgagtagc 840
aaaggagcaa aaggttgaga acagtcagtt catcggctct gagagcattc cagagagcga 900
ggagagtagc acagagcaga aaggtgagag tattattcca gaaaccaaaag ctagtatagt 960
agagcaaaag atgagaatct tgttgaggag tcattggagg ctctgaagaa gagtcaacaa 1020
gagtactttg tgccatggca ttaccatac caccgtgctg aagtgagtagg tgcattctgcg 1080
tctgcacttg caagtgggct tgcaaaagaa gatgatagaa aaggagctgt tgtgtacaac 1140
agatactacc atgtcttttag cgaaggcgaa cttgaaaggt tggcatctgg agtaggcaat 1200
gcaatgatag ttgatagatt ttctgacaag tcgaattggt gtattgtctt tcagaaagaa 1260
gctttaaacc aagattgaac ttgtgtttca aacttatcaa atctttgtgac tattgtgaac 1320
ccattgcatc tgtaatcggg aattattatt gcatttttca tggttgtagt ttgagattct 1380
gtggcagctc attttccctg caatttgggt tctttaaagg gttttgtatt atgtgtaaaa 1440
caaatcaaaag aaagaatctt ctctacatga taacaaaaat gtcagaaaaa tgattt

(2) INFORMATION FOR SEQ ID NO:2735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..313
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2735:

Met Ile Leu Asp Val Leu Arg Thr Phe Ser Thr Arg Thr Arg Asn Leu
1 5 10 15
Pro Ser Ser Gly Phe Tyr Ser Ile Ser Thr Ser Ile Met Arg Asp Ile
20 25 30
Lys Val Lys Ser Asp Ser Lys Glu Phe Leu Thr Ser Ser Asp Glu Glu
35 40 45
Glu Glu Ser Val Ser Ile Arg Val Ser Ser Ser Ser Leu Ser Ser
50 55 60
Val Lys Ser Thr Pro Glu Ile Glu Lys Lys Tyr Val His Arg Val Tyr
65 70 75 80
Asp Ala Ile Ala Pro His Phe Ser Ser Thr Arg Phe Ala Lys Trp Pro
85 90 95
Lys Val Ala Ala Phe Leu Glu Ser Leu Pro Ser Gly Ser Val Ile Leu
100 105 110
Asp Ala Gly Cys Gly Asn Gly Lys Tyr Leu Gly Leu Asn Pro Ser Cys
115 120 125
Phe Phe Ile Gly Cys Asp Ile Ser His Pro Leu Ile Lys Ile Cys Ser
130 135 140
Asp Lys Gly Gln Glu Val Leu Val Ala Asp Ala Val Asn Xaa Xaa Tyr
145 150 155 160
Arg Glu Glu Phe Gly Asp Ala Ala Ile Ser Ile Ala Val Leu His His
165 170 175
Leu Ser Thr Glu Asn Arg Arg Lys Lys Ala Ile Glu Glu Leu Val Arg
180 185 190
Val Val Lys Pro Gly Gly Phe Val Leu Ile Thr Val Trp Ala Ala Glu
195 200 205
Gln Glu Asp Thr Ser Leu Leu Thr Lys Trp Thr Pro Leu Ser Ala Lys
210 215 220
Tyr Val Glu Glu Trp Val Gly Pro Gly Ser Pro Met Asn Ser Pro Arg
225 230 235 240
Val Arg Asn Asn Pro Phe Phe Ser Leu Glu Ser Ile Pro Glu Thr Glu
245 250 255
Val Ser Thr Lys Glu Gln Lys Val Glu Asn Ser Gln Phe Ile Gly Leu
260 265 270
Glu Ser Ile Pro Glu Ser Glu Glu Ser Xaa Arg Glu Gln Lys Gly Glu
275 280 285
Ser Ile Ile Pro Glu Thr Lys Ala Ser Ile Val Glu Gln Arg Met Arg
290 295 300
Asn Leu Leu Arg Ser His Trp Arg Leu
305 310

(2) INFORMATION FOR SEQ ID NO:2736:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 285 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..285

(D) OTHER INFORMATION: / Ceres Seq. ID 1574046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2736:

Met Arg Asp Ile Lys Val Lys Ser Asp Ser Lys Glu Phe Leu Thr Ser
1 5 10 15
Ser Asp Glu Glu Glu Glu Ser Val Ser Ile Arg Val Ser Ser Ser Ser
20 25 30
Ser Leu Ser Ser Val Lys Ser Thr Pro Glu Ile Glu Lys Lys Tyr Val
35 40 45
His Arg Val Tyr Asp Ala Ile Ala Pro His Phe Ser Ser Thr Arg Phe
50 55 60
Ala Lys Trp Pro Lys Val Ala Ala Phe Leu Glu Ser Leu Pro Ser Gly

65	70	75	80
Ser Val Ile Leu	Asp Ala Gly Cys Gly Asn Gly Lys Tyr Leu Gly Leu		
	85	90	95
Asn Pro Ser Cys Phe Phe Ile Gly Cys Asp Ile Ser His Pro Leu Ile			
	100	105	110
Lys Ile Cys Ser Asp Lys Gly Gln Glu Val Leu Val Ala Asp Ala Val			
	115	120	125
Asn Xaa Xaa Tyr Arg Glu Glu Phe Gly Asp Ala Ala Ile Ser Ile Ala			
	130	135	140
Val Leu His His Leu Ser Thr Glu Asn Arg Arg Lys Lys Ala Ile Glu			
	145	150	155
Glu Leu Val Arg Val Val Lys Pro Gly Gly Phe Val Leu Ile Thr Val			
	165	170	175
Trp Ala Ala Glu Gln Glu Asp Thr Ser Leu Leu Thr Lys Trp Thr Pro			
	180	185	190
Leu Ser Ala Lys Tyr Val Glu Glu Trp Val Gly Pro Gly Ser Pro Met			
	195	200	205
Asn Ser Pro Arg Val Arg Asn Asn Pro Phe Phe Ser Leu Glu Ser Ile			
	210	215	220
Pro Glu Thr Glu Val Ser Thr Lys Glu Gln Lys Val Glu Asn Ser Gln			
	225	230	235
Phe Ile Gly Leu Glu Ser Ile Pro Glu Ser Glu Glu Ser Xaa Arg Glu			
	245	250	255
Gln Lys Gly Glu Ser Ile Ile Pro Glu Thr Lys Ala Ser Ile Val Glu			
	260	265	270
Gln Arg Met Arg Asn Leu Leu Arg Ser His Trp Arg Leu			
	275	280	285

(2) INFORMATION FOR SEQ ID NO:2737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1342
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2737:

attgtgttgc	cttcttcttt	ctttctgact	caaaacctta	aatcaattct	cgcgattaag	60
caaaacctta	gatttattct	actcttcgaa	gtcgatttca	atggaaaggt	ctcctgcagc	120
catcgcgagg	aagacatggg	agctagagaa	caacattctc	ccagtggaac	caaccgattc	180
agcctccgac	agtatattcc	actacgacga	cgcttcacaa	gcacaaatcc	agcaggagaa	240
gccatggccc	tcctgatccta	actacttcaa	gcgcgttcac	atctcagccc	ttgctctctt	300
caagatgggt	gttcacgctc	gctccgggtg	cacaaatcag	atcatgggtc	ttatgcaggg	360
taaaaccgag	gggtgatccaa	tcactgttat	ggatgctttt	gctttgcgtg	ttgaagggtac	420
tgagactagg	gttaatgctc	agtctgatgc	ctatgagtat	atggttgaat	acctctcagc	480
cagcaagctg	gctgggaggt	tgagagaacgt	tgttggatgg	tatcactctc	acctggggtta	540
tggatgttgg	ctctcgggta	ttgatgtttc	gacacagatg	cttaaccaac	agtatcagga	600
gccattctta	gctgtttgtta	ttgatccaac	aaggactgtt	tcggctggta	aggttgagat	660
tgggggcattc	agaacatatc	cagagggaca	taagatctcg	gatgatcatg	tttctgagta	720
tcagactatc	ccctcttaaca	agattgagga	ctttggtgta	cattgcaaac	agtaactactc	780
attggacatc	acttatttca	agtcattctc	cgatagtcac	cttctggatc	tCcttcggaa	840
caagtaactg	gtgaacatc	ttttcttctc	cccaactgtt	ggcaatggag	actatgtttg	900
cgggcacaata	tcgactctgg	ctgagaagct	cgagcaagcg	gagagtcacg	tcgctaactc	960
ccggttatgga	ggaattgcgc	cagccgggtca	ccaaaggagg	aaaggagtag	agcctccaact	1020
cgcgaagata	actcgggata	gtgcacaagt	aactgtcgag	caggtccatg	gactaatgtc	1080
acaggttatc	aaagacatct	tggtcaaatc	cgctcgtcag	tccaagaagt	ctgcgtcagca	1140
ctcatcagat	ccagagccca	tgattacatc	gtgaagttgg	tctattcttt	tggtttttttg	1200
ctgcggaaat	tgtactatcg	tttgacccag	tttatgaggc	aatgcccaat	gttccctata	1260
tctctagtgt	agtatctgct	tcagacaaag	atctttgggt	tattaatga	cattaacata	1320

aatcgatcat tatgtttttg tg

(2) INFORMATION FOR SEQ ID NO:2738:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..357

(D) OTHER INFORMATION: / Ceres Seq. ID 1574048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2738:

Met Glu Gly Ser Ser Ser Ala Ile Ala Arg Lys Thr Trp Glu Leu Glu
1 5 10 15
Asn Asn Ile Leu Pro Val Glu Pro Thr Asp Ser Ala Ser Asp Ser Ile
20 25 30
Phe His Tyr Asp Asp Ala Ser Gln Ala Lys Ile Gln Glu Lys Pro
35 40 45
Trp Ala Ser Asp Pro Asn Tyr Phe Lys Arg Val His Ile Ser Ala Leu
50 55 60
Ala Leu Leu Lys Met Val Val His Ala Arg Ser Gly Gly Thr Ile Glu
65 70 75 80
Ile Met Gly Leu Met Gln Gly Lys Thr Glu Gly Asp Thr Ile Ile Val
85 90 95
Met Asp Ala Phe Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn
100 105 110
Ala Gln Ser Asp Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Ser
115 120 125
Lys Leu Ala Gly Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His
130 135 140
Pro Gly Tyr Gly Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Met
145 150 155 160
Leu Asn Gln Gln Tyr Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro
165 170 175
Thr Arg Thr Val Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr
180 185 190
Tyr Pro Glu Gly His Lys Ile Ser Asp Asp His Val Ser Glu Tyr Gln
195 200 205
Thr Ile Pro Leu Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln
210 215 220
Tyr Tyr Ser Leu Asp Ile Thr Tyr Phe Lys Ser Ser Leu Asp Ser His
225 230 235 240
Leu Leu Asp Leu Leu Arg Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser
245 250 255
Ser Pro Leu Leu Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp
260 265 270
Leu Ala Glu Lys Leu Glu Gln Ala Glu Ser Gln Leu Ala Asn Ser Arg
275 280 285
Tyr Gly Gly Ile Ala Pro Ala Gly His Gln Arg Arg Lys Glu Asp Glu
290 295 300
Pro Gln Leu Ala Lys Ile Thr Arg Asp Ser Ala Lys Ile Thr Val Glu
305 310 315 320
Gln Val His Gly Leu Met Ser Gln Val Ile Lys Asp Ile Leu Phe Asn
325 330 335
Ser Ala Arg Gln Ser Lys Lys Ser Ala Asp Asp Ser Ser Asp Pro Glu
340 345 350
Pro Met Ile Thr Ser
355

(2) INFORMATION FOR SEQ ID NO:2739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..289
(D) OTHER INFORMATION: / Ceres Seq. ID 1574049
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2739:

Met Val Val His Ala Arg Ser Gly Gly Thr Ile Glu Ile Met Gly Leu
1 5 10 15
Met Gln Gly Lys Thr Glu Gly Asp Thr Ile Ile Val Met Asp Ala Phe
20 25 30
Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn Ala Gln Ser Asp
35 40 45
Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Ser Lys Leu Ala Gly
50 55 60
Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His Pro Gly Tyr Gly
65 70 75 80
Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Met Leu Asn Gln Gln
85 90 95
Tyr Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro Thr Arg Thr Val
100 105 110
Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr Tyr Pro Glu Gly
115 120 125
His Lys Ile Ser Asp Asp His Val Ser Glu Tyr Gln Thr Ile Pro Leu
130 135 140
Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln Tyr Tyr Ser Leu
145 150 155 160
Asp Ile Thr Tyr Phe Lys Ser Ser Leu Asp Ser His Leu Leu Asp Leu
165 170 175
Leu Arg Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser Ser Pro Leu Leu
180 185 190
Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp Leu Ala Glu Lys
195 200 205
Leu Glu Gln Ala Glu Ser Gln Leu Ala Asn Ser Arg Tyr Gly Gly Ile
210 215 220
Ala Pro Ala Gly His Gln Arg Arg Lys Glu Asp Glu Pro Gln Leu Ala
225 230 235 240
Lys Ile Thr Arg Asp Ser Ala Lys Ile Thr Val Glu Gln Val His Gly
245 250 255
Leu Met Ser Gln Val Ile Lys Asp Ile Leu Phe Asn Ser Ala Arg Gln
260 265 270
Ser Lys Lys Ser Ala Asp Asp Ser Ser Asp Pro Glu Pro Met Ile Thr
275 280 285
Ser

(2) INFORMATION FOR SEQ ID NO:2740:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..276
(D) OTHER INFORMATION: / Ceres Seq. ID 1574050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2740:

Met Gly Leu Met Gln Gly Lys Thr Glu Gly Asp Thr Ile Ile Val Met

1	5	10	15
Asp Ala Phe Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn Ala			
20	25	30	35
Gln Ser Asp Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Ser Lys			
40	45	50	55
Leu Ala Gly Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His Pro			
60	65	70	75
Gly Tyr Gly Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Met Leu			
80	85	90	95
Asn Gln Gln Tyr Gln Glu Pro Phe Leu Ala Val Ile Asp Pro Thr			
100	105	110	115
Arg Thr Val Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr Tyr			
120	125	130	135
Pro Glu Gly His Lys Ile Ser Asp Asp His Val Ser Glu Tyr Gln Thr			
140	145	150	155
Ile Pro Leu Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln Tyr			
160	165	170	175
Tyr Ser Leu Asp Ile Thr Tyr Phe Lys Ser Ser Leu Asp Ser His Leu			
180	185	190	195
Leu Asp Leu Leu Arg Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser Ser			
200	205	210	215
Pro Leu Leu Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp Leu			
220	225	230	235
Ala Glu Lys Leu Glu Gln Ala Glu Ser Gln Leu Ala Asn Ser Arg Tyr			
240	245	250	255
Gly Gly Ile Ala Pro Ala Gly His Gln Arg Arg Lys Glu Asp Glu Pro			
260	265	270	275
Gln Leu Ala Lys Ile Thr Arg Asp Ser Ala Lys Ile Thr Val Glu Gln			
280	285	290	295
Val His Gly Leu Met Ser Gln Val Ile Lys Asp Ile Leu Phe Asn Ser			
300	305	310	315
Ala Arg Gln Ser Lys Lys Ser Ala Asp Asp Ser Ser Pro Glu Pro			
320	325	330	335
Met Ile Thr Ser			

(2) INFORMATION FOR SEQ ID NO:2741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1950 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1950
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2741:

aacagagtcg	cacacactaa	aatggcggtt	cgcgttttgc	tctcttcttc	actcaccgca	60
ctctctcatc	tctccgcggt	tctctcttct	ttcgcccgtt	cttctctccg	cgacgttgac	120
gaagagatc	tcagcttctc	cgaagatctc	aaagaagacg	acgttccggc	cgctgactca	180
ctctcttctc	caactggatt	tgacgaattc	gaaggaggag	aagaagaaga	tcccgatgat	240
tacaacgacg	atgacgatga	agaagagagt	ttttccgata	taggtaattc	ggattccgat	300
cogttaccga	cgccggagat	tgatgagaaa	gacgttgtgg	ttatcaagga	cggttaacttc	360
actgatgtga	ttgagaataa	tcaatacgtt	ttgggttgagt	tttatgtccc	gtgggtgtgt	420
cattgtcagt	ctcttgcctc	tgagtatgct	gcgtctgcca	cgagctctaa	ggaagatggt	480
gtgtgttttg	ctaagattga	tgccgaggag	gagaatgagt	tagctcaagg	gtatcgttgt	540
cagggccttc	cgacgcttct	ttttctcggt	gatgtgtgag	acaagcctta	cactggagga	600
aggactaaag	aaacaattgt	gacatgggtg	aagaagaaga	ttggtcctgg	tgtgtataat	660
ctaactacat	tagatgatgc	tgagaaaagt	ttgacttctg	ggaacaaaat	tgtttttgga	720
tacttgaact	ccttggtggg	tggtgagcac	gatcagctta	atgctgtctc	caaagctgaa	780
gcagatgtga	acttttatca	aacagtgaat	cctgatgttg	caaagatggt	tcaccttgat	840

ccggagtgcta	aaaggcctgc	tcttgctcta	gttaagaagg	aagaggagaa	aattagccat	900
tttgatggag	aatttggttaa	gtctgtctcta	gttagttttg	tgctctgccaa	caagcttgtct	960
ttggctctctg	ttttccacag	agagactgct	ccggaatttt	ttgagagtgc	taatcaagaaa	1020
cagtttgtgt	tggtttgtaac	caaaaatgaa	tctgaaaagg	ttcttacgga	atttcaagaa	1080
gcagcgaaat	cattcaaaagg	aaagctcatc	tttgtatctg	tggtatctgga	taatgaggat	1140
taagggaagc	cagtcgctga	atacttttgt	gtgtctggaa	atggctccaa	acttattggc	1200
tacacaggga	atgaagacca	taaaaaatac	tttttcgatg	gcgagatcca	gtcagataaa	1260
attaagatat	ttgggggagc	tttctggaac	gacaagttaa	agccttttca	taagtacagc	1320
ccattctctg	aaaagaacga	tgaagatgtg	aaaatagtgg	ttggagataa	ctttgatgaa	1380
attgtctctg	acgatttctaa	agatgtgctt	ctcgaggtct	acgcaccatg	gtgtggccat	1440
tgccaagccc	ttgagccaat	gtataacaaa	cttgccaagc	atttacgaag	tattgattct	1500
ctcgctcata	ccaagatgga	tggaacaacc	aatgaacatc	ccaaggcaaa	ggctgagggg	1560
ttccctacca	ttctctctct	ccCtgcgggc	aacaagactt	cagagccgat	tactgtagat	1620
acagaccgca	ctgTggttgc	attttacaag	ttcttaagga	aacacgcaac	gatccattc	1680
aaactggaga	aacctgcctc	aaccgaatca	cctaaaactg	cagagtccac	accaaaagta	1740
gaaactacgc	agaccaaaga	atcacccgat	agcacgacaa	agagtacgca	aagtgaactg	1800
aaggacgaat	tggtatcaga	aaagggatata	atatatatta	catgtctcct	taagtgtgta	1860
tatgtatgat	cagaattgtc	acatcatgag	tttgacttag	ataaagatgg	gaattaaagt	1920
aattttagtt	ttgagaaga	caatttcttc				

(2) INFORMATION FOR SEQ ID NO:2742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..604
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2742:

Asn	Arg	Val	Ala	His	Thr	Lys	Met	Ala	Phe	Arg	Val	Leu	Leu	Leu	Phe
1				5					10					15	
Ser	Leu	Thr	Ala	Leu	Leu	Ile	Phe	Ser	Ala	Val	Ser	Pro	Ser	Phe	Ala
				20				25					30		
Ala	Ser	Ser	Ser	Asp	Asp	Val	Asp	Glu	Asp	Leu	Ser	Phe	Leu	Glu	
				35			40				45				
Asp	Leu	Lys	Glu	Asp	Asp	Val	Pro	Gly	Ala	Asp	Ser	Leu	Ser	Ser	Ser
				50			55				60				
Thr	Gly	Phe	Asp	Glu	Phe	Glu	Gly	Gly	Glu	Glu	Asp	Pro	Asp	Met	
65				70					75						
Tyr	Asn	Asp	Asp	Asp	Asp	Glu	Glu	Gly	Asp	Phe	Ser	Asp	Leu	Gly	Asn
				85					90					95	
Pro	Asp	Ser	Asp	Pro	Leu	Pro	Thr	Pro	Glu	Ile	Asp	Glu	Lys	Asp	Val
				100				105					110		
Val	Val	Ile	Lys	Glu	Arg	Asn	Phe	Thr	Asp	Val	Ile	Glu	Asn	Asn	Gln
				115			120					125			
Tyr	Val	Leu	Val	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Gln	Ser
				130			135				140				
Leu	Ala	Pro	Glu	Tyr	Ala	Ala	Ala	Ala	Thr	Glu	Leu	Lys	Glu	Asp	Gly
145				150					155					160	
Val	Val	Leu	Ala	Lys	Ile	Asp	Ala	Thr	Glu	Glu	Asn	Glu	Leu	Ala	Gln
				165				170						175	
Glu	Tyr	Arg	Val	Gln	Gly	Phe	Pro	Thr	Leu	Leu	Phe	Phe	Val	Asp	Gly
				180				185					190		
Glu	His	Lys	Pro	Tyr	Thr	Gly	Gly	Arg	Thr	Lys	Glu	Thr	Ile	Val	Thr
				195			200					205			
Trp	Val	Lys	Lys	Lys	Ile	Gly	Pro	Gly	Val	Tyr	Asn	Leu	Thr	Thr	Leu
				210			215				220				
Asp	Asp	Ala	Glu	Lys	Val	Leu	Thr	Ser	Gly	Asn	Lys	Val	Val	Leu	Gly
225				230					235						

Tyr Leu Asn Ser Leu Val Gly Val Glu His Asp Gln Leu Asn Ala Ala
245 250 255
Ser Lys Ala Glu Asp Asp Val Asn Phe Tyr Gln Thr Val Asn Pro Asp
260 265 270
Val Ala Lys Met Phe His Leu Asp Pro Glu Ser Lys Arg Pro Ala Leu
275 280 285
Val Leu Val Lys Lys Glu Glu Glu Lys Ile Ser His Phe Asp Gly Glu
290 295 300
Phe Val Lys Ser Ala Leu Val Ser Phe Val Ser Ala Asn Lys Leu Ala
305 310 315
Leu Val Ser Val Phe Thr Arg Glu Thr Ala Pro Glu Ile Phe Glu Ser
325 330 335
Ala Ile Lys Lys Gln Leu Leu Leu Phe Val Thr Lys Asn Glu Ser Glu
340 345 350
Lys Val Leu Thr Glu Phe Gln Glu Ala Ala Lys Ser Phe Lys Gly Lys
355 360 365
Leu Ile Phe Val Ser Val Asp Leu Asp Asn Glu Asp Tyr Gly Lys Pro
370 375 380
Val Ala Glu Tyr Phe Gly Val Ser Gly Asn Gly Pro Lys Leu Ile Gly
385 390 395
Tyr Thr Gly Asn Glu Asp His Lys Lys Tyr Phe Phe Asp Gly Glu Ile
405 410 415
Gln Ser Asp Lys Ile Lys Ile Phe Gly Glu Asp Phe Leu Asn Asp Lys
420 425 430
Leu Lys Pro Phe Tyr Lys Ser Asp Pro Ile Pro Glu Lys Asn Asp Glu
435 440 445
Asp Val Lys Ile Val Val Gly Asp Asn Phe Asp Glu Ile Val Leu Asp
450 455 460
Asp Ser Lys Asp Val Leu Leu Glu Val Tyr Ala Pro Trp Cys Gly His
465 470 475
Cys Gln Ala Leu Glu Pro Met Tyr Asn Lys Leu Ala Lys His Leu Arg
485 490 495
Ser Ile Asp Ser Leu Val Ile Thr Lys Met Asp Gly Thr Thr Asn Glu
500 505 510
His Pro Lys Ala Lys Ala Glu Gly Phe Pro Thr Ile Leu Phe Phe Pro
515 520 525
Ala Gly Asn Lys Thr Ser Glu Pro Ile Thr Val Asp Thr Asp Arg Thr
530 535 540
Val Val Ala Phe Tyr Lys Phe Leu Arg Lys His Ala Thr Ile Pro Phe
545 550 555
Lys Leu Glu Lys Pro Ala Ser Thr Glu Ser Pro Lys Thr Ala Glu Ser
565 570 575
Thr Pro Lys Val Glu Thr Thr Glu Thr Lys Glu Ser Pro Asp Ser Thr
580 585 590
Thr Lys Ser Ser Gln Ser Asp Ser Lys Asp Glu Leu
595 600

(2) INFORMATION FOR SEQ ID NO:2743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..597
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574061

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2743:

Met Ala Phe Arg Val Leu Leu Leu Phe Ser Leu Thr Ala Leu Leu Ile
1 5 10 15
Phe Ser Ala Val Ser Pro Ser Phe Ala Ala Ser Ser Ser Asp Asp Val

20										25					30				
Asp	Asp	Glu	Glu	Asp	Leu	Ser	Phe	Leu	Glu	Asp	Leu	Lys	Glu	Asp	Asp	Val			
Pro	Gly	Ala	Asp	Ser	Leu	Ser	Ser	Ser	Thr	Gly	Phe	Asp	Glu	Phe	Glu				
Gly	Gly	Glu	Glu	Glu	Asp	Pro	Asp	Met	Tyr	Asn	Asp	Asp	Asp	Asp	Asp	Glu			
65					70					75						80			
Glu	Gly	Asp	Phe	Ser	Asp	Leu	Gly	Asn	Pro	Asp	Ser	Asp	Pro	Leu	Pro				
Thr	Pro	Glu	Ile	Asp	Glu	Lys	Asp	Val	Val	Val	Ile	Lys	Glu	Arg	Asn				
Phe	Thr	Asp	Val	Ile	Glu	Asn	Asn	Gln	Tyr	Val	Leu	Val	Glu	Phe	Tyr				
Ala	Pro	Trp	Cys	Gly	His	Cys	Gln	Ser	Leu	Ala	Pro	Glu	Tyr	Ala	Ala				
Ala	Ala	Thr	Glu	Leu	Lys	Glu	Asp	Gly	Val	Val	Leu	Ala	Lys	Ile	Asp				
145					150					155					160				
Ala	Thr	Glu	Glu	Asn	Glu	Leu	Ala	Gln	Glu	Tyr	Arg	Val	Gln	Gly	Phe				
Pro	Thr	Leu	Leu	Phe	Phe	Val	Asp	Gly	Glu	His	Lys	Pro	Tyr	Thr	Gly				
Gly	Arg	Thr	Lys	Glu	Thr	Ile	Val	Thr	Trp	Val	Lys	Lys	Lys	Ile	Gly				
Pro	Gly	Val	Tyr	Asn	Leu	Thr	Thr	Leu	Asp	Asp	Ala	Glu	Lys	Val	Leu				
Thr	Ser	Gly	Asn	Lys	Val	Val	Leu	Gly	Tyr	Leu	Asn	Ser	Leu	Val	Gly				
225					230					235					240				
Val	Glu	His	Asp	Gln	Leu	Asn	Ala	Ala	Ser	Lys	Ala	Glu	Asp	Asp	Val				
Asn	Phe	Tyr	Gln	Thr	Val	Asn	Pro	Asp	Val	Ala	Lys	Met	Phe	His	Leu				
Asp	Pro	Glu	Ser	Lys	Arg	Pro	Ala	Leu	Val	Leu	Val	Lys	Lys	Glu	Glu				
Glu	Lys	Ile	Ser	His	Phe	Asp	Gly	Glu	Phe	Val	Lys	Ser	Ala	Leu	Val				
Ser	Phe	Val	Ser	Ala	Asn	Lys	Leu	Ala	Leu	Val	Ser	Val	Phe	Thr	Arg				
305					310					315					320				
Glu	Thr	Ala	Pro	Glu	Ile	Phe	Glu	Ser	Ala	Ile	Lys	Lys	Gln	Leu	Leu				
Leu	Phe	Val	Thr	Lys	Asn	Glu	Ser	Glu	Lys	Val	Leu	Thr	Glu	Phe	Gln				
Glu	Ala	Ala	Lys	Ser	Phe	Lys	Gly	Lys	Leu	Ile	Phe	Val	Ser	Val	Asp				
Leu	Asp	Asn	Glu	Asp	Tyr	Gly	Lys	Pro	Val	Ala	Glu	Tyr	Phe	Gly	Val				
Ser	Gly	Asn	Gly	Pro	Lys	Leu	Ile	Gly	Tyr	Thr	Gly	Asn	Glu	Asp	His				
385					390					395					400				
Lys	Lys	Tyr	Phe	Phe	Asp	Gly	Glu	Ile	Gln	Ser	Asp	Lys	Ile	Lys	Ile				
Phe	Gly	Glu	Asp	Phe	Leu	Asn	Asp	Lys	Leu	Lys	Pro	Phe	Thr	Lys	Ser				
Asp	Pro	Ile	Pro	Glu	Lys	Asn	Asp	Glu	Asp	Val	Lys	Ile	Val	Val	Gly				
Asp	Asn	Phe	Asp	Glu	Ile	Val	Leu	Asp	Asp	Ser	Lys	Asp	Val	Leu	Leu				
Glu	Val	Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Gln	Ala	Leu	Glu	Pro	Met				
465					470					475					480				
Tyr	Asn	Lys	Leu	Ala	Lys	His	Leu	Arg	Ser	Ile	Asp	Ser	Leu	Val	Ile				
Thr	Lys	Met	Asp	Gly	Thr	Thr	Asn	Glu	His	Pro	Lys	Ala	Lys	Ala	Glu				
			500						505				510						

Gly Phe Pro Thr Ile Leu Phe Phe Pro Ala Gly Asn Lys Thr Ser Glu
515 520 525
Pro Ile Thr Val Asp Thr Asp Arg Thr Val Val Ala Phe Tyr Lys Phe
530 535 540
Leu Arg Lys His Ala Thr Ile Pro Phe Lys Leu Glu Lys Pro Ala Ser
545 550 555 560
Thr Glu Ser Pro Lys Thr Ala Glu Ser Thr Pro Lys Val Glu Thr Thr
565 570 575
Glu Thr Lys Glu Ser Pro Asp Ser Thr Thr Lys Ser Ser Gln Ser Asp
580 585 590
Ser Lys Asp Glu Leu
595

(2) INFORMATION FOR SEQ ID NO:2744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..525
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2744:

Met Tyr Asn Asp Asp Asp Asp Glu Glu Gly Asp Phe Ser Asp Leu Gly
1 5 10 15
Asn Pro Asp Ser Asp Pro Leu Pro Thr Pro Glu Ile Asp Glu Lys Asp
20 25 30
Val Val Val Ile Lys Glu Arg Asn Phe Thr Asp Val Ile Glu Asn Asn
35 40 45
Gln Tyr Val Leu Val Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Gln
50 55 60
Ser Leu Ala Pro Glu Tyr Ala Ala Ala Ala Thr Glu Leu Lys Glu Asp
65 70 75 80
Gly Val Val Leu Ala Lys Ile Asp Ala Thr Glu Glu Asn Glu Leu Ala
85 90 95
Gln Glu Tyr Arg Val Gln Gly Phe Pro Thr Leu Leu Phe Phe Val Asp
100 105 110
Gly Glu His Lys Pro Tyr Thr Gly Gly Arg Thr Lys Glu Thr Ile Val
115 120 125
Thr Trp Val Lys Lys Lys Ile Gly Pro Gly Val Tyr Asn Leu Thr Thr
130 135 140
Leu Asp Asp Ala Glu Lys Val Leu Thr Ser Gly Asn Lys Val Val Leu
145 150 155 160
Gly Tyr Leu Asn Ser Leu Val Gly Val Glu His Asp Gln Leu Asn Ala
165 170 175
Ala Ser Lys Ala Glu Asp Asp Val Asn Phe Tyr Gln Thr Val Asn Pro
180 185 190
Asp Val Ala Lys Met Phe His Leu Asp Pro Glu Ser Lys Arg Pro Ala
195 200 205
Leu Val Leu Val Lys Lys Glu Glu Lys Ile Ser His Phe Asp Gly
210 215 220
Glu Phe Val Lys Ser Ala Leu Val Ser Phe Val Ser Ala Asn Lys Leu
225 230 235 240
Ala Leu Val Ser Val Phe Thr Arg Glu Thr Ala Pro Glu Ile Phe Glu
245 250 255
Ser Ala Ile Lys Lys Gln Leu Leu Leu Phe Val Thr Lys Asn Glu Ser
260 265 270
Glu Lys Val Leu Thr Glu Phe Gln Glu Ala Ala Lys Ser Phe Lys Gly
275 280 285
Lys Leu Ile Phe Val Ser Val Asp Leu Asp Asn Glu Asp Tyr Gly Lys

290	295	300
Pro Val Ala Glu Tyr Phe Gly Val Ser Gly Asn Gly Pro Lys Leu Ile		
305	310	315
Gly Tyr Thr Gly Asn Glu Asp His Lys Lys Tyr Phe Phe Asp Gly Glu		
	325	330
Ile Gln Ser Asp Lys Ile Lys Ile Phe Gly Glu Asp Phe Leu Asn Asp		
	340	345
Lys Leu Lys Pro Phe Tyr Lys Ser Asp Pro Ile Pro Glu Lys Asn Asp		
	355	360
Glu Asp Val Lys Ile Val Val Gly Asp Asn Phe Asp Glu Ile Val Leu		
	370	375
Asp Asp Ser Lys Asp Val Leu Leu Glu Val Tyr Ala Pro Trp Cys Gly		
	385	390
His Cys Gln Ala Leu Glu Pro Met Tyr Asn Lys Leu Ala Lys His Leu		
	405	410
Arg Ser Ile Asp Ser Leu Val Ile Thr Lys Met Asp Gly Thr Thr Asn		
	420	425
Glu His Pro Lys Ala Lys Ala Glu Gly Phe Pro Thr Ile Leu Phe Phe		
	435	440
Pro Ala Gly Asn Lys Thr Ser Glu Pro Ile Thr Val Asp Thr Asp Arg		
	450	455
Thr Val Val Ala Phe Tyr Lys Phe Leu Arg Lys His Ala Thr Ile Pro		
	465	470
Phe Lys Leu Glu Lys Pro Ala Ser Thr Glu Ser Pro Lys Thr Ala Glu		
	485	490
Ser Thr Pro Lys Val Glu Thr Thr Glu Thr Lys Glu Ser Pro Asp Ser		
	500	505
Thr Thr Lys Ser Ser Gln Ser Asp Ser Lys Asp Glu Leu		
	515	520
		525

(2) INFORMATION FOR SEQ ID NO:2745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..978
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2745:

atcagtcact	tattcagact	gttggaaatta	caaagatggg	tgtgtatgtt	gaagccagta	60
ctggctttgg	gcaatctcct	gagagtattc	atactcacta	tgggattatg	tcgaacaaga	120
atgaattgtt	ttccaccatt	ctgcacaaag	agagaagacc	agaagcaacg	caagcttaca	180
tcacaagaaa	caaataccac	cttcacgaag	cattcaatgt	aagtttcac	ttggagaaac	240
ttgcttacc	gatctctaga	gggcatttga	gcttggctaa	cacaaatgtt	gatgacaacc	300
cttcagtcac	cttcaattac	tttaaacacc	cggtggatct	ccaacgctgt	gttggaagcca	360
ttcgctctgt	ttccaaagtg	gtgacgtcta	agcgcttctt	aaactacacg	cagKtgGaca	420
agcaaacggt	acacaagatg	cttagcttaa	gcgtcaagcg	aaacatcaat	ctaaagggcaa	480
agcaactgaa	cgataccaaa	tcaatggctc	agttctgcaa	agacactgtt	gtcaaatctt	540
ggcactacac	tgtgtgagtg	cttgtgggta	aagtgtgtag	ccctaaccgc	aaagtctctg	600
gtgtcgacag	gcttagagtg	attgatgttt	caacgcttga	cgagctccca	ggaaccaaac	660
cgcaagctac	tatgatgatg	atgggaagat	acatggggag	caagattctt	cgggagagac	720
ttggaataac	agctgtgttg	tagttttcag	attgagcttt	tatggtagac	aaatctgtag	780
cagataattc	tgatgtggaa	ttgtgttgga	gaatatctct	ctctgtctcc	ttctctgtta	840
tttgatattc	gattcattga	agtataggat	catattgtct	aatgaactgt	gttaacctct	900
attgggcaat	cggtctgtgt	gcttattagc	tttgtgtgaa	agttaatcac	gttttctgtt	960
tcaatactct	tacaatcg					

(2) INFORMATION FOR SEQ ID NO:2746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..246
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574067
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2746:
Gln Ser Leu Ile Gln Thr Val Gly Ile Thr Lys Met Gly Val Tyr Val
1 5 10 15
Glu Ala Ser Thr Gly Phe Gly Gln Ser Pro Glu Ser Ile His Thr His
 20 25 30
Tyr Gly Ile Met Ser Asn Lys Asn Glu Leu Phe Ser Thr Ile Pro Ala
 35 40 45
Lys Gln Arg Arg Pro Glu Ala Thr Gln Ala Tyr Ile Thr Arg Asn Lys
 50 55 60
Tyr Gln Leu His Glu Ala Phe Asn Gly Ser Phe Ile Leu Glu Lys Leu
65 70 75 80
Ala Tyr Pro Ile Ser Arg Gly His Leu Ser Leu Val Asn Thr Asn Val
 85 90 95
Asp Asp Asn Pro Ser Val Thr Phe Asn Tyr Phe Lys His Pro Val Asp
 100 105 110
Leu Gln Arg Cys Val Glu Ala Ile Arg Leu Val Ser Lys Val Val Thr
 115 120 125
Ser Lys Arg Phe Leu Asn Tyr Thr Gln Xaa Asp Lys Gln Asn Val His
 130 135 140
Lys Met Leu Ser Leu Ser Val Lys Ala Asn Ile Asn Leu Arg Pro Lys
145 150 155 160
Gln Leu Asn Asp Thr Lys Ser Met Ala Gln Phe Cys Lys Asp Thr Val
 165 170 175
Val Thr Ile Trp His Tyr His Gly Gly Cys Leu Val Gly Lys Val Val
 180 185 190
Ser Pro Asn Arg Lys Val Leu Gly Val Asp Arg Leu Arg Val Ile Asp
 195 200 205
Gly Ser Thr Phe Asp Glu Ser Pro Gly Thr Asn Pro Gln Ala Thr Met
210 215 220
Met Met Met Gly Arg Tyr Met Gly Val Lys Ile Leu Arg Glu Arg Leu
225 230 235 240
Gly Asn Lys Ala Gly Val
 245
(2) INFORMATION FOR SEQ ID NO:2747:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..235
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574068
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2747:
Met Gly Val Tyr Val Glu Ala Ser Thr Gly Phe Gly Gln Ser Pro Glu
1 5 10 15
Ser Ile His Thr His Tyr Gly Ile Met Ser Asn Lys Asn Glu Leu Phe
 20 25 30
Ser Thr Ile Pro Ala Lys Gln Arg Arg Pro Glu Ala Thr Gln Ala Tyr
 35 40 45
Ile Thr Arg Asn Lys Tyr Gln Leu His Glu Ala Phe Asn Gly Ser Phe
50 55 60

[illegible]

1	Ile	Pro	Asn	Cys	Leu	Phe	Arg	Val	Gly	Gly	Ser	Ala	Ile	Leu	Leu	Ser
				5						10					15	
Asn	Lys	Gly	Lys	Asp	Arg	Arg	Arg	Ser	Lys	Tyr	Lys	Leu	Val	His	Thr	
			20					25					30			
Val	Arg	Thr	His	Lys	Gly	Ala	Val	Glu	Lys	Ala	Phe	Asn	Cys	Val	Tyr	
		35					40					45				
Gln	Glu	Gln	Asp	Asp	Asn	Gly	Lys	Thr	Gly	Val	Ser	Leu	Ser	Lys	Asp	
		50				55					60					
Leu	Met	Ala	Ile	Ala	Gly	Glu	Ala	Leu	Lys	Ala	Asn	Ile	Thr	Thr	Leu	
65					70					75					80	
Gly	Pro	Leu	Val	Leu	Pro	Ile	Ser	Glu	Gln	Ile	Leu	Phe	Phe	Met	Thr	
				85					90					95		
Leu	Val	Thr	Lys	Lys	Leu	Phe	Asn	Ser	Lys	Leu	Lys	Pro	Tyr	Ile	Pro	
			100					105					110			
Asp	Phe	Lys	Leu	Ala	Phe	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	
		115					120					125				
Ala	Val	Ile	Asp	Glu	Leu	Glu	Lys	Asn	Leu	Gln	Leu	Ser	Gln	Thr	His	
		130					135					140				
Val	Glu	Ala	Ser	Arg	Met	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	
145					150					155					160	
Ser	Ser	Ile	Trp	Tyr	Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	
				165					170				175			

Lys Lys Gly Asn Arg Val Trp Gln Ile Ala Phe Gly Ser Gly Phe Lys
180 185 190
Cys Asn Ser Ala Val Trp Met Ala Leu Asn Asn Val Lys Pro Ser Val
195 200 205
Ser Ser Pro Trp Glu His Cys Ile Asp Arg Tyr Pro Val Lys Leu Asp
210 215 220

Phe
225

(2) INFORMATION FOR SEQ ID NO:2751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 - (B) LOCATION: 1..160
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1574076
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2751:

Met	Ala	Ile	Ala	Gly	Glu	Ala	Leu	Lys	Ala	Asn	Ile	Thr	Thr	Leu	Gly
1				5				10						15	
Pro	Leu	Val	Leu	Pro	Ile	Ser	Glu	Gln	Ile	Leu	Phe	Phe	Met	Thr	Leu
			20				25						30		
Val	Thr	Lys	Lys	Leu	Phe	Asn	Ser	Lys	Leu	Lys	Pro	Tyr	Ile	Pro	Asp
			35				40						45		
Phe	Lys	Leu	Ala	Phe	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala
			50				55					60			
Val	Ile	Asp	Glu	Leu	Glu	Lys	Asn	Leu	Gln	Leu	Ser	Gln	Thr	His	Val
			65				70				75			80	
Glu	Ala	Ser	Arg	Met	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser
				85					90					95	
Ser	Ile	Trp	Tyr	Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys
			100					105					110		
Lys	Gly	Asn	Arg	Val	Trp	Gln	Ile	Ala	Phe	Gly	Ser	Gly	Phe	Lys	Cys
			115				120						125		
Asn	Ser	Ala	Val	Trp	Met	Ala	Leu	Asn	Asn	Val	Lys	Pro	Ser	Val	Ser
			130				135					140			
Ser	Pro	Trp	Glu	His	Cys	Ile	Asp	Arg	Tyr	Pro	Val	Lys	Leu	Asp	Phe
			145			150				155				160	

(2) INFORMATION FOR SEQ ID NO:2752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2752:

Met	Thr	Leu	Val	Thr	Lys	Lys	Leu	Phe	Asn	Ser	Lys	Leu	Lys	Pro	Tyr
1				5				10					15		
Ile	Pro	Asp	Phe	Lys	Leu	Ala	Phe	Asp	His	Phe	Cys	Ile	His	Ala	Gly
			20					25					30		
Gly	Arg	Ala	Val	Ile	Asp	Glu	Leu	Glu	Lys	Asn	Leu	Gln	Leu	Ser	Gln
			35				40					45			
Thr	His	Val	Glu	Ala	Ser	Arg	Met	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr

(2) INFORMATION FOR SEO ID NO:2753:

(A) LENGTH: 1167 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

- (D) OTHER INFORMATION: / Ceres Seq. ID 1574086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2753:

aaatccttat	gtcaggagat	ccatctctct	agtgaattgc	cotttctact	tcaagattgg	60
actcttcgct	catgggtgac	ggctgctcgt	tcttcacatc	ctgtctaca	tctcccacac	120
agctctctct	tcaaacatgt	accaaaggcc	tgacatgatt	accocctggg	ttgacgctca	180
gggccacaacca	ctcgaccocg	gtgaagtata	ggagacactt	gagattttct	ttgagattat	240
tttttagagtg	cttgaaaagt	gtgtgcagat	ggagagcctc	acaatttggg	acaacctctg	300
tgacacacatg	attggcaacg	tatatgttca	gtttaaaggaa	gagatgcagc	ctcgacgtcg	360
tttgcgaagct	ctgcaagagta	gtgtctatct	aggacgtccc	ataattgtcg	attctctctc	420
tgtagcgagat	ttccgcgaag	ccacgctgtg	cgagtatgaa	gaaaaacaac	gcaaccgtgg	480
tggtgatctgt	aatctttcatc	atgtgaagct	ttgttcgagg	gaactaagtg	gaaaattctc	540
tgccgagatat	cgcgcatcat	accgcagaag	aagtaagaac	aggagcagaa	caggagtgat	600
tagcccgagg	aaacaagagag	ataatgaccg	acgtgatctc	tctcacagag	aattcagcta	660
tcgggacagag	gatcgcgagt	tttaccgtta	tggaaagtga	aaaaggagca	gtgagaggct	720
ggagagggcaa	gagggggagc	gattacaagg	taggagacaa	gcaagcccta	aacggaggag	780
gagccccgggt	ggcggggagg	gaaagaagtga	ggagaggagg	gcaagtgatt	agcataggaa	840
caagaaacagg	gagggaaagg	aagaaggagg	agcataaaaa	cagttcttta	ctcaaatcac	900
aatttgtctct	atttgtgttc	tcgcctctgt	tctctcggtt	tattctgaaa	tcggtaaatt	960
ctggtgatgat	atttttcatt	ttgctgttct	aatttggaac	ttgaattgag	tggaaacaac	1020
ttcttttagat	tataaaatgt	ttggggttgt	ttcttttgat	tttttttagt	gaaaaaccgc	1080
tcgtctccctc	tgtttatgat	tttcaacaat	gtttctttaga	accttgtact	atcttcttgt	1140
cgtttaaactt	taaaagagtt	ctagtttt				

(2) INFORMATION FOR SEQ ID NO:2754:

(A) LENGTH: 291 amino acids

- ```
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
```

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..291
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1574087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2754:

Asn	Pro	Tyr	Val	Arg	Arg	Ser	His	Ser	Leu	Val	Asn	Cys	Pro	Phe	Tyr
1				5					10					15	
Phe	Lys	Ile	Gly	Ala	Cys	Arg	His	Gly	Asp	Arg	Cys	Ser	Arg	Leu	His
			20					25					30		
Asn	Arg	Pro	Thr	Ile	Ser	Pro	Thr	Leu	Leu	Leu	Ser	Asn	Met	Tyr	Gln
	35						40					45			

Met	Tyr	Gln	Arg	Pro	Asp	Met	Ile	Thr	Pro	Gly	Val	Asp	Ala	Gln	Gly
1				5					10					15	
Gln	Pro	Leu	Asp	Pro	Arg	Lys	Ile	Gln	Glu	His	Phe	Glu	Asp	Phe	Phe
			20					25					30		
Glu	Asp	Leu	Phe	Glu	Glu	Leu	Gly	Lys	Phe	Gly	Glu	Ile	Glu	Ser	Leu
		35					40					45			
Asn	Ile	Cys	Asp	Asn	Leu	Ala	Asp	His	Met	Ile	Gly	Asn	Val	Tyr	Val
	50					55					60				
Gln	Phe	Lys	Glu	Glu	Asp	Gln	Ala	Ala	Ala	Ala	Leu	Gln	Ala	Leu	Gln
65					70					75				80	
Gly	Arg	Phe	Tyr	Ser	Gly	Arg	Pro	Ile	Ile	Ala	Asp	Phe	Ser	Pro	Val
				85					90					95	
Thr	Asp	Phe	Arg	Glu	Ala	Thr	Cys	Arg	Gln	Tyr	Glu	Glu	Asn	Asn	Cys
			100					105					110		
Asn	Arg	Gly	Gly	Tyr	Cys	Asn	Phe	Met	His	Val	Lys	Leu	Val	Ser	Arg
		115					120					125			
Glu	Leu	Arg	Arg	Lys	Leu	Phe	Gly	Arg	Tyr	Arg	Arg	Ser	Tyr	Arg	Arg

(2) INFORMATION FOR SEQ ID NO:2756:

(A) LENGTH: 240 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAM

(B) LOCATION: 1..240

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:2756:

Ile Thr Pro Gly Val Asp Ala Gln Gly Gln Pr

(2) INFORMATION FOR SEQ ID NO:2757:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..662
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574093

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2757:

```

attttttctt tctctctctc ctccctaagc aaaactaaaa caagctatgg ctggtatgct    60
tcccgagatt gagtgtgcaa ggaggcggcg ctccacgggt ggtgctctc cgattgaatc    120
ctcgaacaca gctctctgtg cggtctggcg gggacacgtc tggacacggc gaccatcggt    180
ctctctttac actaccaact atgagagcca ccaggcccat gtctcctct cggagagaag    240
tgttaggaaat aaatctttat gagaagacaa cgaatgagaaa cttgacggag cagccaaaat    300
ggcaaaagcag agggottaaca agcgggtcag aatcccacca cgtacaagtt caggcaaaat    360
ggtaaaagaca aagggaataa attggagcaa gaaagggtta aacctctcgg ggaattaccg    420
accgaggttg Gtcgggttaa agaagagccg aggaaggttg atggaatggt tcaagcggcg    480
agttagggaa caacaagatt gtgctatatg tctagaccgg ttcaagaagg gtgagacctt    540
ggtacacctt ccatgtgccc ataagtttca ctccatattg ttattgcctt ggctagacac    600
taatgtttat tgcccatatt gtagaactga tatttggaaat taaatgttat atttttgatg    660
tc

```

- (2) INFORMATION FOR SEQ ID NO:2758:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..198
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574094

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2758:

```

Met Ala Gly Met Leu Pro Gly Val Glu Cys Ala Arg Arg Arg Arg Phe
1      5      10      15
His Gly Gly Ala Pro Pro Ile Glu Ser Ser Asn Thr Ala Ser Val Ala
20      25      30
Ala Ala Ala Gly His Val Trp Thr Arg Arg Pro Ser Phe Ser Leu Tyr
35      40      45
Thr Thr Asn His Glu Ser His Gln Ala His Val Ser Phe Ser Glu Arg
50      55      60
Ser Val Arg Asn Lys Ser Tyr Gly Glu Asp Asn Asp Glu Lys Leu Asp
65      70      75      80
Gly Ala Ala Lys Glu Ala Lys Gln Arg Leu Asn Lys Arg Leu Arg Ile
85      90      95
Pro Pro Arg Thr Ser Ser Gly Lys Met Val Lys Thr Lys Gly Ile Asn
100      105      110
Trp Ser Lys Glu Arg Val Asn Leu Ser Gly Thr Tyr Arg Pro Arg Trp
115      120      125
Val Gly Leu Lys Lys Ser Arg Gly Arg Leu Met Glu Trp Phe Lys Arg
130      135      140
Arg Val Arg Glu Gln Gln Asp Cys Ala Ile Cys Leu Asp Arg Phe Lys
145      150      155      160
Lys Gly Glu Thr Leu Val His Leu Pro Cys Ala His Lys Phe His Ser
165      170      175
Ile Cys Leu Leu Pro Trp Leu Asp Thr Asn Val Tyr Cys Pro Tyr Cys
180      185      190
Arg Thr Asp Ile Trp Asn
195

```

- (2) INFORMATION FOR SEQ ID NO:2759:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 195 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..195
(D) OTHER INFORMATION: / Ceres Seq. ID 1574095
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2759:

Met	Leu	Pro	Gly	Val	Glu	Cys	Ala	Arg	Arg	Arg	Phe	His	Gly	Gly
1			5					10					15	
Ala	Pro	Pro	Ile	Glu	Ser	Ser	Asn	Thr	Ala	Ser	Val	Ala	Ala	Ala
			20				25					30		
Gly	His	Val	Trp	Thr	Arg	Arg	Pro	Ser	Phe	Ser	Leu	Tyr	Thr	Thr
		35					40				45			Asn
His	Glu	Ser	His	Gln	Ala	His	Val	Ser	Phe	Ser	Glu	Arg	Ser	Val
	50				55				60					Arg
Asn	Lys	Ser	Tyr	Gly	Glu	Asp	Asn	Asp	Glu	Lys	Leu	Asp	Gly	Ala
65				70					75					80
Lys	Glu	Ala	Lys	Gln	Arg	Leu	Asn	Lys	Arg	Leu	Arg	Ile	Pro	Pro
			85						90				95	Arg
Thr	Ser	Ser	Gly	Lys	Met	Val	Lys	Thr	Lys	Gly	Ile	Asn	Trp	Ser
			100				105					110		Lys
Glu	Arg	Val	Asn	Leu	Ser	Gly	Thr	Tyr	Arg	Pro	Arg	Trp	Val	Gly
		115				120					125			Leu
Lys	Lys	Ser	Arg	Gly	Arg	Leu	Met	Glu	Trp	Phe	Lys	Arg	Arg	Val
		130				135				140				Arg
Glu	Gln	Gln	Asp	Cys	Ala	Ile	Cys	Leu	Asp	Arg	Phe	Lys	Lys	Gly
145				150					155					160
Thr	Leu	Val	His	Leu	Pro	Cys	Ala	His	Lys	Phe	His	Ser	Ile	Cys
			165						170				175	Leu
Leu	Pro	Trp	Leu	Asp	Thr	Asn	Val	Tyr	Cys	Pro	Tyr	Cys	Arg	Thr
			180				185						190	Asp
Ile	Trp	Asn												
		195												

(2) INFORMATION FOR SEQ ID NO:2760:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1396 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1396
(D) OTHER INFORMATION: / Ceres Seq. ID 1574100
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2760:

aaagatgaaa	agtaataacc	ttcctctctt	gccctttttg	ctggctctgg	tgaacatatg	60
aaaaattttt	cttgctcaag	ttaatgataa	aaggtttgtg	taggtattgt	tgctctggct	120
ctgggtggtg	gtctatgaaa	tcaacccata	tcgtgaatgg	actgcaacat	ggatctcttc	180
tcoccatggg	attggggagca	tttgatcatg	tccaatccgt	caaggactga	agatgacagc	240
aaacagctac	ctactgagtg	ggaaattgaa	aaaggtgaag	gaattgaatc	tatagttcca	300
cattttctcag	gcccttgagag	agtcagtaGg	tggtctctgc	accagcttct	ggcacactgc	360
tgtatcgaaa	agctccacagt	cgacctctat	caactcatca	tctcccgaag	ccaaacgatg	420
caagcttgca	tcagaaagt	cccttgagag	tctttgcagc	aacatagact	ttgtccaggt	480
gaaggctccc	acagctctcg	aggtatccgt	tgctcagctc	gaatcagatc	tttgtttaaa	540
actaggaag	cggacatact	ctggaagaata	ctggggtaga	aacaataatg	aaatttcagc	600
ggtttctatg	aagtgtgtaa	ctccatctgt	tgtcgtggg	aaatccaaat	tgtgtggtca	660
gagcatgcc	gtcccgcgt	gccaaattga	tggctgtgaa	ctggatctct	catctgctaa	720

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gggttatcat cgtaagcaca aagtctgcga aaagcattca aagtgcctaa aagttagcgt 780
gagtgccctg gaacgtcggt tctgcacaac gtgtagcagg ttccatgctg tctctgaatt 840
tgatgagaag aaacgaagct ccgcaaaacg tctttctcat cataatgcga ggcgtcgtaa 900
gccacaagga gtatttttcaa tgaatccgca gagggtgtat gatcgaagac agcatacaaa 960
tatgttgttg aatgggggtg cctttaacgc gagatctgaa gaaatgtatg aatggggtaa 1020
taacacttat gatacaagac ctagacaaac ggaaaaaaac tttactctga gcttccagag 1080
aggtaatggc tctgaggacc agctggttgc tagtagcagc cgtatgttCc tctacatctc 1140
aaacctcagg tgggttccca gcaggaagt ccaagtttca acttcattggc gaagatgtgg 1200
gagaatactc aggagtcttc catgaatctc aagatatcca ccgtgctctc tctcttctgt 1260
caacctcttc ggatccctcg gcccaaccac atgtgcagcc attttctcta ctctgttcat 1320
atgatgttgg accaaaatag atgagtaagt aatgtgtaat ttgtaaacct gttactcagt 1380
aggtggatac ttttcc

```

(2) INFORMATION FOR SEQ ID NO:2761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2761:

```

Met Asp Cys Asn Met Val Ser Ser Ser Gln Trp Asp Trp Glu His Leu
1      5      10      15
Ile Met Ser Asn Pro Ser Arg Thr Glu Asp Asp Ser Lys Gln Leu Pro
      20      25      30
Thr Glu Trp Glu Ile Glu Lys Gly Glu Gly Ile Glu Ser Ile Val Pro
      35      40      45
His Phe Ser Gly Leu Glu Arg Val Ser Arg Trp Leu Cys His Gln Leu
      50      55      60
Leu Ala His Cys Cys Ile Glu Lys Leu Thr Val Asp Leu Tyr Gln Leu
      65      70      75
Ile Ile Ser Arg Ser Gln Thr Met Gln Ala Cys Ile Arg Lys Phe Pro
      85      90      95
Trp Arg Phe Leu Gln Gln His Arg Leu Cys Pro Gly Glu Gly Ser His
      100     105     110
Ser Ser Arg Gly Ile Arg Cys Leu Ser
      115     120

```

(2) INFORMATION FOR SEQ ID NO:2762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..205
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2762:

```

Met Lys Leu Leu Thr Pro Ser Val Val Ala Gly Lys Ser Lys Lys Cys
1      5      10      15
Gly Gln Ser Met Pro Val Pro Arg Cys Gln Ile Asp Gly Cys Glu Leu
      20      25      30
Asp Leu Ser Ser Ala Lys Gly Tyr His Arg Lys His Lys Val Cys Glu
      35      40      45
Lys His Ser Lys Cys Pro Lys Val Ser Val Ser Gly Leu Glu Arg Arg
      50      55      60
Phe Cys Gln Gln Cys Ser Arg Phe His Ala Val Ser Glu Phe Asp Glu

```

65					70					75					80
Lys	Lys	Arg	Ser	Cys	Arg	Lys	Arg	Leu	Ser	His	His	Asn	Ala	Arg	Arg
				85						90					95
Arg	Lys	Pro	Gln	Gly	Val	Phe	Ser	Met	Asn	Pro	Glu	Arg	Val	Tyr	Asp
			100					105					110		
Arg	Arg	Gln	His	Thr	Asn	Met	Leu	Trp	Asn	Gly	Val	Ser	Leu	Asn	Ala
		115					120				125				
Arg	Ser	Glu	Glu	Met	Tyr	Glu	Trp	Gly	Asn	Asn	Thr	Tyr	Asp	Thr	Lys
		130				135					140				
Pro	Arg	Gln	Thr	Glu	Lys	Ser	Phe	Thr	Leu	Ser	Phe	Gln	Arg	Gly	Asn
		145			150				155					160	
Gly	Ser	Glu	Asp	Gln	Leu	Val	Ala	Ser	Ser	Ser	Arg	Met	Phe	Leu	Tyr
			165					170					175		
Ile	Ser	Asn	Leu	Arg	Trp	Val	Pro	Ser	Arg	Lys	Val	Gln	Val	Ser	Thr
		180					185					190			
Ser	Trp	Arg	Arg	Cys	Gly	Arg	Ile	Leu	Arg	Ser	Pro	Pro			
		195				200					205				

(2) INFORMATION FOR SEQ ID NO:2763:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2763:

Met	Pro	Val	Pro	Arg	Cys	Gln	Ile	Asp	Gly	Cys	Glu	Leu	Asp	Leu	Ser
1					5				10					15	
Ser	Ala	Lys	Gly	Tyr	His	Arg	Lys	His	Lys	Val	Cys	Glu	Lys	His	Ser
			20					25				30			
Lys	Cys	Pro	Lys	Val	Ser	Val	Ser	Gly	Leu	Glu	Arg	Arg	Phe	Cys	Gln
		35				40					45				
Gln	Cys	Ser	Arg	Phe	His	Ala	Val	Ser	Glu	Phe	Asp	Glu	Lys	Lys	Arg
		50			55					60					
Ser	Cys	Arg	Lys	Arg	Leu	Ser	His	His	Asn	Ala	Arg	Arg	Arg	Lys	Pro
65					70				75					80	
Gln	Gly	Val	Phe	Ser	Met	Asn	Pro	Glu	Arg	Val	Tyr	Asp	Arg	Arg	Gln
			85					90					95		
His	Thr	Asn	Met	Leu	Trp	Asn	Gly	Val	Ser	Leu	Asn	Ala	Arg	Ser	Glu
			100				105					110			
Glu	Met	Tyr	Glu	Trp	Gly	Asn	Asn	Thr	Tyr	Asp	Thr	Lys	Pro	Arg	Gln
		115					120				125				
Thr	Glu	Lys	Ser	Phe	Thr	Leu	Ser	Phe	Gln	Arg	Gly	Asn	Gly	Ser	Glu
		130				135					140				
Asp	Gln	Leu	Val	Ala	Ser	Ser	Ser	Arg	Met	Phe	Leu	Tyr	Ile	Ser	Asn
		145			150				155				160		
Leu	Arg	Trp	Val	Pro	Ser	Arg	Lys	Val	Gln	Val	Ser	Thr	Ser	Trp	Arg
			165					170				175			
Arg	Cys	Gly	Arg	Ile	Leu	Arg	Ser	Pro	Pro						
		180				185									

(2) INFORMATION FOR SEQ ID NO:2764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1454
(D) OTHER INFORMATION: / Ceres Seq. ID 1574104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2764:

ctgggtgaaa	catagaaaag	tttctcttgc	tcaagttaat	gataaaaagg	tgagagcaat	60
aaaagctgat	aagccttgtc	tgttccttgg	aattttgaat	tttcttttct	tatcttactt	120
atagatttgg	tagttgaggg	tgtcgtcgat	aagttgttgt	aggatttgtt	gctctggctc	180
tggttgtagg	tctatgaaat	caaccocat	cgtgaatgga	ctgcaacatg	gtatcttcgt	240
cccagtgagg	tggggagcat	ttagatcatg	ccaatccgtc	aaggactgaa	gatgacagca	300
aacagctacc	tactgagtgg	gaaattgaaa	aagggtgaagg	aattgaatct	atagttccac	360
attcttcagg	ccttgagaga	gtcagtagtg	gctctgCcac	cagctctctg	caactgctgt	420
tatcgaaaag	ctcacagctg	acctctatca	actcatcatc	tcccgaagcc	aaacagatga	480
agcttgcac	agaaagtctc	cctggagatt	cttcgagcaa	catagacttt	gtccagtgta	540
aggtccccac	agctctcgag	gtatccgttg	cctcagctga	atcagatttt	tgtttaaaac	600
taggaaagcg	gacatactct	gaagaatact	ggggtagaaa	caataatgaa	atttcagcgg	660
tttctatgaa	gttggttaact	ccatctgttg	tcgtctggaa	atccaaattg	tgtggtcaga	720
gcatgccagt	cccgcgttgc	caaatgatg	gctgtgaact	ggatctctca	tctgctaagg	780
gttatcatcg	taagcacaaa	gtctgcgaaa	agcattcaaa	gtgcccgaag	gttagcgtga	840
gtggctcgga	acgtcgggtc	tgccaaacgt	gtagcaggtt	ccatgctgtc	tctgaatttg	900
atgagaagaa	acgaagctgc	cgaaaacgtc	tttctcatca	taatgcgagg	cgctgtaagc	960
cacaaggagt	attttcaatg	aatcccgaga	gggtgtatga	tcgaagacag	catacaaata	1020
tggtgtgaaa	tggtgtgtcc	cttaacgcga	gatctgAaag	aaatgtatga	atggggtaat	1080
aacacttatg	atacaaaagc	tagacaaacg	gaaaaaagct	ttactctgag	cttccagagta	1140
ggtaatggct	ctgaggacca	gctggttgct	agtagcagcc	gtatgtttct	tacatctcaa	1200
acctcaggtg	gggtccacgc	aggaaagtc	aagtttcaac	ttcatggcga	agatgtggga	1260
gaatactcga	gagtcctcca	tgaatctcaa	gatatccacc	gtgctctctc	tcttctgtca	1320
acctctctgg	atccctctgc	ccaaccacat	gtgcagccat	tttctctact	ctgttcaat	1380
gatgtgtgac	caaaaatgat	gagtaagtaa	tgtgtaattt	gtaaacctgt	tactcagttg	1440
gtggatactt	ttcc					

(2) INFORMATION FOR SEQ ID NO:2765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..284
(D) OTHER INFORMATION: / Ceres Seq. ID 1574105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2765:

Met	Asp	Cys	Asn	Met	Val	Ser	Ser	Ser	Gln	Trp	Asp	Trp	Glu	His	Leu
1			5						10				15		
Ile	Met	Ser	Asn	Pro	Ser	Arg	Thr	Glu	Asp	Asp	Ser	Lys	Gln	Leu	Pro
			20					25					30		
Thr	Glu	Trp	Glu	Ile	Glu	Lys	Gly	Glu	Gly	Ile	Glu	Ser	Ile	Val	Pro
			35				40					45			
His	Phe	Ser	Gly	Leu	Glu	Arg	Val	Ser	Ser	Gly	Ser	Ala	Thr	Ser	Phe
			50			55				60					
Trp	His	Thr	Ala	Val	Ser	Lys	Ser	Ser	Gln	Ser	Thr	Ser	Ile	Asn	Ser
			65			70			75				80		
Ser	Ser	Pro	Glu	Ala	Lys	Arg	Cys	Lys	Leu	Ala	Ser	Glu	Ser	Ser	Pro
			85					90					95		
Gly	Asp	Ser	Cys	Ser	Asn	Ile	Asp	Phe	Val	Gln	Val	Lys	Ala	Pro	Thr
			100				105					110			
Ala	Leu	Glu	Val	Ser	Val	Ala	Ser	Ala	Glu	Ser	Asp	Leu	Cys	Leu	Lys
			115			120					125				
Leu	Gly	Lys	Arg	Thr	Tyr	Ser	Glu	Glu	Tyr	Trp	Gly	Arg	Asn	Asn	Asn
			130			135				140					
Glu	Ile	Ser	Ala	Val	Ser	Met	Lys	Leu	Leu	Thr	Pro	Ser	Val	Val	Ala
			145			150				155					160

Gly Lys Ser Lys Leu Cys Gly Gln Ser Met Pro Val Pro Arg Cys Gln
165 170 175
Ile Asp Gly Cys Glu Leu Asp Leu Ser Ser Ala Lys Gly Tyr His Arg
180 185 190
Lys His Lys Val Cys Glu Lys His Ser Lys Cys Pro Lys Val Ser Val
195 200 205
Ser Gly Leu Glu Arg Arg Phe Cys Gln Gln Cys Ser Arg Phe His Ala
210 215 220
Val Ser Glu Phe Asp Glu Lys Lys Arg Ser Cys Arg Lys Arg Leu Ser
225 230 235
His His Asn Ala Arg Arg Arg Lys Pro Gln Gly Val Phe Ser Met Asn
245 250 255
Pro Glu Arg Val Tyr Asp Arg Arg Gln His Thr Asn Met Leu Trp Asn
260 265 270
Gly Val Ser Leu Asn Ala Arg Ser Glu Arg Asn Val
275 280

(2) INFORMATION FOR SEQ ID NO:2766:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..280

(D) OTHER INFORMATION: / Ceres Seq. ID 1574106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2766:

Met Val Ser Ser Ser Gln Trp Asp Trp Glu His Leu Ile Met Ser Asn
1 5 10 15
Pro Ser Arg Thr Glu Asp Asp Ser Lys Gln Leu Pro Thr Glu Trp Glu
20 25 30
Ile Glu Lys Gly Glu Gly Ile Glu Ser Ile Val Pro His Phe Ser Gly
35 40 45
Leu Glu Arg Val Ser Ser Gly Ser Ala Thr Ser Phe Trp His Thr Ala
50 55 60
Val Ser Lys Ser Ser Gln Ser Thr Ser Ile Asn Ser Ser Ser Pro Glu
65 70 75 80
Ala Lys Arg Cys Lys Leu Ala Ser Glu Ser Ser Pro Gly Asp Ser Cys
85 90 95
Ser Asn Ile Asp Phe Val Gln Val Lys Ala Pro Thr Ala Leu Glu Val
100 105 110
Ser Val Ala Ser Ala Glu Ser Asp Leu Cys Leu Lys Leu Gly Lys Arg
115 120 125
Thr Tyr Ser Glu Glu Tyr Trp Gly Arg Asn Asn Asn Glu Ile Ser Ala
130 135 140
Val Ser Met Lys Leu Leu Thr Pro Ser Val Val Ala Gly Lys Ser Lys
145 150 155 160
Leu Cys Gly Gln Ser Met Pro Val Pro Arg Cys Gln Ile Asp Gly Cys
165 170 175
Glu Leu Asp Leu Ser Ser Ala Lys Gly Tyr His Arg Lys His Lys Val
180 185 190
Cys Glu Lys His Ser Lys Cys Pro Lys Val Ser Val Ser Gly Leu Glu
195 200 205
Arg Arg Phe Cys Gln Gln Cys Ser Arg Phe His Ala Val Ser Glu Phe
210 215 220
Asp Glu Lys Lys Arg Ser Cys Arg Lys Arg Leu Ser His His Asn Ala
225 230 235 240
Arg Arg Arg Lys Pro Gln Gly Val Phe Ser Met Asn Pro Glu Arg Val
245 250 255
Tyr Asp Arg Arg Gln His Thr Asn Met Leu Trp Asn Gly Val Ser Leu

260 265 270
Asn Ala Arg Ser Glu Arg Asn Val
275 280
(2) INFORMATION FOR SEQ ID NO:2767:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 267 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..267
(D) OTHER INFORMATION: / Ceres Seq. ID 1574107
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2767:
Met Ser Asn Pro Ser Arg Thr Glu Asp Asp Ser Lys Gln Leu Pro Thr
1 5 10 15
Glu Trp Glu Ile Glu Lys Gly Glu Gly Ile Glu Ser Ile Val Pro His
20 25 30
Phe Ser Gly Leu Glu Arg Val Ser Ser Gly Ser Ala Thr Ser Phe Trp
35 40 45
His Thr Ala Val Ser Lys Ser Ser Gln Ser Thr Ser Ile Asn Ser Ser
50 55 60
Ser Pro Glu Ala Lys Arg Cys Lys Leu Ala Ser Glu Ser Ser Pro Gly
65 70 75 80
Asp Ser Cys Ser Asn Ile Asp Phe Val Gln Val Lys Ala Pro Thr Ala
85 90 95
Leu Glu Val Ser Val Ala Ser Ala Glu Ser Asp Leu Cys Leu Lys Leu
100 105 110
Gly Lys Arg Thr Tyr Ser Glu Glu Tyr Trp Gly Arg Asn Asn Asn Glu
115 120 125
Ile Ser Ala Val Ser Met Lys Leu Leu Thr Pro Ser Val Val Ala Gly
130 135 140
Lys Ser Lys Leu Cys Gly Gln Ser Met Pro Val Pro Arg Cys Gln Ile
145 150 155 160
Asp Gly Cys Glu Leu Asp Leu Ser Ser Ala Lys Gly Tyr His Arg Lys
165 170 175
His Lys Val Cys Glu Lys His Ser Lys Cys Pro Lys Val Ser Val Ser
180 185 190
Gly Leu Glu Arg Arg Phe Cys Gln Gln Cys Ser Arg Phe His Ala Val
195 200 205
Ser Glu Phe Asp Glu Lys Lys Arg Ser Cys Arg Lys Arg Leu Ser His
210 215 220
His Asn Ala Arg Arg Arg Lys Pro Gln Gly Val Phe Ser Met Asn Pro
225 230 235 240
Glu Arg Val Tyr Asp Arg Arg Gln His Thr Asn Met Leu Trp Asn Gly
245 250 255
Val Ser Leu Asn Ala Arg Ser Glu Arg Asn Val
260 265

(2) INFORMATION FOR SEQ ID NO:2768:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1658 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1658
(D) OTHER INFORMATION: / Ceres Seq. ID 1574122
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2768:

```

aatttctcaa taacgctctc agagagacca ttgtatgaag ctctcgcgtt ctggaatttg 60
aaaaggaact tgttatggag ataactcacc tgaacgttgt gccccagatgc tctgtgggta 120
cttggagtag taaattagaa accaaaagat tgggtccaaa tcggtcaaat ttgttatctt 180
caggggtcaa aaaatccaga cttgtgattc gaagtggaaa ttccgatggt tatgtttgtg 240
gtgagaatga tgacttgggt cgtatagcca gaagaggaga atcaacgtca aagggttttg 300
ttcctgggtt gctcgtatga tcaaatgggt aaattgctgc tcgaatcagt cattctcaact 360
gcgagtggaa gcccaagctt agagtacatt atgagaaagc cggttgtgac aatctcgatg 420
ctcctgcggt gttgtttctt cctggccttg gcgttggttc atttcaacta gagaagcagc 480
ttaccgatatt gggaagggat tatcgagtat gggtatttga ttttcttgga cagggtttat 540
ctctccctatt tgaagatcct actaccatga ctgaagaaac cagttcctcg gaagataagg 600
aacacattttg gggatttggg gacaaaactg aaccgtgggc tgatcaactt gtattctctc 660
tggatctctg gagggatcaa gttcagttat ttgtagaaga ggttatcggg gagcctgtgt 720
acattgctgg gaactcactt ggagggtatg tagctctcta ctttgacgca acccatcctc 780
acctgggttaa ggggtgttacc ttgcctaatg caacaccttt ctgggggttc ttccctaact 840
cagtaagatc cccaaagcta ccacgtctct ttccatggcc cggagcattc cctctgccgg 900
aaaagatgaa aaaaatcaca gaattgggtg gcaaaaagat aagtgtatct gaagcatag 960
ctgagatcact taacacagtc tacaacagac attctaccaaa tgttgataaa gtattctcac 1020
gtattgtgga ggtcacacag catccggctg ctgcagcatc gtttgcttca attatgctg 1080
ctcctgtgtg agagctatct ttctccgaag ctttatctag gtgtaaggaa aacaatgttc 1140
agatatgtct catgtatgga agagaagatc catgggtgag accgttatgg ggaagaagaa 1200
taaaagaagg aatcccccaa gctccatact acgagatcag cccagcgggt cactgcccac 1260
acgatgaagt cccgtgaggt gtgaactatc tgatgcggcg gtggatcaag cactggaagt 1320
ctgggtggtt tgaaNgcgct cccgcttttg gaggacactg aagaagattg ggaggagtcc 1380
aggaattgga gagaaattga gttcccgaga gatggttgga aaaaagcagt gaactctgtg 1440
ttatatgggt caaactatac gtactggaga ggagttagag aatctttcag atccagtttt 1500
ataagggtgt ttggaggaaa gtctgcatag aagaagcatg gaacagtcgt ctagtgtaaa 1560
ttaattgtaa tctatgttgc atccgatgct agcatatata tgttgtctgt agaatacagt 1620

```

(2) INFORMATION FOR SEQ ID NO:2769:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 428 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..428

(D) OTHER INFORMATION: / Ceres Seq. ID 1574123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2769:

```

Met Glu Ile Ile Ser Leu Asn Val Val Pro Gln Cys Ser Val Val Thr
1 5 10 15
Trp Ser Ser Phe Leu Ala Thr Lys Arg Leu Val Pro Asn Arg Ser Ser
20 25 30
Leu Leu Phe Ser Gly Val Lys Lys Ser Arg Leu Val Ile Arg Ser Gly
35 40 45
Asn Ser Asp Gly Tyr Val Val Gly Glu Asn Asp Asp Leu Gly Arg Ile
50 55 60
Ala Arg Arg Gly Glu Ser Thr Ser Lys Val Leu Ile Pro Gly Leu Pro
65 70 75 80
Asp Glu Ser Asn Gly Glu Ile Ala Ala Arg Ile Ser His Ser His Cys
85 90 95
Glu Trp Lys Pro Lys Leu Arg Val His Tyr Glu Lys Ala Gly Cys Asp
100 105 110
Asn Leu Asp Ala Pro Ala Val Leu Phe Leu Pro Gly Phe Gly Val Gly
115 120 125
Ser Phe His Tyr Glu Lys Gln Leu Thr Asp Leu Gly Arg Asp Tyr Arg
130 135 140
Val Trp Ala Ile Asp Phe Leu Gly Gln Gly Leu Ser Leu Pro Thr Glu
145 150 155 160
Asp Pro Thr Thr Met Thr Glu Glu Thr Ser Ser Ser Glu Asp Lys Glu

```

Met	Thr	Glu	Glu	Thr	Ser	Ser	Ser	Glu	Asp	Lys	Glu	Pro	Phe	Trp	Gly
1				5					10					15	
Phe	Gly	Asp	Lys	Thr	Glu	Pro	Trp	Ala	Asp	Gln	Leu	Val	Phe	Ser	Leu
			20					25					30		
Asp	Leu	Trp	Arg	Asp	Gln	Val	Gln	Tyr	Phe	Val	Glu	Glu	Val	Ile	Gly
		35					40					45			
Glu	Pro	Val	Tyr	Ile	Ala	Gly	Asn	Ser	Leu	Gly	Gly	Tyr	Val	Ala	Leu
		50				55					60				
Tyr	Phe	Ala	Ala	Thr	His	Pro	His	Leu	Val	Lys	Gly	Val	Thr	Leu	Leu
65					70					75				80	
Asn	Ala	Thr	Pro	Phe	Trp	Gly	Phe	Phe	Pro	Asn	Pro	Val	Arg	Ser	Pro
			85						90					95	
Lys	Leu	Ala	Arg	Leu	Phe	Pro	Trp	Pro	Gly	Ala	Phe	Pro	Leu	Pro	Glu
			100					105					110		
Arg	Val	Lys	Lys	Ile	Thr	Glu	Leu	Val	Trp	Gln	Lys	Ile	Ser	Asp	Pro
		115					120					125			

Glu Ser Ile Ala Glu Ile Leu Lys Gln Val Tyr Thr Asp His Ser Thr
130 135 140
Asn Val Asp Lys Val Phe Ser Arg Ile Val Glu Val Thr Gln His Pro
145 150 155 160
Ala Ala Ala Ala Ser Phe Ala Ser Ile Met Leu Ala Pro Gly Gly Glu
165 170 175
Leu Ser Phe Ser Glu Ala Leu Ser Arg Cys Lys Glu Asn Asn Val Gln
180 185 190
Ile Cys Leu Met Tyr Gly Arg Glu Asp Pro Trp Val Arg Pro Leu Trp
195 200 205
Gly Lys Lys Ile Lys Lys Glu Ile Pro Asn Ala Pro Tyr Tyr Glu Ile
210 215 220
Ser Pro Ala Gly His Cys Pro His Asp Glu Val Pro Glu Val Val Asn
225 230 235 240
Tyr Leu Met Arg Gly Trp Ile Lys His Leu Glu Ser Gly Gly Phe Glu
245 250 255
Xaa Ala Pro Ala Phe Gly Gly His
260

(2) INFORMATION FOR SEQ ID NO:2771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1267
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2771:

accacatcac	caatcctcaa	aacagagtaa	cccaaaaaac	agagcaatct	ctaaaaaatc	60
tcaagaaaac	tcactaaaat	gggttcaacg	gcggagacac	aattaactcc	gggtcgaagt	120
accgacgacg	aagctgccc	cttcgccaat	caactagcca	gtgcttcctg	tcttccgat	180
ggctttaaaa	tcgccttag	agcttgacct	tcttgagatt	atggccaaga	atggtttctc	240
catgtctcct	acagagatcg	cttctaaact	tcggacccaa	aacctggaag	ctccggtcat	300
gctcgaccgt	atctcccgtc	ttcttaacgt	ttactccgtc	ttaaacctgc	ccaaccgtaa	360
actttccggt	gatggcggtg	aacggattta	cgggcttggg	ccggttttga	agtatttgac	420
caagaacgaa	gatgggtggt	ccattgctgc	tctttgtcct	atgaaccaag	acaaggttct	480
catggaaaag	tggtaccatt	tgaaggatgc	aattcttgat	gggtgggattc	cattcaacaa	540
ggcttatgga	atgacgcgtg	tcgagtacca	cgggactgac	cctagattca	acaaggttct	600
taacaatgga	atgtctaac	attccacaat	caccatgaag	aagattcttg	agacctataa	660
gggttttgaa	ggattgaact	ctttggttga	tgttgggtgt	ggcattgggtg	ctacactcaa	720
aatgatgttc	tccaagtacc	ctaatcttaa	agggatcaac	tttgatctcc	cacatgtcat	780
tgaagatgct	cctctctcat	ctggattatg	gcattgttga	ggagatatgt	ttgtaagtgt	840
ccctaaaaggt	gatggccatg	tcatgaagtg	gatattgcat	gactggagtg	acgaacattg	900
cgtgaaatc	ttgaaaaact	gctacgagtc	acttccagag	gatggaaaaa	tgatattagc	960
agagtgtata	cttcacagaga	caccagactc	aagcctctca	acccaaacaa	tagtccatgt	1020
cagattgcatt	atgttggctc	acaatcccg	aggcaacgaga	acgaacggaga	aagagtttga	1080
ggcattagcc	aaagcatcag	gcttcaagg	catcaaaagt	Gtctgcgaag	cttttgggtg	1140
taaccttatt	gagttactca	aaagactcta	aaaacaaaca	agtttcttat	gaagatgatt	1200
tatatgtaaa	cattatctca	tatctccttc	cacggttcca	aaactatgct	gtttaataat	1260
gggttttt						

(2) INFORMATION FOR SEQ ID NO:2772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..330

(D) OTHER INFORMATION: / Ceres Seq. ID 1574134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2772:

Met	Ala	Leu	Lys	Ser	Ala	Leu	Glu	Leu	Asp	Leu	Leu	Glu	Ile	Met	Ala
1			5						10					15	
Lys	Asn	Gly	Ser	Pro	Met	Ser	Pro	Thr	Glu	Ile	Ala	Ser	Lys	Leu	Pro
			20					25					30		
Thr	Lys	Asn	Pro	Glu	Ala	Pro	Val	Met	Leu	Asp	Arg	Ile	Leu	Arg	Leu
			35				40					45			
Leu	Thr	Ser	Tyr	Ser	Val	Leu	Thr	Cys	Ser	Asn	Arg	Lys	Leu	Ser	Gly
			50			55					60				
Asp	Gly	Val	Glu	Arg	Ile	Tyr	Gly	Leu	Gly	Pro	Val	Cys	Lys	Tyr	Leu
65				70					75					80	
Thr	Lys	Asn	Glu	Asp	Gly	Val	Ser	Ile	Ala	Leu	Cys	Leu	Met	Asn	
			85					90						95	
Gln	Asp	Lys	Val	Leu	Met	Glu	Ser	Trp	Tyr	His	Leu	Lys	Asp	Ala	Ile
			100				105						110		
Leu	Asp	Gly	Gly	Ile	Pro	Phe	Asn	Lys	Ala	Tyr	Gly	Met	Ser	Ala	Phe
			115				120					125			
Glu	Tyr	His	Gly	Thr	Asp	Pro	Arg	Phe	Asn	Lys	Val	Phe	Asn	Asn	Gly
			130				135				140				
Met	Ser	Asn	His	Ser	Thr	Ile	Thr	Met	Lys	Lys	Ile	Leu	Glu	Thr	Tyr
145				150						155				160	
Lys	Gly	Phe	Glu	Gly	Leu	Thr	Ser	Leu	Val	Asp	Val	Gly	Gly	Gly	Ile
			165						170					175	
Gly	Ala	Thr	Leu	Lys	Met	Ile	Val	Ser	Lys	Tyr	Pro	Asn	Leu	Lys	Gly
			180					185						190	
Ile	Asn	Phe	Asp	Leu	Pro	His	Val	Ile	Glu	Asp	Ala	Pro	Ser	His	Pro
			195				200					205			
Gly	Ile	Glu	His	Val	Gly	Gly	Asp	Met	Phe	Val	Ser	Val	Pro	Lys	Gly
			210			215					220				
Asp	Ala	Ile	Phe	Met	Lys	Trp	Ile	Cys	His	Asp	Trp	Ser	Asp	Glu	His
225				230						235				240	
Cys	Val	Lys	Phe	Leu	Lys	Asn	Cys	Tyr	Glu	Ser	Leu	Pro	Glu	Asp	Gly
			245						250					255	
Lys	Val	Ile	Leu	Ala	Glu	Cys	Ile	Leu	Pro	Glu	Thr	Pro	Asp	Ser	Ser
			260				265						270		
Leu	Ser	Thr	Lys	Gln	Val	Val	His	Val	Asp	Cys	Ile	Met	Leu	Ala	His
			275				280					285			
Asn	Pro	Gly	Gly	Lys	Glu	Arg	Thr	Glu	Lys	Glu	Phe	Glu	Ala	Leu	Ala
			290			295					300				
Lys	Ala	Ser	Gly	Phe	Lys	Gly	Ile	Lys	Val	Val	Cys	Asp	Ala	Phe	Gly
305				310						315					320
Val	Asn	Leu	Ile	Glu	Leu	Leu	Lys	Lys	Leu						
			325						330						

(2) INFORMATION FOR SEQ ID NO:2773:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..316

(D) OTHER INFORMATION: / Ceres Seq. ID 1574135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2773:

Met	Ala	Lys	Asn	Gly	Ser	Pro	Met	Ser	Pro	Thr	Glu	Ile	Ala	Ser	Lys
1			5							10				15	
Leu	Pro	Thr	Lys	Asn	Pro	Glu	Ala	Pro	Val	Met	Leu	Asp	Arg	Ile	Leu
			20					25					30		

Arg Leu Leu Thr Ser Tyr Ser Val Leu Thr Cys Ser Asn Arg Lys Leu
35 40 45
Ser Gly Asp Gly Val Glu Arg Ile Tyr Gly Leu Gly Pro Val Cys Lys
50 55 60
Tyr Leu Thr Lys Asn Glu Asp Gly Val Ser Ile Ala Ala Leu Cys Leu
65 70 75 80
Met Asn Gln Asp Lys Val Leu Met Glu Ser Trp Tyr His Leu Lys Asp
85 90 95
Ala Ile Leu Asp Gly Gly Ile Pro Phe Asn Lys Ala Tyr Gly Met Ser
100 105 110
Ala Phe Glu Tyr His Gly Thr Asp Pro Arg Phe Asn Lys Val Phe Asn
115 120 125
Asn Gly Met Ser Asn His Ser Thr Ile Thr Met Lys Lys Ile Leu Glu
130 135 140
Thr Tyr Lys Gly Phe Glu Gly Leu Thr Ser Leu Val Asp Val Gly Gly
145 150 155 160
Gly Ile Gly Ala Thr Leu Lys Met Ile Val Ser Lys Tyr Pro Asn Leu
165 170 175
Lys Gly Ile Asn Phe Asp Leu Pro His Val Ile Glu Asp Ala Pro Ser
180 185 190
His Pro Gly Ile Glu His Val Gly Gly Asp Met Phe Val Ser Val Pro
195 200 205
Lys Gly Asp Ala Ile Phe Met Lys Trp Ile Cys His Asp Trp Ser Asp
210 215 220
Glu His Cys Val Lys Phe Leu Lys Asn Cys Tyr Glu Ser Leu Pro Glu
225 230 235 240
Asp Gly Lys Val Ile Leu Ala Glu Cys Ile Leu Pro Glu Thr Pro Asp
245 250 255
Ser Ser Leu Ser Thr Lys Gln Val Val His Val Asp Cys Ile Met Leu
260 265 270
Ala His Asn Pro Gly Gly Lys Glu Arg Thr Glu Lys Glu Phe Glu Ala
275 280 285
Leu Ala Lys Ala Ser Gly Phe Lys Gly Ile Lys Val Val Cys Asp Ala
290 295 300
Phe Gly Val Asn Leu Ile Glu Leu Leu Lys Lys Leu
305 310 315

(2) INFORMATION FOR SEQ ID NO:2774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..309
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2774:

Met Ser Pro Thr Glu Ile Ala Ser Lys Leu Pro Thr Lys Asn Pro Glu
1 5 10 15
Ala Pro Val Met Leu Asp Arg Ile Leu Arg Leu Leu Thr Ser Tyr Ser
20 25 30
Val Leu Thr Cys Ser Asn Arg Lys Leu Ser Gly Asp Gly Val Glu Arg
35 40 45
Ile Tyr Gly Leu Gly Pro Val Cys Lys Tyr Leu Thr Lys Asn Glu Asp
50 55 60
Gly Val Ser Ile Ala Ala Leu Cys Leu Met Asn Gln Asp Lys Val Leu
65 70 75 80
Met Glu Ser Trp Tyr His Leu Lys Asp Ala Ile Leu Asp Gly Gly Ile
85 90 95
Pro Phe Asn Lys Ala Tyr Gly Met Ser Ala Phe Glu Tyr His Gly Thr

100										105										110											
Asp	Pro	Arg	Phe	Asn	Lys	Val	Phe	Asn	Asn	Gly	Met	Ser	Asn	His	Ser	Thr	Ile	Thr	Met	Lys	Lys	Ile	Leu	Glu	Thr	Tyr	Lys	Gly	Phe	Glu	Gly
115							120									130															
Thr	Ile	Thr	Met	Lys	Lys	Ile	Leu	Glu	Thr	Tyr	Lys	Gly	Phe	Glu	Gly	Leu	Thr	Ser	Leu	Val	Asp	Val	Gly	Gly	Gly	Ile	Gly	Ala	Thr	Leu	Lys
130							135									145															
Met	Ile	Val	Ser	Lys	Tyr	Pro	Asn	Leu	Lys	Gly	Ile	Asn	Phe	Asp	Leu	155															
165							170									175															
Pro	His	Val	Ile	Glu	Asp	Ala	Pro	Ser	His	Pro	Gly	Ile	Glu	His	Val	180															
185							190									195															
Gly	Gly	Asp	Met	Phe	Val	Ser	Val	Pro	Lys	Gly	Asp	Ala	Ile	Phe	Met	200															
205							210									215															
Lys	Trp	Ile	Cys	His	Asp	Trp	Ser	Asp	Glu	His	Cys	Val	Lys	Phe	Leu	220															
225							230									235															
Lys	Asn	Cys	Tyr	Glu	Ser	Leu	Pro	Glu	Asp	Gly	Lys	Val	Ile	Leu	Ala	240															
245							250									255															
Glu	Cys	Ile	Leu	Pro	Glu	Thr	Pro	Asp	Ser	Ser	Leu	Ser	Thr	Lys	Gln	260															
265							270									275															
Val	Val	His	Val	Asp	Cys	Ile	Met	Leu	Ala	His	Asn	Pro	Gly	Gly	Lys	280															
285							290									295															
Glu	Arg	Thr	Glu	Lys	Glu	Phe	Glu	Ala	Leu	Ala	Lys	Ala	Ser	Gly	Phe	300															
305																															
Lys	Gly	Ile	Lys	Val	Val	Cys	Asp	Ala	Phe	Gly	Val	Asn	Leu	Ile	Glu																
310																															
Leu	Leu	Lys	Lys	Leu																											

(2) INFORMATION FOR SEQ ID NO:2775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..686
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2775:

aaaaaccac	cattcaaac	aaacacaaa	acaaaaaaa	aaacatttcc	ccaaaaaaa	60
aaaaacagag	gatgaacaa	aaccagagca	agtttttgag	aataatctca	acgcctctaa	120
gagcttttag	caaggccat	gattttctac	tgagaagcat	cacoggttgc	gcaGctcgga	180
ctcaatattc	ctctccgcg	tcogtctcgc	ctctttttcc	aagaagccgg	agctctctct	240
cgcgcgcctt	ctctctctcc	gcacatctcc	ggagaaccac	cgatttcggg	atagatgaag	300
attacagcga	gctagtgaga	gctgcgtcgg	tgaggagtgt	agggcacaag	aatgatagat	360
acatgttgat	acaagagaag	ctgcaacagc	agaagcaaca	gaagcaagga	gggttgcta	420
agagctcgag	tgctgggagt	gcgaggatag	aggaagagga	agaaacagag	gaaggatctg	480
tgaatccgaa	Ggtgaagaag	actaagaaag	tctctgatct	tttgatctct	cgtagcaaat	540
cttacgccgt	tactactagt	accctatct	tgtaacttct	cttcttattt	tttctctctc	600
ttaattttag	tattttgtgg	attgattatc	attttctagc	tcgatttttc	gtgcactgtg	660
aaatactatt	ttctagcttt	gatttt				

(2) INFORMATION FOR SEQ ID NO:2776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..190

Lys	Pro	Thr	Ile	Gln	Thr	Lys	His	Lys	Asn	Lys	Lys	Lys	Asn	Ile	Ser
1				5					10					15	
Pro	Lys	Lys	Lys	Lys	Gln	Arg	Met	Lys	Gln	Asn	Gln	Ser	Lys	Phe	Leu
			20					25					30		
Arg	Ile	Ile	Ser	Thr	Pro	Leu	Arg	Ala	Leu	Gly	Lys	Ala	Arg	Asp	Phe
		35					40					45			
Tyr	Val	Arg	Ser	Ile	Thr	Gly	Cys	Ala	Ala	Arg	Thr	Gln	Tyr	Ser	Ser
	50					55					60				
Ser	Ala	Ser	Val	Ser	Ala	Pro	Phe	Pro	Arg	Ser	Arg	Ser	Ser	Ser	Ser
65					70					75				80	
Ala	Ala	Phe	Ser	Ser	Ser	Ala	Ser	Ser	Arg	Arg	Thr	Thr	Asp	Phe	Gly
				85					90					95	
Ile	Asp	Glu	Asp	Tyr	Ser	Glu	Leu	Val	Arg	Ala	Ala	Ser	Val	Arg	Ser
			100					105					110		
Leu	Gly	His	Lys	Asn	Glu	Ile	Asp	Met	Leu	Ile	Gln	Glu	Lys	Leu	Gln
		115					120					125			
Gln	Gln	Lys	Gln	Gln	Lys	Gln	Gly	Gly	Leu	Pro	Lys	Ser	Ser	Ser	Ala
		130				135					140				
Gly	Met	Ala	Arg	Ile	Glu	Glu	Glu	Glu	Glu	Thr	Glu	Glu	Gly	Ser	Val
145					150					155					160
Asn	Pro	Lys	Val	Lys	Lys	Thr	Lys	Lys	Val	Ser	Asp	Leu	Leu	Tyr	Pro
				165					170					175	
Arg	Ser	Lys	Ser	Tyr	Ala	Val	Thr	Thr	Ser	Thr	Pro	Ile	Leu		
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:2778:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 892 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..892
(D) OTHER INFORMATION: / Ceres Seq. ID 1574148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2778:

aatcaaaaaa	ctatccactc	tcagcccgaa	aatttttctc	tgattcatta	cgacagagag	60
aaccatgccg	gcgaacacaga	ggaccgccga	gGtcaacaga	aacctgatc	tgatcagggg	120
gtgttgtaaa	tactcgagat	ccagatgta	ccataagaga	ggttgtggg	ctatcaaggc	180
caaaaatgga	ggcgttttcc	cacgtcacga	cgctaaatct	aaggttgatg	ctccgggtgga	240
gaagccaccg	aagtctctatc	cagctgaaga	tgttaaagaa	ccctccccc	acagggcgac	300
ggcaaaacca	accaagctca	gagctagcat	tactccaggt	acagtgttga	ttatccctgc	360
tggtgagttc	aagggaaga	gagttgtctt	ccttaagcag	cttgctctg	gtttgcttct	420
tgtgactgga	ccattcaaga	tcaatggtgt	tcctttgaga	cgtgttaacc	agggcctatgt	480
gattggcact	tccacaaagg	ttgacatttc	tggagtcacc	ctcgataaat	tcgatgataa	540
gtactttggc	aaggttgctg	agaagaaaaa	gaagaagaca	gaaggagagt	tccttgaggc	600
tgagaaagag	gagaagaagg	agatccacca	ggtgaagaaa	gatgaccaga	aagctgtgga	660
tgcagctttg	atcaaaagca	ttgaagcagt	tcagagttg	aagacttacc	ttggcgcaag	720
gtttctcattg	aaacaaggaa	tgaagcccca	tgagcttggt	ttctagattt	cattactttt	780
ttcttgaggt	ctctagagta	tctgtctctc	gaagtgtttt	accttctaaa	tggtgtgttt	840
gttctgtgtc	actgaacaca	tacaattttt	ggcttatata	ttctctgttc	tt	

(2) INFORMATION FOR SEQ ID NO:2779:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..233
(D) OTHER INFORMATION: / Ceres Seq. ID 1574149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2779:

Met	Pro	Ala	Lys	Gln	Arg	Thr	Pro	Lys	Val	Asn	Arg	Asn	Pro	Asp	Leu
1				5					10					15	
Ile	Arg	Gly	Val	Gly	Lys	Tyr	Ser	Arg	Ser	Gln	Met	Tyr	His	Lys	Arg
			20					25					30		
Gly	Leu	Trp	Ala	Ile	Lys	Ala	Lys	Asn	Gly	Gly	Val	Phe	Pro	Arg	His
			35			40						45			
Asp	Ala	Lys	Ser	Lys	Val	Asp	Ala	Pro	Val	Glu	Lys	Pro	Pro	Lys	Phe
			50			55					60				
Tyr	Pro	Ala	Glu	Asp	Val	Lys	Lys	Pro	Leu	Pro	Asn	Arg	Arg	Thr	Ala
			65		70				75					80	
Lys	Pro	Thr	Lys	Leu	Arg	Ala	Ser	Ile	Thr	Pro	Gly	Thr	Val	Leu	Ile
			85					90						95	
Ile	Leu	Ala	Gly	Arg	Phe	Lys	Gly	Lys	Arg	Val	Val	Phe	Leu	Lys	Gln
			100					105					110		
Leu	Ala	Ser	Gly	Leu	Leu	Leu	Val	Thr	Gly	Pro	Phe	Lys	Ile	Asn	Gly
			115			120						125			
Val	Pro	Leu	Arg	Arg	Val	Asn	Gln	Ala	Tyr	Val	Ile	Gly	Thr	Ser	Thr
			130			135					140				
Lys	Val	Asp	Ile	Ser	Gly	Val	Thr	Leu	Asp	Lys	Phe	Asp	Asp	Lys	Tyr
			145			150				155				160	
Phe	Gly	Lys	Val	Ala	Glu	Lys	Lys	Lys	Lys	Lys	Thr	Glu	Gly	Glu	Phe
			165					170						175	
Phe	Glu	Ala	Glu	Lys	Glu	Glu	Lys	Lys	Glu	Ile	Pro	Gln	Val	Lys	Lys

180 185 190
Asp Asp Gln Lys Ala Val Asp Ala Ala Leu Ile Lys Ala Ile Glu Ala
195 200 205
Val Pro Glu Leu Lys Thr Tyr Leu Gly Ala Arg Phe Ser Leu Lys Gln
210 215 220
Gly Met Lys Pro His Glu Leu Val Phe
225 230

(2) INFORMATION FOR SEQ ID NO:2780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..206
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2780:

Met Tyr His Lys Arg Gly Leu Trp Ala Ile Lys Ala Lys Asn Gly Gly
1 5 10 15
Val Phe Pro Arg His Asp Ala Lys Ser Lys Val Asp Ala Pro Val Glu
20 25 30
Lys Pro Pro Lys Phe Tyr Pro Ala Glu Asp Val Lys Lys Pro Leu Pro
35 40 45
Asn Arg Arg Thr Ala Lys Pro Thr Lys Leu Arg Ala Ser Ile Thr Pro
50 55 60
Gly Thr Val Leu Ile Ile Leu Ala Gly Arg Phe Lys Gly Lys Arg Val
65 70 75 80
Val Phe Leu Lys Gln Leu Ala Ser Gly Leu Leu Val Thr Gly Pro
85 90 95
Phe Lys Ile Asn Gly Val Pro Leu Arg Arg Val Asn Gln Ala Tyr Val
100 105 110
Ile Gly Thr Ser Thr Lys Val Asp Ile Ser Gly Val Thr Leu Asp Lys
115 120 125
Phe Asp Asp Lys Tyr Phe Gly Lys Val Ala Glu Lys Lys Lys Lys
130 135 140
Thr Glu Gly Glu Phe Phe Glu Ala Glu Lys Glu Glu Lys Lys Glu Ile
145 150 155 160
Pro Gln Val Lys Lys Asp Asp Gln Lys Ala Val Asp Ala Ala Leu Ile
165 170 175
Lys Ala Ile Glu Ala Val Pro Glu Leu Lys Thr Tyr Leu Gly Ala Arg
180 185 190
Phe Ser Leu Lys Gln Gly Met Lys Pro His Glu Leu Val Phe
195 200 205

(2) INFORMATION FOR SEQ ID NO:2781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1013 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1013
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2781:

cacaacttac tcttgctcgca tgcttaacgcc gttgacgcat tcagaaaaatg caaacagtggt 60
gctgaggagta aaatagggaat tgcacacagt ccagcttggt tcgaaccaca agaccttgag 120
catgtggag gttccattga acgtgtgctt gatttcatcc taggatggca ttgggtcca 180
acaacttatg gagattatcc acaatcgatg aaggatcgtg tcggtcatag attgccaaaa 240

(2) INFORMATION FOR SEQ ID NO:2782:

(A) LENGTH: 278 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ix) FEATURE:

(1A) FEATURE:
(A) NAME

(A) NAME/KEY: peptide
(B) LOCATION: 1 278

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO: 2762:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2782:
Asp Leu Leu Leu Ser His Ala Thr Ala Val A

Phe	Asn	Leu	Leu	Ser	His	Ala	Tyr	Val	Asp	Ala	Phe
Cys	Lys	Gln	Cys	Gly	Gly	Lys	Ile	Gly	Ile	His	Ser
Trp	Phe	Glu	Pro	Gln	Asp	Leu	Glu	His	Val	Gly	Gly
Val	Leu	Asp	Phe	Ile	Leu	Gly	Trp	His	Leu	Ala	Pro
Asp	Tyr	Pro	Gln	Ser	Met	Lys	Asp	Arg	Val	Gly	His
Phe	Thr	Glu	Ala	Gly	Lys	Lys	Leu	Leu	Lys	Gly	Ser
Gly	Met	Asn	Tyr	Tyr	Thr	Ser	Val	Phe	Ala	Lys	Glu
Pro	Lys	Asn	Pro	Ser	Trp	Thr	Thr	Asp	Ser	Leu	Val
Lys	Ser	Val	Asp	Gly	Tyr	Lys	Ile	Gly	Ser	Lys	Pro
Leu	Asp	Val	Tyr	Ser	Lys	Gly	Leu	Arg	Tyr	Leu	Lys
Asp	Asn	Tyr	Gly	Asp	Pro	Glu	Val	Ile	Ile	Ala	Glu
Glu	Asp	Leu	Gly	Glu	Lys	His	Asn	Asp	Val	Asn	Phe
His	Asn	Arg	Lys	Tyr	Tyr	Ile	Gln	Arg	His	Leu	Leu
Ala	Ile	Cys	Lys	Asp	Lys	Val	Asn	Val	Thr	Gly	Tyr
Leu	Met	Asp	Asn	Phe	Glu	Trp	Gln	Asp	Gly	Tyr	Lys
Leu	Tyr	Tyr	Ile	Asp	Phe	Gln	Asn	Asn	Leu	Thr	Arg
Ser	Gly	Lys	Trp	Tyr	Ser	Glu	Phe	Leu	Lys	Pro	Gln
Lys	Leu	Arg	Glu	Glu	Leu						

(2) INFORMATION FOR SEQ ID NO:2783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..209

(D) OTHER INFORMATION: / Ceres Seq. ID 1574153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2783:

Met Lys Asp Arg Val Gly His Arg Leu Pro Lys Phe Thr Glu Ala Glu
1 5 10 15
Lys Lys Leu Leu Lys Gly Ser Thr Asp Tyr Val Gly Met Asn Tyr Tyr
20 25 30
Thr Ser Val Phe Ala Lys Glu Ile Ser Pro Asp Pro Lys Asn Pro Ser
35 40 45
Trp Thr Thr Asp Ser Leu Val Asp Trp Asp Ser Lys Ser Val Asp Gly
50 55 60
Tyr Lys Ile Gly Ser Lys Pro Phe Asn Gly Lys Leu Asp Val Tyr Ser
65 70 75 80
Lys Gly Leu Arg Tyr Leu Leu Lys Tyr Ile Lys Asp Asn Tyr Gly Asp
85 90 95
Pro Glu Val Ile Ile Ala Glu Asn Gly Tyr Gly Glu Asp Leu Gly Glu
100 105 110
Lys His Asn Asp Val Asn Phe Gly Thr Gln Asp His Asn Arg Lys Tyr
115 120 125
Tyr Ile Gln Arg His Leu Leu Ser Met His Asp Ala Ile Cys Lys Asp
130 135 140
Lys Val Asn Val Thr Gly Tyr Phe Val Trp Ser Leu Met Asp Asn Phe
145 150 155 160
Glu Trp Gln Asp Gly Tyr Lys Ala Arg Phe Gly Leu Tyr Tyr Ile Asp
165 170 175
Phe Gln Asn Asn Leu Thr Arg His Gln Lys Val Ser Gly Lys Trp Tyr
180 185 190
Ser Glu Phe Leu Lys Pro Gln Phe Pro Thr Ser Lys Leu Arg Glu Glu
195 200 205
Leu

(2) INFORMATION FOR SEQ ID NO:2784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..181

(D) OTHER INFORMATION: / Ceres Seq. ID 1574154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2784:

Met Asn Tyr Tyr Thr Ser Val Phe Ala Lys Glu Ile Ser Pro Asp Pro
1 5 10 15
Lys Asn Pro Ser Trp Thr Thr Asp Ser Leu Val Asp Trp Asp Ser Lys
20 25 30
Ser Val Asp Gly Tyr Lys Ile Gly Ser Lys Pro Phe Asn Gly Lys Leu
35 40 45
Asp Val Tyr Ser Lys Gly Leu Arg Tyr Leu Leu Lys Tyr Ile Lys Asp
50 55 60
Asn Tyr Gly Asp Pro Glu Val Ile Ile Ala Glu Asn Gly Tyr Gly Glu

Met Ala Thr Glu Ser Tyr Glu Ala Ala Ile Lys Gly Leu Asn Asp Leu
1 5 10 15
Leu Ser Thr Lys Ala Asp Leu Gly Asn Val Ala Ala Ala Lys Ile Lys

Met	Val	Pro	Pro	Glu	Asp	Gln	Lys	Arg	His	Ser	Gly	Val	Gly	Ala	Ala
1			5						10					15	
Val	Glu	Tyr	Ala	Val	Val	His	Leu	Lys	Val	Glu	Asn	Ile	Leu	Val	Ile
			20					25					30		
Gly	His	Ser	Cys	Gly	Gly	Ile	Lys	Gly	Leu	Met	Ser	Ile	Glu	Asp	
		35				40					45				
Asp	Ala	Ala	Pro	Thr	Gln	Ser	Asp	Phe	Ile	Glu	Asn	Trp	Val	Lys	Ile
	50					55					60				
Gly	Ala	Ser	Ala	Arg	Asn	Lys	Ile	Lys	Glu	Glu	His	Lys	Asp	Leu	Ser
65				70						75				80	
Tyr	Asp	Asp	Gln	Cys	Asn	Lys	Cys	Glu	Lys	Glu	Ala	Val	Asn	Val	Ser
			85					90					95		
Leu	Gly	Asn	Leu	Leu	Ser	Tyr	Pro	Phe	Val	Arg	Ala	Glu	Val	Val	Lys
			100					105					110		
Asn	Thr	Leu	Ala	Ile	Arg	Gly	Gly	His	Thr	Asn	Phe	Val	Lys	Gly	Thr
		115				120						125			
Phe	Asp	Leu	Trp	Glu	Leu	Asp	Phe	Lys	Thr	Thr	Pro	Ala	Phe	Ala	Phe
	130					135					140				

Ser
145

(2) INFORMATION FOR SEQ ID NO:2788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..683
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2788:

aacaacttaa	acagatat	ttt	cataaggaaa	atgaagggtg	agtttttcac	attgatggca	60
ataatgtctc	tctcttagc	cttctcgta	gtccatggag	gaggagagtc	tggaacacct		120
tctaatagcg	cogctacccc	gactagccca	accgaaGgat	ccagtgggtc	aagtgggtca		180
gctcatggac	ctaattgggg	atatagtktg	ggatgggggt	cagccccggg	aggtgtttat		240
ggctatgggt	ctgggtcggg	tcgctacca	gatggaggag	gaaaaggggc	tggattcggg		300
tttggttcgg	ggctcaggtc	aggaactgga	tttgggtctg	gctcggggag	aggaggagcc		360
acagacgggtg	gttctggcca	tggaaagtgg	accggacacg	ctgggttaagg	cgggtggctca		420
ggaagtggaa	atggtagaag	atctcctgtg	cgtagagaga	ggagccaaca	ccgctaaaag		480
aagttttctt	gttattatta	ctaccttaac	acaatcacac	atgcgtaaga	tgataaagat		540
aaaagaagga	aaaagaaaaa	tactatagta	gcattcttaat	taattaatgc	ataaataagg		600
accaaaaggaa	taagtagtgtg	ggctttaatt	accgctgtac	tttgtaatat	aactaaacct		660
ataatatatt	gtgtctctgc	gcc					

(2) INFORMATION FOR SEQ ID NO:2789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2789:

Asn	Asn	Leu	Asn	Arg	Tyr	Phe	Ile	Arg	Lys	Met	Lys	Gly	Glu	Phe	Phe
1				5					10					15	
Thr	Leu	Met	Ala	Ile	Met	Ser	Leu	Leu	Leu	Ala	Phe	Ser	Leu	Val	His
			20					25					30		
Gly	Gly	Gly	Glu	Ser	Gly	Thr	Pro	Ser	Asn	Ala	Ala	Ala	Thr	Pro	Thr
			35				40					45			
Ser	Pro	Thr	Glu	Gly	Ser	Ser	Gly	Ser	Ser	Gly	Ser	Ala	His	Gly	Pro
			50				55				60				
Asn	Trp	Gly	Tyr	Ser	Xaa	Gly	Trp	Gly	Ser	Ala	Pro	Gly	Gly	Gly	Tyr
			65			70				75				80	
Gly	Tyr	Gly	Ser	Gly	Ser	Gly	Ser	Ser	Pro	Asp	Gly	Gly	Gly	Lys	Gly
			85						90					95	
Ala	Gly	Phe	Gly	Phe	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Gly	Phe	Gly
			100						105					110	
Ser	Gly	Ser	Gly	Gly	Gly	Gly	Ala	Thr	Asp	Gly	Gly	Ser	Gly	His	Gly
			115				120						125		
Ser	Gly	Thr	Gly	His	Ala	Gly									
			130			135									

(2) INFORMATION FOR SEQ ID NO:2790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..157
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574164
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2790:
Met Glu Glu Glu Ser Leu Glu His Leu Met Gln Pro Leu Pro Arg
1 5 10 15
Leu Ala Gln Pro Lys Asp Pro Val Val Gln Val Val Gln Leu Met Asp
 20 25 30
Leu Ile Gly Asp Ile Val Xaa Asp Gly Val Gln Pro Arg Glu Val Val
 35 40 45
Met Ala Met Val Leu Val Arg Val Arg His Gln Met Glu Glu Glu Lys
50 55 60
Gly Leu Asp Ser Gly Leu Val Arg Gly Gln Val Gln Glu Leu Asp Leu
65 70 75 80
Gly Leu Ala Arg Glu Glu Glu Pro Gln Thr Val Val Leu Ala Met
 85 90 95
Glu Val Gly Pro Asp Thr Leu Val Lys Ala Val Ala Gln Glu Val Glu
100 105 110
Met Val Lys Asp Leu Leu Val Val Glu Arg Gly Ala Asn Thr Ala Lys
115 120 125
Arg Ser Phe Leu Val Ile Ile Thr Thr Leu Thr Gln Ser His Met Arg
130 135 140
Lys Met Ile Arg Leu Lys Glu Gly Lys Arg Lys Ile Leu
145 150 155

(2) INFORMATION FOR SEQ ID NO:2791:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 147 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..147
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574165
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2791:
Met Gln Pro Leu Pro Arg Leu Ala Gln Pro Lys Asp Pro Val Val Gln
1 5 10 15
Val Val Gln Leu Met Asp Leu Ile Gly Asp Ile Val Xaa Asp Gly Val
 20 25 30
Gln Pro Arg Glu Val Val Met Ala Met Val Leu Val Arg Val Arg His
35 40 45
Gln Met Glu Glu Glu Lys Gly Leu Asp Ser Gly Leu Val Arg Gly Gln
50 55 60
Val Gln Glu Leu Asp Leu Gly Leu Ala Arg Glu Glu Glu Pro Gln
65 70 75 80
Thr Val Val Leu Ala Met Glu Val Gly Pro Asp Thr Leu Val Lys Ala
 85 90 95
Val Ala Gln Glu Val Glu Met Val Lys Asp Leu Leu Val Val Glu Arg
100 105 110
Gly Ala Asn Thr Ala Lys Arg Ser Phe Leu Val Ile Ile Thr Thr Leu
115 120 125
Thr Gln Ser His Met Arg Lys Met Ile Arg Leu Lys Glu Gly Lys Arg
130 135 140
Lys Ile Leu
145

(2) INFORMATION FOR SEQ ID NO:2792:
 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..2133
(D) OTHER INFORMATION: / Ceres Seq. ID 1574194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2792:

atgcccttcg	gactcaagaa	cgccggggca	acctatcaac	gottcgtcaa	caaaatcttc	60
gcattacaga	gtccggaagc	atggaaagt	tacatgcagc	acatgttggt	gaaatccatg	120
acagagaaa	atcacatata	ccatttacgc	gaatgtttca	agcagcttaa	cctctacaac	180
gtcaagctca	atcctgcaaa	gtgcgccttc	ggagtaagat	ccggcatcga	ggcaaatccg	240
aagcaaatcg	aggcattgtt	cggaatggcg	tcacctcaga	acaagccaga	agtgacgtgc	300
ctaaocggaa	gagttgcggc	ccttaaccgt	tctatctctc	gtcacaaccga	aaaatgttta	360
gccttttacc	ttgtgcttcg	gggaaacaaa	aagttcgaat	ggacgaccgc	atgcgaagaa	420
gctttttcag	aactcaagaa	gtacctggca	actccaccca	tcctcgcaaa	accgcgtaac	480
ggagaaccac	ataacttgta	tggtgctgta	tcagataacta	cggtcagcgg	agaattagtc	540
cgagaagaca	gaggcgagca	gaaactgatt	ttttacgtct	cgcaaatctt	caccagcgca	600
gaatctcgct	atccgcaaat	ggaaaaaact	gctttagcag	tcgtaatgtc	ggctcagaag	660
cttcgaccc	acttccaatc	ccattccatc	atagtaatgg	gatccatgcc	actctgcgtc	720
atcttacaca	gtccaagcca	atcaggacgt	ctggctaagt	ggacaatcga	gctcagcgaa	780
tacgacatcg	agtatcagaa	caaaacatgt	gcacaaatgc	gtcgtctcat	cgaagcaagg	840
ctcgggtgta	ggcatccgct	tcacctcacc	aacaggagag	gtcctcgagt	agtcattaag	900
attaaacttc	gaggctacca	acaatgtggc	cgactcatcg	cgaatcaatt	caacggagaa	960
tacacaactc	aggacaaaaa	gatggaagcc	tacctgatcc	atgttcaaaa	ctatcgcaag	1020
aatttcgacg	aattcggatt	gcaaaggatt	ccacgaggag	aaaatacatc	ggctgatgcc	1080
ctggctgcct	tagctctcac	atctgcacac	atctcgaaaa	gagtcacccc	gggtgaaattc	1140
attgagaagc	caagtattga	ctcggcgaaa	gaagaacatg	tcctcccaat	acaaatcagc	1200
gcggatcaag	acgacccaca	tgaactgcaac	tcagaatgga	tggaacccat	cataagctat	1260
atcccggaag	ggaaattgac	ctcagacaaa	tggaaagctc	ggaaacttta	agctcagcgt	1320
gcacgtttcg	tctcagttaga	tgcaaaaact	tacaaatggc	gattatccgg	gcctttagtg	1380
acatgcgtgg	aagcagaagc	gatttgcaag	atcatgaagg	aaattcacgg	tggtctgtgc	1440
ggaaatcatt	ccggggggaag	ggcttttagcc	attaaaaata	aacgccaagg	atttttctgg	1500
ccgacaatga	tcaaaagacta	mgaaaatttt	tcaaaaacat	gcgaaaaatg	tcaaaagccat	1560
gcgcaaacaa	tccatcagcc	ggccgagctc	ttgtcttcaa	tcgctcgccc	gtaaccattc	1620
atcgatgggt	caatggatat	aattggacca	atgcacccct	cgaaggagaa	aaaaatagtt	1680
ctcgtcctga	cagactattt	ctctaagtgg	atagaggccg	aattttacgc	cagcataaag	1740
gacgtcgaag	tcgagaaact	cggtgtgaaa	catatccctat	gtcgccacgg	gataccttat	1800
gagatcgtta	cgataaacgg	ctcgcagttt	atatcgacc	gcttccaagg	cttctgtgat	1860
aaatggggaa	ttcgacttag	caagtcaaca	ccacaatatc	cccaaggaaa	cgcccaagcc	1920
gaggccggca	acgaagaaca	aggtgttcta	tggtgtcatc	ggacaactcc	tcgccgagcc	1980
acaagagaaa	ccccctttgc	ctccgtctac	ggaacgggat	gcgtaattcc	agctgaaatg	2040
attgtaccaa	gcctacgcgc	aagtcctatc	cccgaggacg	atcctgataa	tactcagagg	2100
ccccctgacg	aactcgatct	gatcgatgaa	tga			

(2) INFORMATION FOR SEQ ID NO:2793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 710 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..710
(D) OTHER INFORMATION: / Ceres Seq. ID 1574195
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2793:

Met	Tyr	Gly	Leu	Lys	Asn	Ala	Gly	Ala	Thr	Tyr	Gln	Arg	Phe	Val
1			5				10				15			
Asn	Lys	Ile	Phe	Ala	Leu	Gln	Ile	Gly	Lys	Thr	Met	Glu	Val	Tyr

20										25					30				
Asp	Asp	Met	Leu	Val	Lys	Ser	Met	Thr	Glu	Lys	Asp	His	Ile	Ser	His				
35	35	35					40				45								
Leu	Arg	Glu	Cys	Phe	Lys	Gln	Leu	Asn	Leu	Tyr	Asn	Val	Lys	Leu	Asn				
50	50					55				60									
Pro	Ala	Lys	Cys	Arg	Phe	Gly	Val	Arg	Ser	Gly	Ile	Glu	Ala	Asn	Pro				
65					70				75						80				
Lys	Gln	Ile	Glu	Ala	Leu	Phe	Gly	Met	Ala	Ser	Pro	Gln	Asn	Lys	Arg				
				85					90					95					
Glu	Val	Gln	Cys	Leu	Thr	Gly	Arg	Val	Ala	Ala	Leu	Asn	Arg	Phe	Ile				
			100					105						110					
Ser	Arg	Ser	Thr	Glu	Lys	Cys	Leu	Ala	Phe	Tyr	Val	Val	Leu	Arg	Gly				
		115					120					125							
Asn	Lys	Lys	Phe	Glu	Trp	Thr	Thr	Arg	Cys	Glu	Glu	Ala	Phe	Gln	Glu				
	130					135					140								
Leu	Lys	Lys	Tyr	Leu	Ala	Thr	Pro	Pro	Ile	Leu	Lys	Pro	Val	Ile					
145					150					155				160					
Gly	Glu	Pro	Gln	Tyr	Leu	Tyr	Val	Ala	Val	Ser	Asp	Thr	Thr	Val	Ser				
				165					170					175					
Gly	Glu	Leu	Val	Arg	Glu	Asp	Arg	Gly	Glu	Gln	Lys	Leu	Ile	Phe	Tyr				
			180					185					190						
Val	Ser	Gln	Thr	Phe	Thr	Ser	Ala	Glu	Ser	Arg	Tyr	Pro	Gln	Met	Glu				
		195					200					205							
Lys	Ser	Ala	Leu	Ala	Val	Val	Met	Ser	Ala	Gln	Lys	Leu	Arg	Pro	Tyr				
	210					215					220								
Phe	Gln	Ser	His	Ser	Ile	Ile	Val	Met	Gly	Ser	Met	Pro	Leu	Cys	Val				
225					230					235				240					
Ile	Leu	His	Ser	Pro	Ser	Gln	Ser	Gly	Arg	Leu	Ala	Lys	Trp	Thr	Ile				
				245					250					255					
Glu	Leu	Ser	Glu	Tyr	Asp	Ile	Glu	Tyr	Gln	Asn	Lys	Thr	Cys	Ala	Lys				
								265						270					
Ser	Arg	Leu	Val	Ile	Glu	Ala	Arg	Leu	Gly	Cys	Arg	His	Pro	Ser	His				
	275						280					285							
Leu	Thr	Asn	Arg	Arg	Gly	Pro	Arg	Val	Val	Ile	Lys	Ile	Lys	Leu	Arg				
	290					295					300								
Gly	Tyr	Gln	Gln	Cys	Gly	Arg	Leu	Ile	Ala	Asn	Gln	Phe	Asn	Gly	Glu				
305					310				315					320					
Tyr	Thr	Thr	Gln	Asp	Lys	Lys	Met	Glu	Ala	Tyr	Leu	Ile	His	Val	Gln				
				325					330					335					
Asn	Leu	Ala	Lys	Asn	Phe	Asp	Glu	Phe	Glu	Leu	Thr	Arg	Ile	Pro	Arg				
			340					345					350						
Gly	Glu	Asn	Thr	Ser	Ala	Asp	Ala	Leu	Ala	Ala	Leu	Ala	Ser	Thr	Ser				
	355					360					365								
Asp	Thr	Ile	Leu	Lys	Arg	Val	Ile	Pro	Val	Glu	Phe	Ile	Glu	Lys	Pro				
	370					375					380								
Ser																			

Gln Cys Glu Lys Cys Gln Arg His Ala Gln Thr Ile His Gln Pro Ala
515 520 525
Glu Leu Leu Ser Ser Ile Ala Ser Pro Tyr Pro Phe Met Arg Trp Ser
530 535 540
Met Asp Ile Ile Gly Pro Met His Pro Ser Lys Glu Lys Lys Ile Val
545 550 555 560
Leu Val Leu Thr Asp Tyr Phe Ser Lys Trp Ile Glu Ala Glu Phe Tyr
565 570 575
Ala Ser Ile Lys Asp Ala Gln Val Glu Asn Phe Val Leu Lys His Ile
580 585 590
Leu Cys Arg His Gly Ile Pro Tyr Glu Ile Val Thr Asp Asn Gly Ser
595 600 605
Gln Phe Ile Ser Thr Arg Phe Gln Gly Phe Cys Asp Lys Trp Gly Ile
610 615 620
Arg Leu Ser Lys Ser Thr Pro Gln Tyr Pro Gln Gly Asn Gly Gln Ala
625 630 635 640
Glu Ala Ala Asn Glu Leu Glu Gly Val Leu Trp Leu His Arg Thr Thr
645 650 655
Pro Arg Arg Ala Thr Arg Glu Thr Pro Phe Ala Ser Val Tyr Gly Thr
660 665 670
Glu Cys Val Ile Pro Ala Glu Met Ile Val Pro Ser Leu Arg Arg Ser
675 680 685
Leu Ser Pro Glu Asp Asp Pro Asp Asn Thr Gln Arg Pro Leu Asp Glu
690 695 700
Leu Asp Leu Ile Asp Glu
705 710

(2) INFORMATION FOR SEQ ID NO:2794:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 683 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..683

(D) OTHER INFORMATION: / Ceres Seq. ID 1574197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2794:

Met Glu Val Tyr Ile Asp Asp Met Leu Val Lys Ser Met Thr Glu Lys
1 5 10 15
Asp His Ile Ser His Leu Arg Glu Cys Phe Lys Gln Leu Asn Leu Tyr
20 25 30
Asn Val Lys Leu Asn Pro Ala Lys Cys Arg Phe Gly Val Arg Ser Gly
35 40 45
Ile Glu Ala Asn Pro Lys Gln Ile Glu Ala Leu Phe Gly Met Ala Ser
50 55 60
Pro Gln Asn Lys Arg Glu Val Gln Cys Leu Thr Gly Arg Val Ala Ala
65 70 75 80
Leu Asn Arg Phe Ile Ser Arg Ser Thr Glu Lys Cys Leu Ala Phe Tyr
85 90 95
Val Val Leu Arg Gly Asn Lys Lys Phe Glu Trp Thr Thr Arg Cys Glu
100 105 110
Glu Ala Phe Gln Glu Leu Lys Lys Tyr Leu Ala Thr Pro Pro Ile Leu
115 120 125
Ala Lys Pro Val Ile Gly Glu Pro Gln Tyr Leu Tyr Val Ala Val Ser
130 135 140
Asp Thr Thr Val Ser Gly Glu Leu Val Arg Glu Asp Arg Gly Glu Gln
145 150 155 160
Lys Leu Ile Phe Tyr Val Ser Gln Thr Phe Thr Ser Ala Glu Ser Arg
165 170 175
Tyr Pro Gln Met Glu Lys Leu Ala Leu Val Val Met Ser Ala Gln

Lys	Leu	Arg	Pro	Tyr	Phe	Gln	Ser	His	Ser	Ile	Ile	Val	Met	Gly	Ser
Met	Pro	Leu	Cys	Val	Ile	Leu	His	Ser	Pro	Ser	Gln	Ser	Gly	Arg	Leu
Ala	Lys	Trp	Thr	Ile	Glu	Leu	Ser	Glu	Tyr	Asp	Ile	Glu	Tyr	Gln	Asn
Lys	Thr	Cys	Ala	Lys	Ser	Arg	Leu	Val	Ile	Glu	Ala	Arg	Leu	Gly	Cys
Arg	His	Pro	Ser	His	Leu	Thr	Asn	Arg	Arg	Gly	Pro	Arg	Val	Val	Ile
Lys	Ile	Lys	Leu	Arg	Gly	Tyr	Gln	Gln	Cys	Gly	Arg	Leu	Ile	Ala	Asn
Gln	Phe	Asn	Gly	Glu	Tyr	Thr	Thr	Gln	Asp	Lys	Lys	Met	Glu	Ala	Tyr
Leu	Ile	His	Val	Gln	Asn	Leu	Ala	Lys	Asn	Phe	Asp	Glu	Phe	Glu	Leu
Thr	Arg	Ile	Pro	Arg	Gly	Glu	Asn	Thr	Ser	Ala	Asp	Ala	Leu	Ala	Ala
Leu	Ala	Ser	Thr	Ser	Asp	Thr	Ile	Leu	Lys	Arg	Val	Ile	Pro	Val	Glu
Phe	Ile	Glu	Lys	Pro	Ser	Ile	Glu	Leu	Gly	Lys	Glu	Glu	His	Val	Leu
Pro	Ile	Gln	Ile	Ser	Ala	Asp	Gln	Asp	Asp	Pro	Asp	Asp	Cys	Asn	Ser
Glu	Trp	Met	Glu	Pro	Ile	Ile	Ser	Tyr	Ile	Ser	Glu	Gly	Lys	Leu	Pro
Ser	Asp	Lys	Trp	Lys	Ala	Arg	Lys	Leu	Lys	Ala	Gln	Ala	Ala	Arg	Phe
Val	Leu	Val	Asp	Ala	Lys	Leu	Tyr	Lys	Trp	Arg	Leu	Ser	Gly	Pro	Leu
Met	Thr	Cys	Val	Glu	Ala	Glu	Ala	Ile	Cys	Lys	Ile	Met	Lys	Glu	Ile
His	Gly	Gly	Ser	Cys	Gly	Asn	His	Ser	Gly	Gly	Arg	Ala	Leu	Ala	Ile
Lys	Ile	Lys	Arg	Gln	Gly	Phe	Phe	Trp	Pro	Thr	Met	Ile	Lys	Asp	Xaa
Glu	Asn	Phe	Ser	Lys	Gln	Cys	Glu	Lys	Cys	Gln	Arg	His	Ala	Gln	Thr
Ile	His	Gln	Pro	Ala	Glu	Leu	Leu	Ser	Ser	Ile	Ala	Ser	Pro	Tyr	Pro
Phe	Met	Arg	Trp	Ser	Met	Asp	Ile	Ile	Gly	Pro	Met	His	Pro	Ser	Lys
Glu	Lys	Lys	Ile	Val	Leu	Val	Leu	Thr	Asp	Tyr	Phe	Ser	Lys	Trp	Ile
Glu	Ala	Glu	Phe	Tyr	Ala	Ser	Ile	Lys	Asp	Ala	Gln	Val	Glu	Asn	Phe
Val	Leu	Lys	His	Ile	Lys	Cys	Arg	His	Gly	Ile	Pro	Tyr	Glu	Ile	Val
Thr	Asp	Asn	Gly	Ser	Gln	Phe	Ile	Ser	Thr	Arg	Phe	Gln	Gly	Phe	Cys
Asp	Lys	Trp	Gly	Ile	Arg	Leu	Ser	Lys	Ser	Thr	Pro	Gln	Tyr	Pro	Gln
Gly	Asn	Gly	Gln	Ala	Glu	Ala	Ala	Asn	Glu	Leu	Glu	Gly	Val	Leu	Trp
Leu	His	Arg	Thr	Thr	Pro	Arg	Arg	Ala	Thr	Arg	Glu	Thr	Pro	Phe	Ala
Ser	Val	Tyr	Gly	Thr	Glu	Cys	Val	Ile	Pro	Ala	Glu	Met	Ile	Val	Pro
Ser	Leu	Arg	Arg	Ser	Leu	Ser	Pro	Glu	Asp	Asp	Pro	Asp	Asn	Thr	Gln

Arg Pro Leu Asp Glu Leu Asp Leu Ile Asp Glu
675 680

(2) INFORMATION FOR SEQ ID NO:2795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2795:

accgtcgtcg ttgaggcccc accgaagaca ccaccagttc caaatttcga ttctactccc 60
ttcgactaca ttttgagaga atctggttac aagaacgttt tagtgc

(2) INFORMATION FOR SEQ ID NO:2796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2796:

Thr Val Val Val Glu Ala Pro Pro Lys Thr Pro Pro Val Pro Asn Phe
1 5 10 15
Asp Phe Thr Pro Phe Asp Tyr Ile Leu Glu Lys Ser Ala Tyr Lys Asn
20 25 30
Val Leu Val
35

(2) INFORMATION FOR SEQ ID NO:2797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..33
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2797:

Pro Ser Ser Leu Arg Pro His Arg Arg His His Gln Phe Gln Ile Ser
1 5 10 15
Ile Ser Leu Pro Ser Thr Thr Phe Trp Arg Asn Leu Leu Thr Arg Thr
20 25 30
Phe

(2) INFORMATION FOR SEQ ID NO:2798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1.162
(D) OTHER INFORMATION: / Ceres Seq. ID 1574218
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2798:
acggatacat caaaggcgat agaacaaagc acatcctacc aaaattcttc tacacacacg 60
atctacaaaa gagcgcgat gtacgagttc tacagatccg ttcgaaatgga atattctggc 120
tgactttatt acaaaggcgc tacctactgc tactttcaag aa
(2) INFORMATION FOR SEQ ID NO:2799:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1.40
(D) OTHER INFORMATION: / Ceres Seq. ID 1574219
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2799:
Thr Asp Thr Ser Lys Ala Ile Glu Gln Ser Thr Ser Tyr Gln Asn Ser
1 5 10 15
Ser Thr His Thr Ile Tyr Lys Arg Ala Ala Met Tyr Glu Phe Tyr Arg
20 25 30
Ser Val Arg Met Glu Tyr Ser Gly
35 40
(2) INFORMATION FOR SEQ ID NO:2800:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1.53
(D) OTHER INFORMATION: / Ceres Seq. ID 1574220
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2800:
Gly Tyr Ile Lys Gly Asp Arg Thr Lys His Ile Leu Pro Lys Phe Phe
1 5 10 15
Tyr Thr His Asp Leu Gln Lys Ser Gly Asp Val Arg Val Leu Gln Ile
20 25 30
Arg Ser Asn Gly Ile Phe Trp Leu Thr Tyr Ser Gln Arg Arg Tyr Leu
35 40 45
Leu Leu Leu Ser Arg
50
(2) INFORMATION FOR SEQ ID NO:2801:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 581 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1.581
(D) OTHER INFORMATION: / Ceres Seq. ID 1574260
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2801:
ataatggcat aattccatat ttctccagct gttccgcccga gcgaacgacc cacaaccaga 60
agccaccocat tggcgtagcg gagcgcatcg gacgcatcccg tcccaagagg agaaactccg 120
gccggcgacg cgggggaaaa tggggaagac gccggtgcgg atgaagcgcg tgggtgacgc 180
gctgtcgccc ttccagcaga aggtgatgcc ggggctgtgg aaggacatca ccaccaagat 240
ccaccacaag gtcaccgaga actggatctc cgccaagctc ctccctaccc ccgtcgctcg 300

cacctaccaa tacgccatgt ggtacaaaaga gcaggagaag ctttcccaca gatactaaat 360
gggatgtcct ccaagtttgc gggcgttgct gcagttgaat tttccatgat gggttgtata 420
atctgtcaat gtcatctttt tgctcagttt tagttcaacc catcttcaacc ttcccatatg 480
catatacggg atctgtgcct ggcacacata ttttgaggct agctaaatat gaaccttttg 540
tctcttaagt tgttaaataa agcaaaAtba tctgacagt t

(2) INFORMATION FOR SEQ ID NO:2802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2802:

Asn Gly Ile Ile Pro Tyr Phe Ser Ser Cys Ser Ala Glu Arg Thr Thr
1 5 10 15
His Asn Gln Lys Pro Pro Ile Gly Val Arg Glu Ala Ile Gly Ala Ser
20 25 30
Arg Pro Lys Arg Arg Asn Ser Gly Arg Arg Arg Gly Gly Lys Trp Gly
35 40 45
Arg Arg Arg Cys Gly
50

(2) INFORMATION FOR SEQ ID NO:2803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2803:

Met Gly Lys Thr Pro Val Arg Met Lys Ala Val Val Tyr Ala Leu Ser
1 5 10 15
Pro Phe Gln Gln Lys Val Met Pro Gly Leu Trp Lys Asp Ile Thr Thr
20 25 30
Lys Ile His His Lys Val Thr Glu Asn Trp Ile Ser Ala Thr Leu Leu
35 40 45
Leu Thr Pro Val Val Gly Thr Tyr Gln Tyr Ala Met Trp Tyr Lys Glu
50 55 60
Gln Glu Lys Leu Ser His Arg Tyr
65 70

(2) INFORMATION FOR SEQ ID NO:2804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2804:

Met Lys Ala Val Val Tyr Ala Leu Ser Pro Phe Gln Gln Lys Val Met
1 5 10 15

Pro Gly Leu Trp Lys Asp Ile Thr Thr Lys Ile His His Lys Val Thr
20 25 30
Glu Asn Trp Ile Ser Ala Thr Leu Leu Leu Thr Pro Val Val Gly Thr
35 40 45
Tyr Gln Tyr Ala Met Trp Tyr Lys Glu Gln Glu Lys Leu Ser His Arg
50 55 60

Tyr
65

(2) INFORMATION FOR SEQ ID NO:2805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..809
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2805:

caggatagtt	tgggtacct	cgtcgtcgtc	tcactcaccc	cgccttcacg	cctccctcac	60
caataaaggt	cccgcccttt	tccgacattc	acagggggga	caggaataca	gcggccatgg	120
cctcgattcc	ggcgacgacc	ttcgccgtca	tcttatccgt	cctcttctgt	gcgcggcgtg	180
gcaccgcggt	cgacaacgac	ctccccgact	acgtcatcca	gggcgcggtc	tattgcgaca	240
cctgcgcggt	cgggttcgtg	accaatgtca	ccgagtcacat	cgccggcgcc	aaggtgaggg	300
tggagtgcaa	gcactctggc	accggcaagc	tcgagcgcgc	catcgacggg	gtgaccgacg	360
ggaacggcgc	gtacacgwtc	gagctcaagg	acagccacga	ggaggacatc	tgcgaggtgg	420
ctcttggtga	gagcccgccg	aaggactgac	gaccaggtgc	agggcgacac	ggaccgcgcc	480
ggcgctctgy	tcaccaggaa	cgtcggcgtc	agcgacaacc	tgccgccccc	caaccgcgtc	540
ggctacctca	aggacgtgcc	gctgcccatc	tgccgctcgc	tgctcaaaac	gttggtactcg	600
gacgacgacg	acgdtcagta	atagcacatc	gacgacgacg	dtcgatatgt	aatagcacgt	660
cgctgcgacg	cgacgcgacg	cgtcgacgac	tggtctggac	taaacccaaa	atcctcttca	720
cctggattac	aaatatgtaa	ctgagaaagg	aaaggaaaac	aaaaatgtaa	ctgcgtgggt	780
gtaccaaaatt	ctgagtgctg	gattcttgc				

(2) INFORMATION FOR SEQ ID NO:2806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..207
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2806:

Met	Ala	Ser	Ile	Pro	Ala	Thr	Thr	Phe	Ala	Val	Ile	Leu	Ser	Val	Leu
1				5				10				15			
Phe	Cys	Ala	Ala	Ala	Gly	Thr	Ala	Val	Asp	Asn	Asp	Leu	Pro	Asp	Tyr
				20				25				30			
Val	Ile	Gln	Gly	Arg	Val	Tyr	Cys	Asp	Thr	Cys	Arg	Ala	Gly	Phe	Val
				35				40				45			
Thr	Asn	Val	Thr	Glu	Tyr	Ile	Ala	Gly	Ala	Lys	Val	Arg	Leu	Glu	Cys
				50				55				60			
Lys	His	Phe	Gly	Thr	Gly	Lys	Leu	Glu	Arg	Ser	Ile	Asp	Gly	Val	Thr
				65				70				75			80
Asp	Gly	Asn	Gly	Thr	Tyr	Thr	Xaa	Glu	Leu	Lys	Asp	Ser	His	Glu	Glu
				85				90				95			
Asp	Ile	Cys	Glu	Val	Val	Leu	Val	Glu	Ser	Pro	Arg	Lys	Asp	Trp	Arg
				100				105				110			
Pro	Gly	Ala	Gly	Gly	Gln	Gly	Pro	Arg	Arg	Pro	Xaa	His	Gln	Glu	

Arg	Arg	His	Gln	Arg	Gln	Pro	Ala	Pro	Arg	Gln	Pro	Ala	Arg	Leu	Pro
130						135					140				
Gln	Gly	Arg	Ala	Ala	Ala	His	Leu	Arg	Leu	Ala	Ala	Gln	Thr	Val	Gly
145					150					155					160
Leu	Gly	Arg	Arg	Arg	Xaa	Ser	Val	Ile	Ala	His	Arg	Arg	Arg	Xaa	Ser
				165						170					175
Ile	Cys	Asn	Ser	Thr	Ser	Ser	Thr	Thr	Asp	Arg	Ser	Arg	Arg	Arg	Leu
				180				185						190	
Ala	Gly	Thr	Lys	Pro	Gln	Ile	Leu	Phe	Thr	Trp	Ile	Thr	Asn	Met	
				195			200					205			

(2) INFORMATION FOR SEQ ID NO:2807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..645
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2807:

atcggtgagg	cgagcccgga	gtggaactgt	ggaagcgttg	agcttttttc	ttctttgtct	60
tgctgcgcaa	gaagaaggga	aacgagaggg	ggcgccgcat	ggcgaagagg	ctgctcccgt	120
cgctgaaccg	gggtgctggg	gagaagctgg	tgacgcccga	gaagaccgcc	ggcgccatcc	180
tcgtcccgga	aacatccaag	cagattaggt	tgatgtcttt	cctgagactg	ttgcctcaaa	240
ggctaccocga	acttatcagg	caggtggagc	aagatgttga	gactgtaatc	cacgtttctc	300
agccgggtcc	aataggaatt	Ggtggagcac	aaattcacag	acgcggagat	cttagagggc	360
agggctacag	tgaagaagGg	cagtgataaa	ttggcgaaag	aattggacc	ttgagagaaa	420
tgttagcaga	taattggaaa	aaatataccc	ctggtgtctt	ctatcaaacg	twattgnbvk	480
raatagggtg	ccatggctgg	atgcagttgt	tgccattagt	tagatttgag	cacgatctcg	540
ttatcggggg	ttatgttaac	tggtctaaat	gacacgtctg	tttctctttg	tttcatgggt	600
tgaaaacgttc	atatttagag	aatgcagtaa	ttcgactccg	attcgc		

(2) INFORMATION FOR SEQ ID NO:2808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2808:

Met	Ala	Lys	Arg	Leu	Leu	Pro	Ser	Leu	Asn	Arg	Val	Leu	Val	Glu	Lys
1				5				10				15			
Leu	Val	Gln	Pro	Lys	Lys	Thr	Ala	Gly	Ile	Leu	Val	Pro	Glu	Thr	
			20				25				30				
Ser	Lys	Gln	Ile	Arg	Leu	Met	Ser	Phe	Leu	Arg	Leu	Leu	Pro	Gln	Arg
			35			40				45					
Leu	Pro	Gln	Leu	Ile	Arg	Gln	Val	Glu	Gln	Asp	Val	Glu	Thr	Val	Ile
			50			55				60					
His	Val	Leu	Gln	Pro	Gly	Pro	Ile	Gly	Ile	Gly	Gly	Ala	Gln	Ile	His
65					70				75						80
Arg	Arg	Gly	Asp	Leu	Arg	Gly	Gln	Gly	Tyr	Ser	Glu	Lys	Arg	Gln	Trp
			85						90					95	
Ile	Ile	Gly	Glu	Glu	Ile	Gly	Pro	Leu	Arg	Glu	Met	Leu	Ala	Asp	Lys
			100				105					110			
Trp	Lys	Lys	Tyr	Thr	Pro	Gly	Val	Phe	Tyr	Gln	Gln	Xaa	Leu	Xaa	Xaa

115 120 125
Ile Gly Cys His Gly Trp Met Gln Leu Leu Pro Leu Val Arg Phe Glu
130 135 140
His Asp Leu Leu Ile Gly Ser Tyr Val Asn Cys Ser Lys
145 150 155

(2) INFORMATION FOR SEQ ID NO:2809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1574299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2809:

Met Ser Phe Leu Arg Leu Leu Pro Gln Arg Leu Pro Gln Leu Ile Arg
1 5 10 15
Gln Val Glu Gln Asp Val Glu Thr Val Ile His Val Leu Gln Pro Gly
20 25 30
Pro Ile Gly Ile Gly Gly Ala Gln Ile His Arg Arg Gly Asp Leu Arg
35 40 45
Gly Gln Gly Tyr Ser Glu Lys Arg Gln Trp Ile Ile Gly Glu Glu Ile
50 55 60
Gly Pro Leu Arg Glu Met Leu Ala Asp Lys Trp Lys Lys Tyr Thr Pro
65 70 75 80
Gly Val Phe Tyr Gln Gln Xaa Leu Xaa Xaa Ile Gly Cys His Gly Trp
85 90 95
Met Gln Leu Leu Pro Leu Val Arg Phe Glu His Asp Leu Leu Ile Gly
100 105 110
Ser Tyr Val Asn Cys Ser Lys
115

(2) INFORMATION FOR SEQ ID NO:2810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..766

(D) OTHER INFORMATION: / Ceres Seq. ID 1574312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2810:

agatcagcat tcaaaactagg gtttactcct gccgctccga gaaaacaaa aagcgtcast 60
ccgcgcggctt cctccgcgct ttctcccccgc cgcgcgcgcgc gccgcttcctt cctctacgcc 120
ggcagcgcaa gatgaagctc gtcagggttcc ttatgaagct gaacaatgag acgggtcacca 180
tcgagctcaa gaacggcacg gttgtacacg gccacatcac cgggtgttagc ataagcatga 240
acactcatct gaagacagtg aagctttacac tgaaaggga gaaccctgta acacttgacc 300
acctcagcgt gcgagggaac aacatccgct actacatcct tcccgacagc ttaaacctgg 360
aaacottgct ggtagaggaa acccctaggg tgaagcctaa gaagccaact acaggaagac 420
ctttggggcg tggtcgcggc cgaggctcgt gacgtggtcg gggccggggg Ccagcgtgag 480
ctttatcgtt cccctgctgt cggctccctt gcaagacaag ttctctctac aatgtaaaac 540
dtctttctct tgcacgcgtg gtgaaagaat gttgcactct taccttctg atgaaggtgg 600
acgdaatatc tcaatgtcag tagttcttgc tgtgaaatca cgctgtctac ctggccccc 660
tactcatgcc trctcttaggt ttactactcta gttratttgt aatgttttt ttctccccc 720
tgaatacat gtaagctgcc gcagagcttt ggatgtctag ggttgt

(2) INFORMATION FOR SEQ ID NO:2811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..158
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574313
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2811:

Ile	Ser	Ile	Gln	Thr	Arg	Val	Tyr	Ser	Cys	Arg	Ser	Glu	Lys	Thr	Asn	
1			5						10					15		
Lys	Arg	Xaa	Ser	Ala	Gly	Phe	Leu	Arg	Ala	Phe	Ser	Pro	Pro	Xaa	Pro	
		20						25					30			
Pro	Pro	Leu	Leu	Pro	Tyr	Ala	Arg	His	Ala	Lys	Met	Lys	Leu	Val	Arg	
		35					40					45				
Phe	Leu	Met	Lys	Leu	Asn	Asn	Glu	Thr	Val	Thr	Ile	Glu	Leu	Lys	Asn	
	50				55					60						
Gly	Thr	Val	Val	His	Gly	Thr	Ile	Thr	Gly	Val	Asp	Ile	Ser	Met	Asn	
65				70					75						80	
Thr	His	Leu	Lys	Thr	Val	Lys	Leu	Thr	Leu	Lys	Gly	Lys	Asn	Pro	Val	
			85						90				95			
Thr	Leu	Asp	His	Leu	Ser	Val	Arg	Gly	Asn	Asn	Ile	Arg	Tyr	Tyr	Ile	
		100						105					110			
Leu	Pro	Asp	Ser	Leu	Asn	Leu	Glu	Thr	Leu	Leu	Val	Glu	Glu	Thr	Pro	
		115					120					125				
Arg	Val	Lys	Pro	Lys	Lys	Pro	Thr	Thr	Gly	Lys	Pro	Leu	Gly	Arg	Gly	
	130					135					140					
Arg	Gly	Arg	Gly	Arg	Gly	Arg	Gly	Arg	Gly	Arg	Gly	Pro	Arg			
145				150					155							

(2) INFORMATION FOR SEQ ID NO:2812:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..115
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2812:

Met	Lys	Leu	Val	Arg	Phe	Leu	Met	Lys	Leu	Asn	Asn	Glu	Thr	Val	Thr	
1			5						10				15			
Ile	Glu	Leu	Lys	Asn	Gly	Thr	Val	Val	His	Gly	Thr	Ile	Thr	Gly	Val	
		20						25					30			
Asp	Ile	Ser	Met	Asn	Thr	His	Leu	Lys	Thr	Val	Lys	Leu	Thr	Leu	Lys	
		35					40					45				
Gly	Lys	Asn	Pro	Val	Thr	Leu	Asp	His	Leu	Ser	Val	Arg	Gly	Asn	Asn	
	50					55					60					
Ile	Arg	Tyr	Tyr	Ile	Leu	Pro	Asp	Ser	Leu	Asn	Leu	Glu	Thr	Leu	Leu	
65				70					75					80		
Val	Glu	Glu	Thr	Pro	Arg	Val	Lys	Pro	Lys	Lys	Pro	Thr	Thr	Gly	Lys	
			85					90					95			
Pro	Leu	Gly	Arg	Gly	Arg	Gly	Arg	Gly	Arg	Gly	Arg	Gly	Arg	Gly	Arg	
	100						105						110			
Gly	Pro	Arg														
	115															

(2) INFORMATION FOR SEQ ID NO:2813:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..108
(D) OTHER INFORMATION: / Ceres Seq. ID 1574315
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2813:
Met Lys Leu Asn Asn Glu Thr Val Thr Ile Glu Leu Lys Asn Gly Thr
1 5 10 15
Val Val His Gly Thr Ile Thr Gly Val Asp Ile Ser Met Asn Thr His
20 25 30
Leu Lys Thr Val Lys Leu Thr Leu Lys Gly Lys Asn Pro Val Thr Leu
35 40 45
Asp His Leu Ser Val Arg Gly Asn Asn Ile Arg Tyr Tyr Ile Leu Pro
50 55 60
Asp Ser Leu Asn Leu Glu Thr Leu Leu Val Glu Glu Thr Pro Arg Val
65 70 75 80
Lys Pro Lys Lys Pro Thr Thr Gly Lys Pro Leu Gly Arg Gly Arg Gly
85 90 95
Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Pro Arg
100 105

(2) INFORMATION FOR SEQ ID NO:2814:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 533 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..533
(D) OTHER INFORMATION: / Ceres Seq. ID 1574376
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2814:
aacgaagctt gcttctacga gaggatatag agaggaagaa cagctcgctcc gagaccatga 60
agagcagccc acacctgggtg ctgattccctgt gcctccaggc cgctctgggtc atgggCgtct 120
tcgccgcttt ggctaaaagaa aatgccctgg ttgagagcaa ggccatcgac atcaaacccgg 180
ggcagctcaa gtgctgcacc aactgcaact tctctctctc ggggtctctac acctgcgacg 240
acgtcaaaaa ggactgcgac cccgtctgca agaagtcgct cgctgcctgt cagccctcct 300
actcgggcaa caacaagtgc aggtgcacgc acaccttctt cggcatgtgc ggccccaagt 360
gctagctaga gaggaagaac gcgcgctgct gctagctgct atagcttctgt tcttcccgct 420
ccggccgGcc gccggcCgtt gNcatgttct acgtactgtg tgttgtgcta Ctacgtactg 480
gctttctgtg tgttcggttc ttgtgtttct ctcgacagtg caccttgccg gcc

(2) INFORMATION FOR SEQ ID NO:2815:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..120
(D) OTHER INFORMATION: / Ceres Seq. ID 1574377
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2815:
Arg Ser Leu Leu Arg Glu Asp Ile Glu Arg Lys Asn Ser Ser Ser
1 5 10 15
Glu Thr Met Lys Ser Ser Pro His Leu Val Leu Ile Leu Cys Leu Gln
20 25 30
Ala Ala Leu Val Met Gly Val Phe Ala Ala Leu Ala Lys Glu Asn Ala
35 40 45

Leu Val Glu Ser Lys Ala Ile Asp Ile Asn Pro Gly Gln Leu Lys Cys
50 55 60
Cys Thr Asn Cys Asn Phe Ser Phe Ser Gly Leu Tyr Thr Cys Asp Asp
65 70 75 80
Val Lys Lys Asp Cys Asp Pro Val Cys Lys Lys Cys Val Val Ala Val
85 90 95
His Ala Ser Tyr Ser Gly Asn Asn Lys Phe Arg Cys Thr Asp Thr Phe
100 105 110

Leu Gly Met Cys Gly Pro Lys Cys
115 120

(2) INFORMATION FOR SEQ ID NO:2816:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1574378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2816:

Met Lys Ser Ser Pro His Leu Val Leu Ile Leu Cys Leu Gln Ala Ala
1 5 10 15
Leu Val Met Gly Val Phe Ala Ala Leu Ala Lys Glu Asn Ala Leu Val
20 25 30
Glu Ser Lys Ala Ile Asp Ile Asn Pro Gly Gln Leu Lys Cys Cys Thr
35 40 45
Asn Cys Asn Phe Ser Phe Ser Gly Leu Tyr Thr Cys Asp Asp Val Lys
50 55 60
Lys Asp Cys Asp Pro Val Cys Lys Lys Cys Val Val Ala Val His Ala
65 70 75 80
Ser Tyr Ser Gly Asn Asn Lys Phe Arg Cys Thr Asp Thr Phe Leu Gly
85 90 95
Met Cys Gly Pro Lys Cys
100

(2) INFORMATION FOR SEQ ID NO:2817:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1574379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2817:

Met Gly Val Phe Ala Ala Leu Ala Lys Glu Asn Ala Leu Val Glu Ser
1 5 10 15
Lys Ala Ile Asp Ile Asn Pro Gly Gln Leu Lys Cys Cys Thr Asn Cys
20 25 30
Asn Phe Ser Phe Ser Gly Leu Tyr Thr Cys Asp Asp Val Lys Lys Asp
35 40 45
Cys Asp Pro Val Cys Lys Lys Cys Val Val Ala Val His Ala Ser Tyr
50 55 60
Ser Gly Asn Asn Lys Phe Arg Cys Thr Asp Thr Phe Leu Gly Met Cys
65 70 75 80
Gly Pro Lys Cys

(2) INFORMATION FOR SEQ ID NO:2818:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 818 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..818
(D) OTHER INFORMATION: / Ceres Seq. ID 1574380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2818:

```
gggcccaaca cgaggctccc ggactctcca gttccttcgc tctctgttaa cccrrrrgcgg      60
ccgacgaggg cgngnaccac cgacggcgac gatggggcgc ggcgagggca agtccaagaa      120
acgcgcgtct tctactctct cagcggagga agaagggggg gaacgggaaga ggcGggacaa      180
gaaggagagc aagaggagga gccgagagca caggagggat gacgatgaca gacacaagaa      240
gaaggggaaa cacatcgaca ggaacaaaag aaaagagaga gattcgaagg ataggcattc      300
caeggagaag acgagcaaga gaaaagacaa ggaacgggcc ttcaaaagaa tatccaagga      360
tgactacttt gcaaaagaaca acgagttcgc taccctgggtg aaggaggaaa agggcaaaata      420
tttctcagat ttgtcttcag agtctgctcg tgatcttttc ttgaagtttg tgaacaatg      480
gaacaaaggc aagctgccat cacaatacta tgaggggatt acgagtgccc cacgatcagc      540
gcacaattgg aacatcaaag catgatacgt ttctcggttc atcgggtctt cggcttgaga      600
tgttttttgc ttctcggcgc agatttttct tatagttgca tctagcaact gcttttaata      660
tctcgggttg ttgtatttaa gctgatgttc agaattgctg tctaaagcag gagggtagat      720
cgtgggtctc tctagtatcc agtggttaac atcaacgcta cttttccatt gatcactact      780
gtctgatctc acaatgagca aacatactgt ttctgggg
```

(2) INFORMATION FOR SEQ ID NO:2819:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..187
(D) OTHER INFORMATION: / Ceres Seq. ID 1574381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2819:

```
Gly Pro Thr Arg Gly Ser Arg Thr Pro Gln Phe Leu Arg Ser Val
1      5      10      15
Thr Xaa Xaa Gly Arg Arg Gly Arg Xaa Pro Pro Thr Ala Thr Met Gly
      20      25      30
Gly Gly Glu Gly Lys Ser Lys Lys Arg Arg Ser Ser Thr Ser Ser Ala
      35      40      45
Glu Glu Glu Gly Gly Glu Arg Lys Arg Arg Asp Lys Lys Glu Ser Lys
      50      55      60
Arg Arg Ser Arg Asp Asp Arg Glu Asp Asp Asp Arg His Lys Lys
      65      70      75      80
Lys Gly Lys His Ile Asp Arg Asn Lys Gly Lys Glu Arg Asp Ser Lys
      85      90      95
Asp Arg His Ser Lys Glu Lys Thr Ser Lys Arg Lys Asp Lys Asp Ala
      100      105      110
Ala Phe Lys Glu Ile Ser Lys Asp Asp Tyr Phe Ala Lys Asn Asn Glu
      115      120      125
Phe Ala Thr Trp Leu Lys Glu Glu Lys Gly Lys Tyr Phe Ser Asp Leu
      130      135      140
Ser Ser Glu Ser Ala Arg Asp Leu Phe Leu Lys Phe Val Lys Gln Trp
      145      150      155      160
Asn Lys Gly Lys Leu Pro Ser Gln Tyr Tyr Glu Gly Ile Thr Ser Gly
      165      170      175
Pro Arg Ser Ala His Asn Trp Asn Ile Lys Ala
      180      185
```


(2) INFORMATION FOR SEQ ID NO:2820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2820:

Met	Gly	Gly	Gly	Glu	Gly	Lys	Ser	Lys	Lys	Arg	Arg	Ser	Ser	Thr	Ser
1				5				10						15	
Ser	Ala	Glu	Glu	Glu	Gly	Gly	Glu	Arg	Lys	Arg	Arg	Asp	Lys	Lys	Glu
				20				25					30		
Ser	Lys	Arg	Arg	Ser	Arg	Asp	Asp	Arg	Glu	Asp	Asp	Asp	Asp	Arg	His
				35				40					45		
Lys	Lys	Lys	Gly	Lys	His	Ile	Asp	Arg	Asn	Lys	Gly	Lys	Glu	Arg	Asp
				50				55				60			
Ser	Lys	Asp	Arg	His	Ser	Lys	Glu	Lys	Thr	Ser	Lys	Arg	Lys	Asp	Lys
				65				70				75			80
Asp	Ala	Ala	Phe	Lys	Glu	Ile	Ser	Lys	Asp	Asp	Tyr	Phe	Ala	Lys	Asn
				85				90						95	
Asn	Glu	Phe	Ala	Thr	Trp	Leu	Lys	Glu	Lys	Gly	Lys	Tyr	Phe	Ser	
				100				105						110	
Asp	Leu	Ser	Ser	Glu	Ser	Ala	Arg	Asp	Leu	Phe	Leu	Lys	Phe	Val	Lys
				115				120						125	
Gln	Trp	Asn	Lys	Gly	Lys	Leu	Pro	Ser	Gln	Tyr	Tyr	Glu	Gly	Ile	Thr
				130				135						140	
Ser	Gly	Pro	Arg	Ser	Ala	His	Asn	Trp	Asn	Ile	Lys	Ala			
				145				150						155	

(2) INFORMATION FOR SEQ ID NO:2821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..696
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2821:

gcattccacgc	tcgattcggc	cgttttccgc	atccacggag	ccagggcgacc	gccgcgcgctt	60
ccctaccac	ccttgccggc	cgacgacgag	cgccaccacg	gcaggatgac	gacgctgagg	120
aacctcaaga	tcaagacgct	gacgtgcaag	aggatcgtga	aggAdctcgc	ctcgtacgag	180
aaggagggtg	agaaggaggc	ggccaagacc	gccgacatga	aggagaaggg	cgctgatccc	240
tacgacctca	aacagcagga	gaatgtttt	gctgagtcga	ggatgatggt	cccagactgc	300
cacaaacgac	ttgaaactgc	actggctgac	ttgaaagcaa	cactggctga	actgaaggag	360
tcaaatgagc	aaggtgcgca	gattggagaa	gctgagagta	caatcgcaga	agttgaagca	420
gttgtaacgc	cagcagaaga	ttaaactaaa	aaaactcttg	gtttgctgaa	ctgttagcgc	480
acatcctatt	ttcgcatatt	gagcccttgt	gagcttatta	cgagatgttt	gaggcgtgaa	540
atcctgtacc	attatcatca	cttctatcct	gaaatttgag	tttctgttcc	caagttctaa	600
gcgttaactgt	ttgtgtctgc	ggagagcgca	catccctggc	ttctccggga	agttgttagt	660
gtaaattgaa	attaagaaaa	atggacgaat	ttgaat			

(2) INFORMATION FOR SEQ ID NO:2822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..147
(D) OTHER INFORMATION: / Ceres Seq. ID 1574387
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2822:
Ala Ser Thr Leu Asp Ser Ala Val Phe Arg Ile His Gly Ala Arg Arg
1 5 10 15
Pro Pro Pro Leu Pro Tyr Ser Pro Leu Ala Gly Asp Asp Glu Arg His
 20 25 30
His Gly Arg Met Thr Thr Leu Arg Asn Leu Lys Ile Lys Thr Ser Thr
 35 40 45
Cys Lys Arg Ile Val Lys Xaa Leu Arg Ser Tyr Glu Lys Glu Val Glu
 50 55 60
Lys Glu Ala Ala Lys Thr Ala Asp Met Lys Glu Lys Gly Ala Asp Pro
65 70 75 80
Tyr Asp Leu Lys Gln Gln Glu Asn Val Leu Ala Glu Ser Arg Met Met
 85 90 95
Val Pro Asp Cys His Lys Arg Leu Glu Thr Ala Leu Ala Asp Leu Lys
 100 105 110
Ala Thr Leu Ala Glu Leu Lys Glu Ser Asn Glu Gln Gly Ala Glu Ile
 115 120 125
Gly Glu Ala Glu Ser Thr Ile Ala Glu Val Glu Ala Val Val Lys Pro
130 135 140
Ala Glu Asp
145

(2) INFORMATION FOR SEQ ID NO:2823:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..77
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574388
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2823:
Ile His Ala Arg Phe Gly Arg Phe Pro His Pro Arg Ser Gln Ala Thr
1 5 10 15
Ala Ala Ala Ser Leu Leu Thr Leu Gly Arg Arg Arg Arg Ala Pro Pro
 20 25 30
Arg Gln Asp Asp Asp Ala Glu Glu Pro Gln Asp Gln Asp Val Asp Val
 35 40 45
Gln Glu Asp Arg Glu Gly Xaa Ala Leu Val Arg Glu Gly Gly Gly Glu
 50 55 60
Gly Gly Gly Gln Asp Arg Arg His Glu Gly Glu Gly Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:2824:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..112
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574389
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2824:

Met Thr Thr Leu Arg Asn Leu Lys Ile Lys Thr Ser Thr Cys Lys Arg
1 5 10 15
Ile Val Lys Xaa Leu Arg Ser Tyr Glu Lys Glu Val Glu Lys Glu Ala
20 25 30
Ala Lys Thr Ala Asp Met Lys Glu Lys Gly Ala Asp Pro Tyr Asp Leu
35 40 45
Lys Gln Gln Glu Asn Val Leu Ala Glu Ser Arg Met Met Val Pro Asp
50 55 60
Cys His Lys Arg Leu Glu Thr Ala Leu Ala Asp Leu Lys Ala Thr Leu
65 70 75 80
Ala Glu Leu Lys Glu Ser Asn Glu Gln Gly Ala Glu Ile Gly Glu Ala
85 90 95
Glu Ser Thr Ile Ala Glu Val Glu Ala Val Val Lys Pro Ala Glu Asp
100 105 110

(2) INFORMATION FOR SEQ ID NO:2825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..560
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2825:

ttctttcaga aaacgaaatc cactcaggag cgaggaaaga gggacagagg agggatagat 60
ccccgggctc cagcctctca caaccatccg tcccgatccc gaccagcttt gagatcgaga 120
tggcggagcg ccgtgctgctg accttctctg agatcctctt cgccatcatc ctccccgccc 180
tcggcgctctt cctccgattc ggctgctgca gaatagagtt ctgcattctgc ctgctgctca 240
caatccttgg ctacgtcccc ggaatcatct acgcatctca tgtccttgtt gctctcgact 300
ctgaccagca cgagaggaggaa tactacaccc ttgcttagag catctgggtt tgccaggcgg 360
gcctgcacag ttgagtcgaa atcagttatt tttttctcat gtgattgtc tgacatggca 420
taagcggaac tgggtaacca agtgtgtggt tctatatctc tgttaccacaa cttgtgagct 480
ctctttattg tgcctccagt attcaaAtct gtaattgtga tactacaAga gaataagatg 540
cgcatgtatc tctgagagct

(2) INFORMATION FOR SEQ ID NO:2826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2826:

Phe Phe Gln Lys Thr Lys Ser Thr Gln Glu Arg Gly Lys Arg Asp Arg
1 5 10 15
Gly Gly Ile Asp Pro Arg Ala Pro Arg Leu His Asn His Pro Ser Arg
20 25 30
Ser Arg Pro Ala Leu Arg Ser Arg Trp Arg Thr Ala Ala Ala Pro
35 40 45
Ser Trp Arg Ser Ser Ser Pro Ser Ser Ser Arg Pro Ser Ala Ser Ser
50 55 60
Ser Asp Ser Ala Ala Glu
65 70

(2) INFORMATION FOR SEQ ID NO:2827:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..111
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574405
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2827:
Leu Ser Glu Asn Glu Ile His Ser Gly Ala Arg Lys Glu Gly Gln Arg
1 5 10 15
Arg Asp Arg Ser Pro Gly Ser Thr Pro Pro Gln Pro Ser Val Pro Ile
 20 25 30
Pro Thr Ser Phe Glu Ile Ala Met Ala Asp Gly Arg Cys Cys Thr Phe
 35 40 45
Leu Glu Ile Leu Phe Ala Ile Ile Leu Pro Pro Leu Gly Val Phe Leu
50 55 60
Arg Phe Gly Cys Cys Arg Ile Glu Phe Cys Ile Cys Leu Leu Leu Thr
65 70 75 80
Ile Leu Gly Tyr Val Pro Gly Ile Ile Tyr Ala Ile Tyr Val Leu Val
 85 90 95
Ala Leu Asp Ser Asp Gln His Glu Arg Glu Tyr Tyr Thr Leu Ala
 100 105 110

(2) INFORMATION FOR SEQ ID NO:2828:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..72
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574406
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2828:
Met Ala Asp Gly Arg Cys Cys Thr Phe Leu Glu Ile Leu Phe Ala Ile
1 5 10 15
Ile Leu Pro Pro Leu Gly Val Phe Leu Arg Phe Gly Cys Cys Arg Ile
 20 25 30
Glu Phe Cys Ile Cys Leu Leu Leu Thr Ile Leu Gly Tyr Val Pro Gly
 35 40 45
Ile Ile Tyr Ala Ile Tyr Val Leu Val Ala Leu Asp Ser Asp Gln His
50 55 60
Glu Arg Glu Tyr Tyr Thr Leu Ala
65 70

(2) INFORMATION FOR SEQ ID NO:2829:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 778 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..778
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574421
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2829:
agcaagcaaa gattgcgccg gtgagggtgt tcgggacggc ggacttcgtg aacgctgcga 60
gggttatggc ttgcctggag gaagttggcg tggagtacga ggtcgtcgag gtcgactacg 120

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cgcccatgga gcacaagggc gccacgacc tcgaagaaa ccgcttcggc caaatcccag 180
cgtttcagga cggggacacg atgctctttg aatcccagc aatcgccaag tacgtgctcc 240
gcaaatactc caagtacgct caagtgcacc tgctccgtga gggcaaccgc gaggaagccg 300
ccatggtaga cgtgtggacg gaggtcgagg cgcacacctc cctaccgcgc catcgccccc 360
wtyttctacg agtacgRtg tgtacccgcg cgagcatggc acbacgccc accaggaggt 420
ggtggacag agtgtggaga ggytcaggaa ggtcctcgac gtctacgagg cgcacctgta 480
caagaccaag cagctctatc tcgccgggga ctacttcagc ctgcgccrfs tcaaccagct 540
ccgtacacc tcaccacctc taggacacc gcnacgcgtc gctcttcgag gcgtatcctc 600
acgttaagcg ctggtgggag agagtatatg cagcccgctc gctgcagaag ctgcgccggg 660
atatggtgat caaagcctga ttgcacgtac ctttgtatca tcagattctt ccttgggggtg 720
tatatatgca aggggtacct ttcttgcaar ataaataaag arataataa atccgatc

```

(2) INFORMATION FOR SEQ ID NO:2830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2830:

```

Gln Ala Lys Ile Ala Pro Val Arg Val Phe Gly Thr Ala Asp Phe Val
1      5      10      15
Asn Ala Ala Arg Val Met Ala Cys Leu Glu Glu Val Gly Val Glu Tyr
20     25     30
Glu Val Val Glu Val Asp Tyr Ala Ala Met Glu His Lys Gly Ala Gln
35     40     45
His Leu Ala Arg Asn Pro Phe Gly Gln Ile Pro Ala Phe Gln Asp Gly
50     55     60
Asp Thr Met Leu Phe Glu Ser Arg Ala Ile Ala Lys Tyr Val Leu Arg
65     70     75     80
Lys Tyr Ser Lys Ser Ala Gln Val Asp Leu Leu Arg Glu Gly Asn Pro
85     90     95
Glu Glu Ala Ala Met Val Asp Val Trp Thr Glu Val Glu Ala His Thr
100    105    110
Tyr Leu Pro Gly His Arg Ala Xaa Xaa Leu Arg Val Xaa Trp Cys Thr
115    120    125
Pro Pro Ser Met Ala Xaa Arg Pro Thr Arg Arg Trp Trp Thr Arg Val
130    135    140
Trp Arg Xaa Ser Gly Arg Ser Ser Thr Ser Thr Arg Arg Thr Cys Thr
145    150    155    160
Arg Pro Ser Ser Ser Ile Ser Pro Gly Thr Thr Ser Ala Ser Pro Xaa
165    170    175
Ser Thr Thr Ser Arg Thr Pro Ser Thr Ser
180    185

```

(2) INFORMATION FOR SEQ ID NO:2831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2831:

```

Met Ala Cys Leu Glu Glu Val Gly Val Glu Tyr Glu Val Val Glu Val
1      5      10      15

```

```

Asp Tyr Ala Ala Met Glu His Lys Gly Ala Gln His Leu Ala Arg Asn
                20                25                30
Pro Phe Gly Gln Ile Pro Ala Phe Gln Asp Gly Asp Thr Met Leu Phe
                35                40                45
Glu Ser Arg Ala Ile Ala Lys Tyr Val Leu Arg Lys Tyr Ser Lys Ser
                50                55                60
Ala Gln Val Asp Leu Leu Arg Glu Gly Asn Pro Glu Glu Ala Ala Met
                65                70                75                80
Val Asp Val Trp Thr Glu Val Glu Ala His Thr Tyr Leu Pro Gly His
                85                90                95
Arg Ala Xaa Xaa Leu Arg Val Xaa Trp Cys Thr Pro Pro Ser Met Ala
                100                105                110
Xaa Arg Pro Thr Arg Arg Trp Trp Thr Arg Val Trp Arg Xaa Ser Gly
                115                120                125
Arg Ser Ser Thr Ser Thr Arg Arg Thr Cys Thr Arg Pro Ser Ser Ser
                130                135                140
Ile Ser Pro Gly Thr Thr Ser Ala Ser Pro Xaa Ser Thr Thr Ser Arg
                145                150                155                160
Thr Pro Ser Thr Ser
                165

```

(2) INFORMATION FOR SEQ ID NO:2832:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1574424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2832:

```

Met Glu His Lys Gly Ala Gln His Leu Ala Arg Asn Pro Phe Gly Gln
1          5          10          15
Ile Pro Ala Phe Gln Asp Gly Asp Thr Met Leu Phe Glu Ser Arg Ala
          20          25
Ile Ala Lys Tyr Val Leu Arg Lys Tyr Ser Lys Ser Ala Gln Val Asp
          35          40          45
Leu Leu Arg Glu Gly Asn Pro Glu Glu Ala Ala Met Val Asp Val Trp
          50          55          60
Thr Glu Val Glu Ala His Thr Tyr Leu Pro Gly His Arg Ala Xaa Xaa
          65          70          75          80
Leu Arg Val Xaa Trp Cys Thr Pro Pro Ser Met Ala Xaa Arg Pro Thr
          85          90          95
Arg Arg Trp Trp Thr Arg Val Trp Arg Xaa Ser Gly Arg Ser Ser Thr
          100          105          110
Ser Thr Arg Arg Thr Cys Thr Arg Pro Ser Ser Ile Ser Pro Gly
          115          120          125
Thr Thr Ser Ala Ser Pro Xaa Ser Thr Thr Ser Arg Thr Pro Ser Thr
          130          135          140

```

Ser
145

(2) INFORMATION FOR SEQ ID NO:2833:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 756 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..756

(D) OTHER INFORMATION: / Ceres Seq. ID 1574438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2833:

aaaaaactta	gccgcgtgga	cgcacaccag	caactgccct	cctcgcgcgc	gctgcctccc	60
tccgcgcgac	cgatctaccc	tccgcgcgca	ccatgtcget	gategccggg	gaggacttcc	120
agcatatcct	gcgtttgctg	aacaccaacg	tggatgggaa	gcagaagatc	atgttcgcca	180
tgacctcaat	caagggtgtc	ggcgcccgct	tctccaacat	cgtctgcaag	aaggccgaca	240
tcgacatgaa	caagaggggc	ggcgaGctga	cgccctgatga	gctggagcgc	ctRgatgNac	300
ggctcgtggcc	aaccctaggc	agttcaaggt	gccggactgg	ttoctcaaca	ggaagaagga	360
ttacaaggac	ggcaggttct	cgcaggtcgt	ctccaacgcc	cttgatatga	agctcaaggga	420
cgaccttgag	aggctcaaga	agatcaggaa	ccaccgtggt	ctgcgtcaact	actggggcct	480
ccgtgtccgt	ggccagcaca	ccaagactac	tggcaggcgt	gbaaaagacc	ttggtgtctc	540
caagaagcga	tgagctytat	atcaccccga	caaactcttg	cgcactacc	atgtcggttt	600
gtgtccaaac	agtcctgatg	aagggtttct	gttkaggcwg	tkkcsstgaa	tggtgttktg	660
ctctaggaca	atatcgcggt	tattgaacck	taatatatcg	tgccctggg	atgtgttttt	720
tttttgcac	tttataagta	atttcatttg	gatgag			

(2) INFORMATION FOR SEQ ID NO:2834:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1574439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2834:

Lys	Asn	Leu	Ala	Ala	Trp	Thr	His	Thr	Ser	Thr	Cys	Pro	Pro	Arg	Arg
1		5						10						15	
Arg	Cys	Leu	Pro	Pro	Arg	Asp	Arg	Ser	Thr	Leu	Arg	Arg	His	His	Val
			20					25						30	
Ala	Asp	Arg	Arg	Gly	Gly	Leu	Pro	Ala	Tyr	Pro	Ala	Phe	Ala	Glu	His
			35					40				45			
Gln	Arg	Gly	Trp	Glu	Ala	Glu	Asp	His	Val	Arg	His	Asp	Leu	Asn	Gln
			50				55					60			
Gly	Cys	Arg	Ala	Pro	Leu	Leu	Gln	His	Arg	Leu	Gln	Glu	Gly	Arg	His
			65			70			75					80	
Arg	His	Glu	Gln	Glu	Gly	Arg	Arg	Ala	Asp	Ala					
			85				90								

(2) INFORMATION FOR SEQ ID NO:2835:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1574440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2835:

Met	Ser	Leu	Ile	Ala	Gly	Glu	Asp	Phe	Gln	His	Ile	Leu	Arg	Leu	Leu
1			5						10					15	
Asn	Thr	Asn	Val	Asp	Gly	Lys	Gln	Lys	Ile	Met	Phe	Ala	Met	Thr	Ser
			20					25						30	
Ile	Lys	Gly	Val	Gly	Arg	Arg	Phe	Ser	Asn	Ile	Val	Cys	Lys	Lys	Ala
			35				40					45			
Asp	Ile	Asp	Met	Asn	Lys	Arg	Ala	Gly	Glu	Leu	Thr	Pro	Asp	Glu	Leu
			50			55					60				
Glu	Arg	Xaa	Asp	Xaa	Arg	Ser	Trp	Pro	Thr	Leu	Gly	Ser	Ser	Arg	Cys

65 70 75 80
Arg Thr Gly Ser Ser Thr Gly Arg Arg Ile Thr Arg Thr Ala Gly Ser
85 90 95
Arg Arg Ser Ser Pro Thr Pro Leu Ile
100 105

(2) INFORMATION FOR SEQ ID NO:2836:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1574441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2836:

Met Phe Ala Met Thr Ser Ile Lys Gly Val Gly Arg Arg Phe Ser Asn
1 5 10 15
Ile Val Cys Lys Lys Ala Asp Ile Asp Met Asn Lys Arg Ala Gly Glu
20 25 30
Leu Thr Pro Asp Glu Leu Glu Arg Xaa Asp Xaa Arg Ser Trp Pro Thr
35 40 45
Leu Gly Ser Ser Arg Cys Arg Thr Gly Ser Ser Thr Gly Arg Arg Ile
50 55 60
Thr Arg Thr Ala Gly Ser Arg Arg Ser Ser Pro Thr Pro Leu Ile
65 70 75

(2) INFORMATION FOR SEQ ID NO:2837:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 415 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..415

(D) OTHER INFORMATION: / Ceres Seq. ID 1574446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2837:

tcaaaactaca tctcctttgg gcacgtacgc gtctgatagc tgcagtggtt ggggttggtc 60
tcgtgtctatt cagaacacaca gtacgcgaagaa ctattcgggtg gggccgaaga tgggtgtcgct 120
gaaggtgcaca aagcgcctcgc ccgcaagcgt ttctcaagtgt gggaaagcca aagtgttggtc 180
tgaccccaat gaagtttagt agatctccat ggcgaactcc cgtaagactt atccgctagc 240
tccccccctc cgattaattg ctcaactgggt tggggttgta tggatctctg ggtgaggtgg 300
atggtttatc tggtttcata tattggtatc atggctgcac tattcttttc tactatcatt 360
ttgcagtgctc gtttacctac ggccaccatt gaaaacacta ttggctgtag ctgct

(2) INFORMATION FOR SEQ ID NO:2838:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1574447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2838:

Pro Asn Ser Ser Pro Leu Gly Thr Tyr Ala Ser Asn Ser Cys Ser Gly
1 5 10 15
Trp Gly Trp Leu Arg Ala Ile Gln Lys His Ser Ser Glu Asn Trp Ser

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..193
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574510
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2841:
His Arg Gln Thr Leu Asn Thr Lys Ala Pro His Ile Asn Thr Phe Pro
1 5 10 15
Ser His Leu Phe Pro Ser Pro Ala Ala Ala Ala Pro Ala Pro Ser
 20 25 30
Ser Cys Ser Ala Ser Cys Ser Arg Arg Arg Glu Ala Leu Gln Arg Thr
 35 40 45
Ser Val Asn Met Gly Lys Thr Arg Gly Met Gly Ala Gly Arg Lys Leu
50 55 60
Lys Thr His Arg Arg Asn Gln Arg Trp Ala Asp Lys Ala Tyr Lys Lys
65 70 75 80
Ser His Leu Gly Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His
 85 90 95
Ala Lys Gly Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro
100 105 110
Asn Ser Ala Ile Arg Lys Cys Ala Arg Val Gln Leu Val Lys Asn Gly
115 120 125
Lys Lys Ile Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Tyr Ile
130 135 140
Glu Glu Asn Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His
145 150 155 160
Ala Val Gly Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser
 165 170 175
Gly Val Ser Leu Leu Ala Leu Phe Lys Glu Lys Lys Glu Lys Pro Arg
180 185 190
Ser

(2) INFORMATION FOR SEQ ID NO:2842:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 142 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..142
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574511
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2842:
Met Gly Lys Thr Arg Gly Met Gly Ala Gly Arg Lys Leu Lys Thr His
1 5 10 15
Arg Arg Asn Gln Arg Trp Ala Asp Lys Ala Tyr Lys Lys Ser His Leu
20 25 30
Gly Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His Ala Lys Gly
35 40 45
Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala
50 55 60
Ile Arg Lys Cys Ala Arg Val Gln Leu Val Lys Asn Gly Lys Lys Ile
65 70 75 80
Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn
85 90 95
Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His Ala Val Gly
100 105 110
Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser Gly Val Ser
115 120 125

Leu Leu Ala Leu Phe Lys Glu Lys Lys Glu Lys Pro Arg Ser
130 135 140

(2) INFORMATION FOR SEQ ID NO:2843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2843:

```
Met Gly Ala Gly Arg Lys Leu Lys Thr His Arg Arg Asn Gln Arg Trp
1      5      10      15
Ala Asp Lys Ala Tyr Lys Lys Ser His Leu Gly Asn Glu Trp Lys Lys
20      25      30
Pro Phe Ala Gly Ser Ser His Ala Lys Gly Ile Val Leu Glu Lys Ile
35      40      45
Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala Ile Arg Lys Cys Ala Arg
50      55      60
Val Gln Leu Val Lys Asn Gly Lys Lys Ile Ala Ala Phe Val Pro Asn
65      70      75      80
Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn Asp Glu Val Leu Ile Ala
85      90      95
Gly Phe Gly Arg Lys Gly His Ala Val Gly Asp Ile Pro Gly Val Arg
100     105     110
Phe Lys Val Val Lys Val Ser Gly Val Ser Leu Leu Ala Leu Phe Lys
115     120     125
Glu Lys Lys Glu Lys Pro Arg Ser
130     135
```

(2) INFORMATION FOR SEQ ID NO:2844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..978
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2844:

```
aaaggaaact cactcccaact ttactcctat ccaactgcgcg ctggacgcgt gcgagaggct      60
tgaccaagca gcagcagcag cagcagcgat ggcgcctctg aagctgtacg ggaatccgcgt      120
gtcccccaac gtgggtgcgcg tggccaccgt gctcaacgag aagggcctcg acttcgagat      180
cgtccccgtc gacctcacca ccggcgccca caagcagccc gacttctcta cctctcaacc      240
tttcggccag atccccggctc tcgtcgacgg agacgaakyc tcttcgagtc ccgcgcgcgtc      300
aacccgtata tcgccagcaa gtacgcgtca gggcacggac ctgctccccg cgcacggcgtc      360
ggcggcgcaac tggaggtgtg gctggagggt gagtgcaccc acttctaccc gaacgcgatcg      420
ccgtgggtgt tcacagctgt ctctgaggccg ctctcgggcg cgcccccgam gcggcggttg      480
tggagaagca ccgcggagcag ctgcgcaagg tgctcgacgt gtacgaggcg cacttgcccc      540
gcaacaagta ccCtcgcccg ggacaagttc acgctcgccg acgccaacca cgcgtctctac      600
ctgctctacc tcagcaagac ccccaaggcc gggctcgctc ccgccccgcc ccacgtcaag      660
gctcgtgtgg agggcatcgc cgcccgcgcc cgtttccaga agaccgtcgc cgcctctctac      720
ttgccccgcg cgccctctct ctcgggttga cctcgcttgc cgtcgtctgc gtgcgggatg      780
cgtcggagcc ccgagtgcaa taaaagaggg cgcctctctg tgtgtgttta ttgctctttg      840
tgtgctataa cagcctgtgt aataaacact gttgtcttgc tgtgtgttta ttgctctttg      900
gttggttgtt ccttgcatat cctactagtg ctgatctttt tgtgaagctt ggattggatg      960
gacgcgtttt cttgcgcg
```

(2) INFORMATION FOR SEQ ID NO:2845:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1574524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2845:

```
Lys Glu Thr His Ser His Phe Thr Pro Ile His Cys Gly Leu Asp Ala
1      5      10      15
Cys Glu Arg Leu Asp Gln Ala Ala Ala Ala Ala Met Ala Pro
20      25      30
Leu Lys Leu Tyr Gly Met Pro Leu Ser Pro Asn Val Val Arg Val Ala
35      40      45
Thr Val Leu Asn Glu Lys Gly Leu Asp Phe Glu Ile Val Pro Val Asp
50      55      60
Leu Thr Thr Gly Ala His Lys Gln Pro Asp Phe Leu Thr Leu Asn Pro
65      70      75      80
Phe Gly Gln Ile Pro Ala Leu Val Asp Gly Asp Glu Xaa Ser Ser Ser
85      90      95
Pro Ala Arg Ser Thr Gly Thr Ser Pro Ala Ser Thr Arg Gln Gly Thr
100      105      110
Asp Leu Leu Pro Ala Thr Ala Ser Ala Ala Asn Trp Arg Cys Gly Trp
115      120      125
Arg Trp Ser Arg Thr Thr Ser Thr Arg Thr His Arg Arg Trp Cys Ser
130      135      140
Ser Cys Ser
145
```

(2) INFORMATION FOR SEQ ID NO:2846:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1574525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2846:

```
Met Ala Pro Leu Lys Leu Tyr Gly Met Pro Leu Ser Pro Asn Val Val
1      5      10      15
Arg Val Ala Thr Val Leu Asn Glu Lys Gly Leu Asp Phe Glu Ile Val
20      25      30
Pro Val Asp Leu Thr Thr Gly Ala His Lys Gln Pro Asp Phe Leu Thr
35      40      45
Leu Asn Pro Phe Gly Gln Ile Pro Ala Leu Val Asp Gly Asp Glu Xaa
50      55      60
Ser Ser Ser Pro Ala Arg Ser Thr Gly Thr Ser Pro Ala Ser Thr Arg
65      70      75      80
Gln Gly Thr Asp Leu Leu Pro Ala Thr Ala Ser Ala Ala Asn Trp Arg
85      90      95
Cys Gly Trp Arg Trp Ser Arg Thr Thr Ser Thr Arg Thr His Arg Arg
100      105      110
Trp Cys Ser Ser Cys Ser
115
```

(2) INFORMATION FOR SEQ ID NO:2847:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..110
(D) OTHER INFORMATION: / Ceres Seq. ID 1574526
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2847:
Met Pro Leu Ser Pro Asn Val Val Arg Val Ala Thr Val Leu Asn Glu
1 5 10 15
Lys Gly Leu Asp Phe Glu Ile Val Pro Val Asp Leu Thr Thr Gly Ala
20 25 30
His Lys Gln Pro Asp Phe Leu Thr Leu Asn Pro Phe Gly Gln Ile Pro
35 40 45
Ala Leu Val Asp Gly Asp Glu Xaa Ser Ser Ser Pro Ala Arg Ser Thr
50 55 60
Gly Thr Ser Pro Ala Ser Thr Arg Gln Gly Thr Asp Leu Leu Pro Ala
65 70 75 80
Thr Ala Ser Ala Ala Asn Trp Arg Cys Gly Trp Arg Trp Ser Arg Thr
85 90 95
Thr Ser Thr Arg Thr His Arg Arg Trp Cys Ser Ser Cys Ser
100 105 110

(2) INFORMATION FOR SEQ ID NO:2848:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 677 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..677
(D) OTHER INFORMATION: / Ceres Seq. ID 1574547
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2848:
aaccaccgtt cagaggagta ctcccggttc gagcacacta gtcttccctg cgcttgetcg 60
ctcttctctt cccccatggc gctgctcgcc gtccaggGca tggccatgtc caccgccgcc 120
gcggccctcc catctcaca ccacggcgcc gtctcatcct acgtctccac ctctctctac 180
gcgtcgccag ctctccgcgc ctctcccgcc gcccgagctg cgctcgccgt cgccaccgtc 240
ttgtcgccca cgtcactcct agttcttgac gtctactcgc ggagagggga caagaaaacg 300
aaaaggggca aaaggttcaa ccattcatat ggcaatgcga ggccgcgcaa caagaagaag 360
ggaactgggc ctgcgcggct cttgtctcct ccagctcctc caaggaagga tcagttcgat 420
gatggggaga tcatttcaat cgagattgac gaggacatcc tggaaatagg ttgtccgagtt 480
ctgccttgct ttatatttgc cctgagctta attggcctag ttgtaccaca atcaaatact 540
acataattta agtaattatt tcctgcgcta taattatcga tgggtaggct gccacacttt 600
catttggtca gtaatgttcc tactactgac tgggttcttt attttccttt ccagctgctg 660
agttctttac tctcttc

(2) INFORMATION FOR SEQ ID NO:2849:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..155
(D) OTHER INFORMATION: / Ceres Seq. ID 1574548
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2849:

Asn His Arg Ser Glu Glu Tyr Ser Arg Ser Glu His Thr Ser Leu Pro
1 5 10 15
Cys Ala Cys Ser Leu Leu Leu Ala Pro Met Ala Leu Leu Ala Val Gln
20 25 30
Gly Met Ala Met Ser Thr Ala Ala Ala Leu Pro Ser His Asn His
35 40 45
Gly Ala Val Ser Ser Tyr Val Ser Thr Ser Tyr Ala Leu Ala Ala
50 55 60
Ser Ala Ala Phe Pro Arg Ala Arg Ala Ala Phe Ala Val Gly Thr Val
65 70 75 80
Leu Ser Ala Thr Val Thr Pro Val Leu Asp Val Tyr Cys Gly Arg Gly
85 90 95
Asp Lys Lys Thr Lys Arg Gly Lys Arg Phe Asn His Ser Tyr Gly Asn
100 105 110
Ala Arg Pro Arg Asn Lys Lys Lys Gly Thr Gly Pro Ala Arg Leu Phe
115 120 125
Ala Pro Pro Ala Pro Pro Arg Lys Asp Gln Phe Asp Asp Gly Glu Ile
130 135 140
Ile Ser Ile Glu Ile Asp Glu Asp Ile Leu Glu
145 150 155

(2) INFORMATION FOR SEQ ID NO:2850:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1574549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2850:

Thr Thr Val Pro Arg Ser Thr Pro Val Pro Ser Thr Leu Val Phe Pro
1 5 10 15
Ala Leu Ala Arg Ser Phe Leu Pro Pro Trp Arg Cys Ser Pro Ser Arg
20 25 30
Ala Trp Pro Cys Pro Pro Pro Pro Arg Pro Ser His Leu Thr Thr Thr
35 40 45
Ala Pro Ser His Pro Thr Ser Pro Pro Pro Thr Arg Ser Gln Pro
50 55 60
Pro Pro Pro Ser Pro Ala Pro Glu Leu Arg Ser Pro Ser Ala Pro Ser
65 70 75 80
Cys Arg Pro Pro Ser Leu Gln Phe Leu Thr Ser Thr Ala Gly Glu Gly
85 90 95
Thr Arg Lys Arg Lys Gly Ala Lys Gly Ser Thr Ile His Met Ala Met
100 105 110
Arg Gly Arg Ala Thr Arg Arg Glu Leu Gly Leu Arg Gly Ser Leu
115 120 125
Leu Leu Gln Leu Leu Gln Gly Arg Ile Ser Ser Met Met Gly Arg Ser
130 135 140
Phe Gln Ser Arg Leu Thr Arg Thr Ser Trp Asn Arg Leu Ser Glu Phe
145 150 155
Cys Leu Ala Leu Tyr Leu Pro
165

(2) INFORMATION FOR SEQ ID NO:2851:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..130
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574550
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2851:
Met Ala Leu Leu Ala Val Gln Gly Met Ala Met Ser Thr Ala Ala Ala
1 5 10 15
Ala Leu Pro Ser His Asn His Gly Ala Val Ser Ser Tyr Val Ser Thr
 20 25 30
Ser Ser Tyr Ala Leu Ala Ala Ser Ala Ala Phe Pro Arg Ala Arg Ala
 35 40 45
Ala Phe Ala Val Gly Thr Val Leu Ser Ala Thr Val Thr Pro Val Leu
50 55 60
Asp Val Tyr Cys Gly Arg Gly Asp Lys Lys Thr Lys Arg Gly Lys Arg
65 70 75 80
Phe Asn His Ser Tyr Gly Asn Ala Arg Pro Arg Asn Lys Lys Lys Gly
 85 90 95
Thr Gly Pro Ala Arg Leu Phe Ala Pro Pro Ala Pro Pro Arg Lys Asp
 100 105 110
Gln Phe Asp Asp Gly Glu Ile Ile Ser Ile Glu Ile Asp Glu Asp Ile
 115 120 125
Leu Glu
130

(2) INFORMATION FOR SEQ ID NO:2852:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 615 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..615
(D) OTHER INFORMATION: / Ceres Seq. ID 1574572

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2852:

atccgtattc ccgtcacgcc cccaacacgc ccacaaccgc aagcagcgaa agctccccta 60
accctctccg cgcattccgat cgcaaggaga aagagggaga tgagctacta cgggcagcag 120
ccccccgTck cggtccccgcc gcagcaaggc taccggggca aggacggcta cccgccacgc 180
gggtACccgc cggccggcta ccccccgccg gcgcagggct accctccgca Gggctaccct 240
ccgcagtagc cgcaGccgcc gcctccacag cagcagcaga gcagcgggcc ttccctcatg 300
gagggatgct tggtgtgcct ctgctgctgc tgctctctgg acgctctgct ctgagagtgA 360
gagggggcga cgcagcgatt cgacacggcg acaagtgaA ctactagott tctatgcgag 420
ggagagagag agagagctgg aactggattg agcctggaaT gctatcgctc tattctagct 480
ttgtcagagc ataattatgtc gccctagttt tttatttctc tctgtcaatg ttgacgggat 540
cacagattgt gtgtgttattc gccctgtgga tgttcctgtg ttctgttgga attcaatcct 600
gggatttatt gtgcc

(2) INFORMATION FOR SEQ ID NO:2853:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..117
(D) OTHER INFORMATION: / Ceres Seq. ID 1574573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2853:

Ile Arg Ile Pro Val Thr Pro Pro Thr Arg Pro Gln Pro Glu Ala Ala
1 5 10 15
Lys Ala Pro Leu Thr Leu Ser Ala His Pro Ile Ala Arg Lys Lys Arg

(2) INFORMATION FOR SEQ ID NO:2854:

(A) LENGTH: 131 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAM

(B) LOCATION: 1..131

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:2854:

Tyr Ser Arg His Ala Pro Asn Thr Pro Thr Th

(2) INFORMATION FOR SEQ ID NO:2855:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1574575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2855:

Met	Ser	Tyr	Tyr	Gly	Gln	Gln	Pro	Pro	Val	Xaa	Val	Pro	Pro	Gln	Gln
1				5					10					15	
Gly	Tyr	Pro	Gly	Lys	Asp	Gly	Tyr	Pro	Pro	Ala	Gly	Tyr	Pro	Pro	Ala
			20					25					30		
Gly	Tyr	Pro	Pro	Pro	Ala	Gln	Gly	Tyr	Pro	Pro	Gln	Gly	Tyr	Pro	Pro
		35					40					45			

Gln Tyr Ala Gln Pro Pro Pro Gln Gln Gln Gln Ser Ser Gly Pro
50 55 60
Ser Phe Met Glu Gly Cys Leu Ala Ala Leu Cys Cys Cys Leu Leu
65 70 75 80
Asp Ala Cys Phe

(2) INFORMATION FOR SEQ ID NO:2856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 869 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..869
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2856:

agctagtag	cagcgcaaca	ccaccgatca	gctatacaag	caaggtagct	acctagtaga	60
gtacgtagag	gccgggtctc	cagaagacga	acatgtcgtg	gagctccgac	gagaaccaca	120
ggttcgagca	ggcgctggca	gattacgacg	aggatactcc	aggacgctgg	cagctcgtgr	180
cccaggcggt	cgggcgccgc	aggacggcgg	acgacgtctg	ggcgcaactac	ctgcacctgg	240
agggggacat	cgacgacatg	ggcgccaggg	agcgggcgaa	ccggccgcgc	caacagtacc	300
gccgcaacgc	ccacgacgac	caacaccacg	acggcgccaa	cgccaacgcc	aacgcccacg	360
ccagccgcaa	ccatattagt	cgggcgagca	acggcgcgcg	cgccagcagc	agtaacacta	420
acaacattag	tagtcatcgc	gctactaaca	gcaacgacag	agccaaacgc	ccgcagGaat	480
gagacgcggc	cgggcaggag	agacgatgaa	ccacacaaac	tacgtactat	cctactacca	540
taatatgggt	gatatcgcca	cctttccgcg	tacgaacgtg	tatgctctaa	ttaaaggaata	600
atcctagtag	tagcctatag	ccccagacta	agggcttgtt	cggttagctc	ttaatccata	660
tggattgaat	gggattggat	gggtttgaac	ccaaacaagt	caaaacttct	ctcaattttt	720
tccaattcca	tccaatccat	gtgtattggg	aataacaaaa	caagctctaa	tgtgtattgc	780
tctaattgtg	tggctcatgc	tgccgcgtac	gacggacgta	cgcaagtgtg	aaacettggg	840
cactatttat	atgtataaag	ttatatcgc				

(2) INFORMATION FOR SEQ ID NO:2857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2857:

Met	Ser	Trp	Ser	Ser	Asp	Glu	Asn	His	Arg	Phe	Glu	Gln	Ala	Leu	Ala
1			5							10				15	
Asp	Tyr	Asp	Glu	Asp	Thr	Pro	Gly	Arg	Trp	Gln	Leu	Xaa	Ala	Gln	Ala
			20					25					30		
Val	Gly	Gly	Gly	Arg	Thr	Ala	Asp	Asp	Val	Trp	Arg	His	Tyr	Leu	His
			35				40				45				
Leu	Glu	Gly	Asp	Ile	Asp	Asp	Met	Gly	Ala	Arg	Glu	Arg	Ala	Asn	Arg
			50			55					60				
Arg	Arg	Gln	Gln	Tyr	Arg	Arg	Asn	Ala	Gln	Gln	His	Gln	His	Gln	His
			65			70				75				80	
Gly	Ala	Asn	Ala	Asn	Ala	Asn	Ala	His	Ala	Ser	Arg	Asn	His	Ile	Ser
			85					90						95	
Arg	Arg	Ser	Asn	Gly	Gly	Gly	Ala	Ser	Ser	Ser	Asn	Thr	Asn	Asn	Ile
			100					105					110		
Ser	Ser	His	Arg	Ala	Thr	Asn	Ser	Asn	Asp	Arg	Ala	Lys	Arg	Pro	Gln
			115					120					125		

Glu

(2) INFORMATION FOR SEQ ID NO:2858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2858:

```
Met Gly Ala Arg Glu Arg Ala Asn Arg Arg Arg Gln Gln Tyr Arg Arg
1      5      10      15
Asn Ala Gln Gln His Gln His Gln His Gly Ala Asn Ala Asn Ala Asn
20      25      30
Ala His Ala Ser Arg Asn His Ile Ser Arg Arg Ser Asn Gly Gly Gly
35      40      45
Ala Ser Ser Ser Asn Thr Asn Asn Ile Ser Ser His Arg Ala Thr Asn
50      55      60
Ser Asn Asp Arg Ala Lys Arg Pro Gln Glu
65      70
```

(2) INFORMATION FOR SEQ ID NO:2859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..833
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2859:

```
ttggttcgcg gccacatcac caagctccgg gcgctgctgt acgtcgccgc ccagctgctg 60
gcgtctctcc tgcctgcat cctctccgc tacctcagcg gcggcatggt gaccccgatg 120
cacgcctctg gcgctggcat caacccgatg caggcgcttg tgatggaggt gatcctcacc 180
ttctcgctgc tcttgctcac ctacgcatatg atcctggacc cgcgggacag gtccgcaccca 240
tcggcccgct gctgacgggg ctcatagctg gcgcccaacag cctcgccggc ggcaacttca 300
ccggcccgct catgaacccg gcgcggtcct tcggtcccgcc catggccacc ggggtctgtg 360
ccaaccactg ggtctacttg atcggcccgcc tgctcgccgg gtccctggcc ggctctgtgt 420
acgagctcgt gtccatggtg aacaagacgc acgagccgct gctcaatgga gacatctgac 480
gaccgtcgcc ccccaaggca gtgagcacgg ttcatgcttg tttctgttaa aatagtctgt 540
tacctacaag catgatcatg atattgacca aggtaattaa ttagagaggg ttgctgttaa 600
atagttaccc ttggtgggatt gtgggatgta gaaattgttg ctgggctttg cttttctttt 660
ttcttttttt cttttctctc caaggaaatt tttaagaggg ctgggttctg taaggagatt 720
gtttaggcta ttagttagct atatgtaga aaactagaga atgctatagc ttggacgtga 780
ttttttttca cgtatattgt ttacagatat ggtatttttt atcttccgga tgg
```

(2) INFORMATION FOR SEQ ID NO:2860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2860:

Leu	Val	Arg	Gly	His	Ile	Thr	Lys	Leu	Arg	Ala	Leu	Leu	Tyr	Val	Ala	
1			5					10					15			
Ala	Gln	Leu	Leu	Ala	Ser	Ser	Leu	Ala	Cys	Ile	Leu	Leu	Arg	Tyr	Leu	
			20					25					30			
Ser	Gly	Gly	Met	Val	Thr	Pro	Val	His	Ala	Leu	Gly	Ala	Gly	Ile	Asn	
			35					40					45			
Pro	Met	Gln	Gly	Leu	Val	Met	Glu	Val	Ile	Leu	Thr	Phe	Ser	Leu	Leu	
			50				55					60				
Phe	Val	Thr	Tyr	Ala	Met	Ile	Leu	Asp	Pro	Arg	Xaa	Arg	Ser	Ala	Pro	
					70					75				80		
Ser	Ala	Arg	Cys													

(2) INFORMATION FOR SEQ ID NO:2861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2861:

Gly	Ser	Arg	Pro	His	His	Gln	Ala	Pro	Gly	Ala	Ala	Val	Arg	Arg	Arg	
1			5					10					15			
Pro	Ala	Ala	Gly	Val	Leu	Pro	Arg	Leu	His	Pro	Pro	Pro	Leu	Pro	Gln	
			20					25					30			
Arg	Arg	His	Gly	Asp	Pro	Ser	Ala	Arg	Pro	Gly	Arg	Trp	His	Gln	Pro	
			35					40				45				
Asp	Ala	Gly	Leu	Gly	Asp	Gly	Gly	Asp	Pro	His	Leu	Leu	Ala	Ala	Leu	
			50				55					60				
Arg	His	Leu	Arg	His	Asp	Pro	Gly	Pro	Ala	Xaa	Gln	Val	Arg	Thr	Ile	
					70					75				80		
Gly	Pro	Leu	Leu	Thr	Gly	Leu	Ile	Val	Gly	Ala	Asn	Ser	Leu	Ala	Gly	
					85					90				95		
Gly	Asn	Phe	Thr	Gly	Ala	Ser	Met	Asn	Pro	Ala	Arg	Ser	Phe	Gly	Pro	
					100			105					110			
Ala	Met	Ala	Thr	Gly	Val	Trp	Thr	Asn	His	Trp	Val	Tyr	Trp	Ile	Gly	
					115			120					125			
Pro	Leu	Leu	Gly	Gly	Ser	Leu	Ala	Gly	Phe	Val	Tyr	Glu	Ser	Leu	Phe	
							135					140				
Met	Val	Asn	Lys	Thr	His	Glu	Pro	Leu	Leu	Asn	Gly	Asp	Ile			
							150									

(2) INFORMATION FOR SEQ ID NO:2862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..538
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2862:

atctcatca	caggcaacaa	ggcaccacac	ctcttcttct	tcttctctct	ctctcctagca	60
cagCtagcgc	ctgtctccct	tcgctctgtga	tcattgtcttg	cagcagcggc	aagtgcgact	120
gtggctccag	ctgtctctgc	ggcagctcat	gcaactgcac	gtcccctaac	gtggagaccg	180
ccgccgcgac	cagcatcaag	accacggtcc	tcgccgcgcc	gaccaccaag	gccagcgccg	240

ggcgcttcga ggcggccacc gagggcggcg gctgcgactg caacacctgc aactgcggca 300
ccagctgcgg ctgctcctgc tgcagctgca actgagccgg tcaggcgatg gcgcacgaga 360
gtcgagagga cgacgacgag tcgtataaat ataatagcgg cgtctaaata agatcctgtc 420
aactgcaccc gccattatcg atccatggtc gtcctggggg ttcatgttca tctgtaacgt 480
gctcgcggtc atgtccgtct cgtgccggat ttaatatita tatgcatgta ttgtgttt

(2) INFORMATION FOR SEQ ID NO:2863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1574620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2863:

Pro	His	His	Arg	Gln	Gln	Gly	Thr	Thr	Pro	Leu	Leu	Leu	Leu	Pro	Pro
1			5						10					15	
Pro	Pro	Ser	Thr	Ala	Ser	Ala	Cys	Ser	Pro	Ser	Pro	Val	Ile	Met	Ser
			20					25					30		
Cys	Ser	Ser	Gly	Lys	Cys	Asp	Cys	Gly	Ser	Ser	Cys	Ser	Cys	Gly	Ser
		35					40				45				
Ser	Cys	Asn	Cys	Met	Ser	Pro	Asn	Val	Glu	Thr	Ala	Ala	Ala	Ser	Ser
	50					55				60					
Ile	Lys	Thr	Thr	Val	Leu	Ala	Ala	Pro	Thr	Thr	Lys	Ala	Ser	Ala	Gly
	65			70					75						80
Gly	Phe	Glu	Ala	Ala	Thr	Glu	Gly	Gly	Gly	Cys	Asp	Cys	Asn	Thr	Cys
			85					90					95		
Asn	Cys	Gly	Thr	Ser	Cys	Gly	Cys	Ser	Cys	Cys	Ser	Cys	Asn		
			100				105						110		

(2) INFORMATION FOR SEQ ID NO:2864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1574621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2864:

Met	Ser	Cys	Ser	Ser	Gly	Lys	Cys	Asp	Cys	Gly	Ser	Ser	Cys	Ser	Cys
1					5				10				15		
Gly	Ser	Ser	Cys	Asn	Cys	Met	Ser	Pro	Asn	Val	Glu	Thr	Ala	Ala	Ala
			20					25					30		
Ser	Ser	Ile	Lys	Thr	Thr	Val	Leu	Ala	Ala	Pro	Thr	Thr	Lys	Ala	Ser
		35				40					45				
Ala	Gly	Gly	Phe	Glu	Ala	Ala	Thr	Glu	Gly	Gly	Gly	Cys	Asp	Cys	Asn
	50				55					60					
Thr	Cys	Asn	Cys	Gly	Thr	Ser	Cys	Gly	Cys	Ser	Cys	Cys	Ser	Cys	Asn
	65				70				75					80	

(2) INFORMATION FOR SEQ ID NO:2865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..58
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574622
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2865:
Met Ser Pro Asn Val Glu Thr Ala Ala Ala Ser Ser Ile Lys Thr Thr
1 5 10 15
Val Leu Ala Ala Pro Thr Thr Lys Ala Ser Ala Gly Gly Phe Glu Ala
 20 25 30
Ala Thr Glu Gly Gly Gly Cys Asp Cys Asn Thr Cys Asn Cys Gly Thr
 35 40 45
Ser Cys Gly Cys Ser Cys Cys Ser Cys Asn
50 55

(2) INFORMATION FOR SEQ ID NO:2866:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..657
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2866:

arngccgtct	ttcttcgtta	ctgcgcccg	ctcccggaag	ctcgaccct	ttacagccg	60
cgaagaagat	gcacctgtgg	ccatcgctcc	ggatccgcga	ctcgttcaag	cacggctacc	120
tccagaagct	ggagctcaac	ctcggaaca	tgaagcgcg	gcagCGgcag	cgccagggcc	180
ggcagggaga	gagccaggag	gaccaggag	gccagcccg	cgccaacggg	aagcgccgc	240
tgctcgagga	ccgctcgcca	tcggggctcg	tgcttgccg	cgcgctcgag	ctgcctggg	300
acgcccgtct	gtccctcacc	tgctgctgct	gttgcttctg	ctgcggagCt	tgtagcgag	360
aagaggatca	cccaactgcc	cgctaagaag	caacttcagg	tgctgtataa	ttcatcagat	420
cacgaaaacc	agataatttg	tggcataaat	gaattggagt	caaatagttc	aaatagtttt	480
gatcagcttt	gtacatatgg	ttttctattc	atccttatgc	cgcccataga	tgctattgat	540
aaacgggaaa	aaggatcctt	aatttttttg	ttggaaaccc	gtgtgttagg	tattttgggc	600
gtgtaatcag	gtcgatatctg	tatttaggat	aatctgtggg	gttgctgttt	ctcaact	

(2) INFORMATION FOR SEQ ID NO:2867:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2867:

Xaa Pro Ser Phe Phe Val Thr Cys Pro Arg Ser Pro Lys Leu Glu Pro	
1 5 10 15	
Phe Thr Ala Gly Glu Glu Asp Ala Pro Val Ala Ile Ala Pro Asp Pro	
20 25 30	
Arg Leu Val Gln Ala Arg Leu Pro Glu Ala Gly Ala Gln Pro Arg	
35 40 45	
Gln His Glu Ala Arg Ala Ala Ala Pro Gly Pro Ala Gly Arg Glu	
50 55 60	
Pro Gly Gly Pro Gly Arg Pro Ala Arg Arg Gln Arg Glu Gly Ala Ala	
65 70 75 80	
Ala Arg Gly Pro Leu Ala Ile Gly Val Arg Ala Cys Arg Arg Ala Arg	
85 90 95	

Ala Arg Leu Gly Arg Arg Leu Ala Pro His Leu Leu Leu Leu Leu Leu
100 105 110
Leu Leu Arg Ser Leu
115

(2) INFORMATION FOR SEQ ID NO:2868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1574628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2868:

Xaa Arg Leu Ser Ser Leu Pro Ala Pro Ala Pro Arg Ser Ser Asn Pro
1 5 10 15
Leu Gln Pro Ala Lys Lys Met His Leu Trp Pro Ser Leu Arg Ile Arg
20 25 30
Asp Ser Phe Lys His Gly Tyr Leu Gln Lys Leu Glu Leu Asn Leu Gly
35 40 45
Asn Met Lys Arg Ala Gln Arg Gln Arg Gln Gly Arg Gln Gly Glu Ser
50 55 60
Gln Glu Asp Gln Asp Gly Gln Pro Gly Gly Asn Gly Lys Ala Pro Leu
65 70 75 80
Leu Glu Asp Arg Ser Pro Ser Gly Ser Val Leu Ala Gly Ala Leu Glu
85 90 95
Leu Ala Trp Asp Ala Val Leu Leu Leu Thr Cys Cys Cys Cys Cys Phe
100 105 110
Cys Cys Gly Ala Cys Ser Asp Glu Glu Asp His Pro Thr Ala Arg
115 120 125

(2) INFORMATION FOR SEQ ID NO:2869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1574629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2869:

Met His Leu Trp Pro Ser Leu Arg Ile Arg Asp Ser Phe Lys His Gly
1 5 10 15
Tyr Leu Gln Lys Leu Glu Leu Asn Leu Gly Asn Met Lys Arg Ala Gln
20 25 30
Arg Gln Arg Gln Gly Arg Gln Gly Glu Ser Gln Glu Asp Gln Asp Gly
35 40 45
Gln Pro Gly Gly Asn Gly Lys Ala Pro Leu Leu Glu Asp Arg Ser Pro
50 55 60
Ser Gly Ser Val Leu Ala Gly Ala Leu Glu Leu Ala Trp Asp Ala Val
65 70 75 80
Leu Leu Leu Thr Cys Cys Cys Cys Cys Phe Cys Cys Gly Ala Cys Ser
85 90 95
Asp Glu Glu Asp His Pro Thr Ala Arg
100 105

(2) INFORMATION FOR SEQ ID NO:2870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 853 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..853
(D) OTHER INFORMATION: / Ceres Seq. ID 1574636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2870:

anactcatcc	caaaccagag	cgaagaagaa	tcgccatcac	agcaagctac	gcgcactgaa	60
atcctccaat	ccacaggaca	cagctctact	tcacacgttc	gcagactcgc	acgcaccgag	120
cggctagcga	ntcaacgaga	aatgtcgtgt	gtgaggcgca	cagcgtgttc	gacccatttc	180
ctgtggacct	cttcgacccc	ttcgacagca	tggtccgctc	catcgtgccg	ccgtcgttgt	240
cgctgtcggc	ggcctccgag	acgcgccgct	tcgccagcgc	ccgcctcgac	tggaaaggaa	300
cgcccgaggc	gcaagtgttc	aaggccgacc	tcgccggcgt	gaagaaggag	gaggtcaagg	360
tggaggtgga	ggacggcaac	gtgctgtcta	tcagcgggca	gcgcaacagg	gagaaggagg	420
acaaggcgga	caagtggcac	cgctgggagc	cgagCagcgg	ccagtctcgt	cgccgtcttc	480
gcctgcggga	gaacggcaag	acggaggagg	tgaggggcgc	gctggagaac	ggcgtgctca	540
cggtcacctg	gcccaggccc	gaggtcaaga	agcccgaggc	taagagcatc	cagatctcgc	600
tctgaagaag	acatggacgc	gaggtgaatg	gtcgcgtcgc	gttcgcgtcg	cgccgtcggg	660
tcttgggttt	cagcgacgcg	actcgtgtgt	gtgtgactgt	ggttgctctg	ctttgggtatg	720
tctgtgtgtg	cgtgtgtcgt	ttcagtggtt	cgtggtcatc	gtctgtacat	tgtgtgtgtc	780
ggtgagctcc	cgcactcagt	gtgttgtgtt	ctgcgagtga	ataaataaaa	acaaccagc	840
tgctgtctcg	tgt					

(2) INFORMATION FOR SEQ ID NO:2871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..113
(D) OTHER INFORMATION: / Ceres Seq. ID 1574637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2871:

Xaa	Leu	Ile	Pro	Asn	Gln	Ser	Glu	Glu	Ser	Pro	Ser	Gln	Gln	Ala
1		5					10					15		
Thr	Arg	Thr	Glu	Ile	Leu	Gln	Ser	Thr	Gly	His	Ser	Ser	Thr	Ser
		20					25					30		
Val	Arg	Arg	Leu	Ala	Arg	Thr	Glu	Arg	Leu	Ala	Xaa	Gln	Arg	Met
		35					40					45		
Ser	Leu	Val	Arg	Arg	Thr	Ala	Cys	Ser	Thr	His	Ser	Leu	Trp	Ser
		50					55				60			
Ser	Thr	Pro	Ser	Thr	Ala	Cys	Ser	Ala	Pro	Ser	Cys	Arg	Arg	Cys
		65					70				75			80
Arg	Arg	Arg	Arg	Pro	Pro	Arg	Pro	Pro	Pro	Ser	Pro	Ala	Pro	Ser
				85						90				95
Thr	Gly	Arg	Arg	Arg	Pro	Arg	Arg	Thr	Cys	Ser	Arg	Pro	Thr	Pro
		100						105					110	

Ala

(2) INFORMATION FOR SEQ ID NO:2872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1574638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2872:

```
Met Ser Leu Val Arg Arg Thr Ala Cys Ser Thr His Ser Leu Trp Thr
1      5      10      15
Ser Ser Thr Pro Ser Thr Ala Cys Ser Ala Pro Ser Cys Arg Arg Arg
20      25      30
Cys Arg Arg Arg Arg Pro Pro Arg Pro Pro Ser Pro Ala Pro Ala
35      40      45
Ser Thr Gly Arg Arg Arg Pro Arg Arg Thr Cys Ser Arg Pro Thr Ser
50      55      60
Pro Ala
65
```

(2) INFORMATION FOR SEQ ID NO:2873:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1574639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2873:

```
Met Phe Arg Ser Ile Val Pro Pro Ser Leu Ser Ser Ser Ala Ala Ser
1      5      10      15
Glu Thr Ala Ala Phe Ala Ser Ala Arg Ile Asp Trp Lys Glu Thr Pro
20      25      30
Glu Ala His Val Phe Lys Ala Asp Leu Pro Gly Val Lys Lys Glu Glu
35      40      45
Val Lys Val Glu Val Glu Asp Gly Asn Val Leu Leu Ile Ser Gly Gln
50      55      60
Arg Ser Arg Glu Lys Glu Asp Lys Gly Asp Lys Trp His Arg Val Glu
65      70      75      80
Arg Ser Ser Gly Gln Phe Val Arg Arg Phe Arg Leu Pro Glu Asn Ala
85      90      95
Lys Thr Glu Glu Val Arg Ala Ala Leu Glu Asn Gly Val Leu Thr Val
100      105      110
Thr Val Pro Lys Ala Glu Val Lys Lys Pro Glu Val Lys Ser Ile Gln
115      120      125
Ile Ser Val
130
```

(2) INFORMATION FOR SEQ ID NO:2874:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 962 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..962

(D) OTHER INFORMATION: / Ceres Seq. ID 1574673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2874:

```
aacaagcatc agagctcggt gtcacaaaac ctgaccgatg gcggcccggt gctccacagc      60
tgctccggtg gtcagaacag gatcgcgaga cctctcccc tccttttctt tcacagccgc      120
ggcgctcccc tcggcgcgctc tgaggccggt aggagcggtg gtcgcggtg gagggtacac      180
ctgcaggctc cgcgccgctc cgcccatggg ctccgcgccc tcgtcgctcc aatccccgtc      240
gccgcacacg ccttcaggac aaacccaagg gaaagcagat tataaatcac tgagtgaaga      300
ggagtggaa gaaagcgctga ctgaagagca gtattatgtt actcggcaga agggcactga      360
```


aagagcattc	actggggaat	actggaatac	taaaacccca	ggcattttac	agtgtgtctg	420
ctgcgcaccc	cctctgtttc	agtcacaaac	caaatgtgat	agtggtactg	ggtggccatc	480
ctattataaa	ccaattgggt	aaaatgtcaa	gagcaagctt	gatattgtca	tcatttttat	540
gccccggacc	gaggtgtctc	gtgcaacCtg	tgatgtctcat	ctgggggcatg	tcCTTTttcg	600
atgaacgggcc	accaccaaca	gggaagagat	actgtatcaa	tagtgcattc	ctgaaattga	660
agcccccaata	gtttctggat	actttagcaa	gaagtcaact	ataacgctgg	tcgcgcctat	720
gtaaacttcg	gggttatgta	tataaactac	tcgagttgta	gcataattat	tattctcttt	780
gttatgtaaa	atatgtgttc	acaaacogat	gaaagtatga	aacaaacagc	cgctacttca	840
ctctgtgatt	ctggtctaga	attaaggtgt	tgtttgggtg	acgaattgta	acgtaaatgg	900
caacggtaat	ggtttgcaat	cgagtgaacg	ttgacaacgg	taataaattt	aaatagatct	960
tt						

(2) INFORMATION FOR SEQ ID NO:2875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..188
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2875:

Met	Ala	Ala	Arg	Cys	Ser	Thr	Ala	Ala	Ser	Val	Val	Arg	Thr	Gly	Ser
1			5						10					15	
Arg	Asp	Leu	Ser	Pro	Ser	Phe	Ser	Phe	Thr	Ala	Ala	Ala	Leu	Pro	Ser
			20						25				30		
Ala	Arg	Leu	Arg	Pro	Val	Gly	Ala	Trp	Val	Arg	Gly	Gly	Gly	Tyr	Thr
			35				40					45			
Cys	Arg	Leu	Arg	Ala	Val	Cys	Ala	Met	Gly	Ser	Ala	Pro	Ser	Ser	Ser
			50				55				60				
Gln	Ser	Pro	Ser	Pro	His	Thr	Pro	Ser	Gly	Gln	Thr	Gln	Gly	Lys	Ala
			65				70			75				80	
Asp	Tyr	Lys	Ser	Leu	Ser	Glu	Glu	Glu	Trp	Lys	Lys	Arg	Leu	Thr	Glu
			85						90				95		
Glu	Gln	Tyr	Tyr	Val	Thr	Arg	Gln	Lys	Gly	Thr	Glu	Arg	Ala	Phe	Thr
			100					105					110		
Gly	Glu	Tyr	Trp	Asn	Thr	Lys	Thr	Pro	Gly	Ile	Tyr	Gln	Cys	Val	Cys
			115				120					125			
Cys	Asp	Thr	Pro	Leu	Phe	Gln	Ser	Ser	Thr	Lys	Phe	Asp	Ser	Gly	Thr
			130				135					140			
Gly	Trp	Pro	Ser	Tyr	Tyr	Lys	Pro	Ile	Gly	Glu	Asn	Val	Lys	Ser	Lys
			145				150				155			160	
Leu	Asp	Met	Ser	Ile	Ile	Phe	Met	Pro	Arg	Thr	Glu	Val	Leu	Cys	Ala
			165						170				175		
Thr	Cys	Asp	Ala	His	Leu	Gly	His	Val	Leu	Phe	Arg				
			180												

(2) INFORMATION FOR SEQ ID NO:2876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2876:

Met	Gly	Ser	Ala	Pro	Ser	Ser	Ser	Gln	Ser	Pro	Ser	Pro	His	Thr	Pro
1				5					10				15		

Ser Gly Gln Thr Gln Gly Lys Ala Asp Tyr Lys Ser Leu Ser Glu Glu
20 25 30
Glu Trp Lys Lys Arg Leu Thr Glu Glu Gln Tyr Tyr Val Thr Arg Gln
35 40 45
Lys Gly Thr Glu Arg Ala Phe Thr Gly Glu Tyr Trp Asn Thr Lys Thr
50 55 60
Pro Gly Ile Tyr Gln Cys Val Cys Cys Asp Thr Pro Leu Phe Gln Ser
65 70 75
Ser Thr Lys Phe Asp Ser Gly Thr Gly Trp Pro Ser Tyr Tyr Lys Pro
85 90 95
Ile Gly Glu Asn Val Lys Ser Lys Leu Asp Met Ser Ile Ile Phe Met
100 105 110
Pro Arg Thr Glu Val Leu Cys Ala Thr Cys Asp Ala His Leu Gly His
115 120 125
Val Leu Phe Arg
130

(2) INFORMATION FOR SEQ ID NO:2877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2877:

Met Leu Leu Gly Arg Arg Ala Leu Lys Glu His Ser Leu Gly Asn Thr
1 5 10 15
Gly Ile Leu Lys Pro Gln Ala Phe Ile Ser Val Ser Ala Ala Thr Pro
20 25 30
Leu Cys Phe Ser His Gln Pro Asn Leu Ile Val Val Leu Gly Gly His
35 40 45
Pro Ile Ile Asn Gln Leu Val Lys Met Ser Arg Ala Ser Leu Ile Cys
50 55 60
Gln Ser Phe Leu Cys Pro Gly Pro Arg Cys Ser Val Gln Pro Val Met
65 70 75 80
Leu Ile Trp Gly Met Ser Phe Phe Asp Asp Gly Pro Pro Pro Thr Gly
85 90 95
Lys Arg Tyr Cys Ile Asn Ser Ala Ser Leu Lys Leu Lys Pro Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:2878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..755
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2878:

agatctcaac gcaactaaaa cattttatct tctctatcgc tactccaaga gtacccaatc 60
accogagccat ggccatctca gtcactgcgc tggcgcgcctt gccgcgttct cggctcaaa 120
aagcctcccg cagccgctccc gccagagggt cgtagcgttc atcgtcgtcc gcccggtgcg 180
cgcgaccgcg cggtttgtgg gcggtggcgc cagctgcgcg cccacgcgcg cggatctcgc 240
aaagaaggtg tccagagaca tcaagcaggg ccaggagagc tgcgcagatg acccggtgag 300
cggcgagtg cgtggcggcgt gggacgagct ggaggagctc agcgcggcgc ccagccactt 360
gcgcgaccgg cagaagggcg ccgaccgcct cgaggagtag tgcaaggaca accccgagGa 420

ccgcagcagtg ccCGcagcta cgaggactga accacgcgcg cgcgaggttg gatcgctgtc 480
acttgatctta gctagGcagc ttagctcggc atgatggcga catgtgtaga cgtgcaatgg 540
atcgggtatg atcctctgtt gattcagctct gccttggtgt ggaataaaac gaggtttgct 600
gtttattata agtaacattt aggagctcct actgtagtct caaggcaggt gtaatcctta 660
gaaacatttg atggtgtgct tctagccttg tagtactcga tatgtgcaat tctgtaaagt 720
atcgcagatt ttccacctga gcattgatt gctgc

(2) INFORMATION FOR SEQ ID NO:2879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1574678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2879:

Asp	Leu	Asn	Ala	Thr	Lys	Thr	Phe	Tyr	Leu	Leu	Tyr	Arg	Tyr	Ser	Lys
1			5						10					15	
Ser	Thr	Gln	Ser	Pro	Ser	His	Gly	His	Leu	Ser	His	Cys	Arg	Gly	Arg
			20				25					30			
Leu	Ala	Arg	Phe	Ser	Ala	Gln	Arg	Ser	Leu	Pro	Gln	Pro	Ser	Arg	Gln
			35				40					45			
Arg	Val	Val	Ala	Phe	Ile	Val	Val	Arg	Pro	Val	Arg	Ala	His	Arg	Arg
			50				55					60			
Phe	Val	Gly	Val	Ala	Ala	Ser	Ser	Pro	Pro	Thr	Pro	Pro	Asp	Leu	Ala
			65				70					75			80
Lys	Lys	Val	Ser	Glu	Ser	Ile	Lys	Gln	Ala	Gln	Glu	Thr	Cys	Ala	Asp
							85								
Asp	Pro	Val	Ser	Gly	Glu	Cys	Val	Ala	Ala	Trp	Asp	Glu	Leu	Glu	Glu
							100								
Leu	Ser	Ala	Ala	Ala	Ser	His	Leu	Arg	Asp	Arg	Gln	Lys	Gly	Ala	Asp
							115								
Pro	Leu	Glu	Glu	Tyr	Cys	Lys	Asp	Asn	Pro	Glu	Asp	Arg	Arg	Val	Pro
							120								
Ala	Arg	Thr	Arg	Thr	Glu	Pro	Arg	Ala	Arg	Glu	Val	Gly	Ser	Leu	Ser
							135								
Leu	Asp	Leu	Ala	Arg	Gln	Leu	Ser	Ser	Ala						
							150								
							165								170

(2) INFORMATION FOR SEQ ID NO:2880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2880:

aacgcccctt	tcttgcgagt	gaggccaaag	ccgagcaaac	aaaacgatat	gccgctgcc	60
tgaaccgaga	ccaccacccg	tctgcctcgc	ctcgcctcac	ctcacctcat	ctcacctcgc	120
cgactagggt	tttgtaccgc	cgtggatctc	gccgtccccg	ccatggagctg	ctgcacacgc	180
ggtacctctg	tcgcgcggcg	ggctccgacc	accgggggag	accggatggg	gactaccatc	240
gtcggggctc	gctacagagg	cggcgctgct	ctgggcgcgc	attccaggac	cagcactgga	300
atgtatgtag	ccaacccgtc	ttcagacaag	attactcaac	tgacagacaa	tgtgtatgtc	360
tgtcgtctcg	gatctgctcg	gtatcacaca	gtcatttcgg	attatgtacg	ctatttcctc	420
caccaacaca	caatccagct	tgGacaacca	gctaccgtta	aagtgtcagc	camctTgatt	480
aggtTgctag	cttatcagaA	caagaacatg	ttgcaagctg	gcatgattgt	tggaggatgg	540

```

ggacaagtac gagggaggcc aaattttctc agtccctctc ggtggaacga tcttgaagca    600
accatttgca attggaggtt caggtccagt tacctatatg ctcttcttga tcatgaatgg    660
aaagagggaa tgagtcagga agaggcagag aaatttgtgg tgaaggtagt ttcccttgct    720
atggcccggt atggtgctag tggagggggt gtccgcacag ttacaataaa tgcggatggc    780
gtgaagagga acttttaccc tggcgacaag ctacccctgt ggcacgacga gctggaaccc    840
cagaactcgt tgcttgatat tcttgctgct gggaaccctg atcccatggt gcagtgaaat    900
cgccctccac ttactttgtg aacttttcac tgtatctgac ttgttcttga ttatttctcc    960
ttgaactatg tcagaccaga gtaatttacg aattgtgtgt atcgacacct aataaattca   1020
tgtttagctg ggtgattggc gttttgagtt aatggttact ggtaagcggt ctactgctgt   1080
agttaagcct gtggcaagta ttcaaatatt cagt

```

(2) INFORMATION FOR SEQ ID NO:2881:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..244

(D) OTHER INFORMATION: / Ceres Seq. ID 1574694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2881:

```

Met Asp Val Ser His Ala Gly Ser Ser Val Ala Gly Glu Ala Pro Thr
1           5           10           15
Thr Gly Glu His Arg Met Gly Thr Thr Ile Val Gly Val Cys Tyr Glu
20           25           30
Gly Gly Val Val Leu Gly Ala Asp Ser Arg Thr Ser Thr Gly Met Tyr
35           40           45
Val Ala Asn Arg Ala Ser Asp Lys Ile Thr Gln Leu Thr Asp Asn Val
50           55           60
Tyr Val Cys Arg Ser Gly Ser Ala Ala Asp Thr Gln Val Ile Ser Asp
65           70           75           80
Tyr Val Arg Tyr Phe Leu His Gln His Thr Ile Gln Leu Gly Gln Pro
85           90           95
Ala Thr Val Lys Val Ala Ala Xaa Leu Ile Arg Leu Leu Ala Tyr Gln
100          105          110
Asn Lys Asn Met Leu Gln Ala Gly Met Ile Val Gly Gly Trp Gly Gln
115          120          125
Val Arg Gly Arg Pro Asn Phe Leu Ser Pro Ser Arg Trp Asn Asp Leu
130          135          140
Glu Ala Thr Ile Cys Asn Trp Arg Phe Arg Ser Ser Tyr Leu Tyr Ala
145          150          155          160
Leu Leu Asp His Glu Trp Lys Glu Gly Met Ser Gln Glu Glu Ala Glu
165          170          175
Lys Phe Val Val Lys Val Val Ser Leu Ala Met Ala Arg Asp Gly Ala
180          185          190
Ser Gly Gly Val Val Arg Thr Val Thr Ile Asn Ala Asp Gly Val Lys
195          200          205
Arg Asn Phe Tyr Pro Gly Asp Lys Leu Pro Leu Trp His Asp Glu Leu
210          215          220
Glu Pro Gln Asn Ser Leu Leu Asp Ile Leu Ala Glu Asn Pro Asp
225          230          235          240
Pro Met Val Gln

```

(2) INFORMATION FOR SEQ ID NO:2882:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1574695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2882:

Met Gly Thr Thr Ile Val Gly Val Cys Tyr Glu Gly Gly Val Val Leu
1 5 10 15
Gly Ala Asp Ser Arg Thr Ser Thr Gly Met Tyr Val Ala Asn Arg Ala
20 25 30
Ser Asp Lys Ile Thr Gln Leu Thr Asp Asn Val Tyr Val Cys Arg Ser
35 40 45
Gly Ser Ala Ala Asp Thr Gln Val Ile Ser Asp Tyr Val Arg Tyr Phe
50 55 60
Leu His Gln His Thr Ile Gln Leu Gly Gln Pro Ala Thr Val Lys Val
65 70 75 80
Ala Ala Xaa Leu Ile Arg Leu Leu Ala Tyr Gln Asn Lys Asn Met Leu
85 90 95
Gln Ala Gly Met Ile Val Gly Gly Trp Gly Gln Val Arg Gly Arg Pro
100 105 110
Asn Phe Leu Ser Pro Ser Arg Trp Asn Asp Leu Glu Ala Thr Ile Cys
115 120 125
Asn Trp Arg Phe Arg Ser Ser Tyr Leu Tyr Ala Leu Leu Asp His Glu
130 135 140
Trp Lys Glu Gly Met Ser Gln Glu Glu Ala Glu Lys Phe Val Val Lys
145 150 155 160
Val Val Ser Leu Ala Met Ala Arg Asp Gly Ala Ser Gly Gly Val Val
165 170 175
Arg Thr Val Thr Ile Asn Ala Asp Gly Val Lys Arg Asn Phe Tyr Pro
180 185 190
Gly Asp Lys Leu Pro Leu Trp His Asp Glu Leu Glu Pro Gln Asn Ser
195 200 205
Leu Leu Asp Ile Leu Ala Ala Gly Asn Pro Asp Pro Met Val Gln
210 215 220

(2) INFORMATION FOR SEQ ID NO:2883:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..198

(D) OTHER INFORMATION: / Ceres Seq. ID 1574696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2883:

Met Tyr Val Ala Asn Arg Ala Ser Asp Lys Ile Thr Gln Leu Thr Asp
1 5 10 15
Asn Val Tyr Val Cys Arg Ser Gly Ser Ala Ala Asp Thr Gln Val Ile
20 25 30
Ser Asp Tyr Val Arg Tyr Phe Leu His Gln His Thr Ile Gln Leu Gly
35 40 45
Gln Pro Ala Thr Val Lys Val Ala Ala Xaa Leu Ile Arg Leu Leu Ala
50 55 60
Tyr Gln Asn Lys Asn Met Leu Gln Ala Gly Met Ile Val Gly Gly Trp
65 70 75 80
Gly Gln Val Arg Gly Arg Pro Asn Phe Leu Ser Pro Ser Arg Trp Asn
85 90 95
Asp Leu Glu Ala Thr Ile Cys Asn Trp Arg Phe Arg Ser Ser Tyr Leu
100 105 110
Tyr Ala Leu Leu Asp His Glu Trp Lys Glu Gly Met Ser Gln Glu Glu
115 120 125

Ala Glu Lys Phe Val Val Lys Val Val Ser Leu Ala Met Ala Arg Asp
130 135 140
Gly Ala Ser Gly Gly Val Val Arg Thr Val Thr Ile Asn Ala Asp Gly
145 150 155 160
Val Lys Arg Asn Phe Tyr Pro Gly Asp Lys Leu Pro Leu Trp His Asp
165 170 175
Glu Leu Glu Pro Gln Asn Ser Leu Leu Asp Ile Leu Ala Ala Gly Asn
180 185 190
Pro Asp Pro Met Val Gln
195

(2) INFORMATION FOR SEQ ID NO:2884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..762
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2884:

agctttgttt	ttgtgtgtgt	cagchvgrcg	gtccgagcta	cgccgtggag	ctggggcgggc	60
tggaacggcaa	gacgttcaac	agggccatcg	tgaagcacgt	cctcccgggc	cccggtctta	120
acctggacca	gctcaacgcc	ctcttcgcgc	agaacggcct	cacgcagacg	gacatgatcg	180
cgctctcagg	cggccacacg	atcgggggtga	cgcactgcga	caagttcgtg	cgccggatct	240
acacgttcaa	gcagcggctg	gcgtggaacc	cgccgatgaa	cctggacttc	ctgcgctcgc	300
tgccggcggt	gtgccccctc	agctacagcc	ccacgGcggt	cgccatgctg	gacgtcaacca	360
gcgccgggt	cttcgacaac	gcctacttca	acaacctccg	ctacaacaag	ggcctgctcg	420
ctctcgacca	gggtctcttc	accgaccgcc	gtccctcgcc	cacctgcaac	ctcttcgccc	480
ccaacgccac	cgctctctac	gaggcattcg	tcgcccacat	ggccaagctc	ggcaggatcg	540
gcctcaagac	cggcgccgac	ggcgagatac	gccgcgtctg	cacgcgcgtc	aactaagcct	600
gcattggctg	cttgctctct	gcgtcgctgg	gtttacttta	tttactctot	tcctttctct	660
gtttatatac	gtacgtttgt	cggatggatt	ttggtagcca	tgagatgaca	tccttgctct	720
gagctagcgg	acctgccccc	attgatgat	atagattgat	cc		

(2) INFORMATION FOR SEQ ID NO:2885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..231
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2885:

Ala Leu Phe Leu Val Cys Ala Xaa Xaa Arg Ser Glu Leu Arg Arg Gly	
1 5 10 15	
Ala Gly Ala Ala Gly Arg Gln Asp Val Gln Gln Gly His Arg Gly Ala	
20 25 30	
Arg Pro Pro Gly Pro Arg Leu Gln Pro Gly Pro Ala Gln Arg Pro Leu	
35 40 45	
Arg Ala Glu Arg Pro His Ala Asp Gly His Asp Arg Ala Leu Arg Arg	
50 55 60	
Ala His Asp Arg Gly Asp Ala Leu Arg Gln Val Arg Ala Ala Asp Leu	
65 70 75 80	
His Val Gln Ala Ala Gly Val Glu Pro Ala Asp Glu Pro Gly Leu	
85 90 95	
Pro Ala Leu Ala Ala Gly Val Pro Pro Gln Leu Gln Pro His Gly	
100 105 110	

Val Arg His Ala Gly Arg His His Ala Gln Gly Leu Arg Gln Arg Leu
115 120 125
Leu Gln Gln Pro Pro Leu Gln Gln Gly Pro Ala Arg Leu Arg Pro Gly
130 135 140
Ala Leu His Arg Pro Pro Leu Pro Thr His Arg Gln Pro Leu Arg Arg
145 150 155 160
Gln Arg His Arg Leu Leu Arg Gly Ile Arg Arg His Gly Gln Ala
165 170 175
Arg Gln Asp Arg Pro Gln Asp Arg Arg Arg Arg Asp Thr Pro Arg
180 185 190
Leu His Arg Arg Gln Leu Ser Leu His Trp Leu Leu Ala Ala Cys Val
195 200 205
Arg Gly Phe His Leu Phe His Phe Phe Leu Leu Phe Ile Tyr Val
210 215 220
Arg Leu Ser Asp Gly Phe Trp
225 230

(2) INFORMATION FOR SEQ ID NO:2886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2886:

Leu Cys Phe Trp Cys Val Gln Xaa Xaa Gly Pro Ser Tyr Gly Val Glu
1 5 10 15
Leu Gly Arg Leu Asp Gly Lys Thr Phe Asn Arg Ala Ile Val Lys His
20 25 30
Val Leu Pro Gly Pro Gly Phe Asn Leu Asp Gln Leu Asn Ala Leu Phe
35 40 45
Ala Gln Asn Gly Leu Thr Gln Thr Asp Met Ile Ala Leu Ser Gly Ala
50 55 60
His Thr Ile Gly Val Thr His Cys Asp Lys Phe Val Arg Arg Ile Tyr
65 70 75 80
Thr Phe Lys Gln Arg Leu Ala Trp Asn Pro Pro Met Asn Leu Asp Phe
85 90 95
Leu Arg Ser Leu Arg Arg Val Cys Pro Leu Ser Tyr Ser Pro Thr Ala
100 105 110
Phe Ala Met Leu Asp Val Thr Thr Pro Arg Val Phe Asp Asn Ala Tyr
115 120 125
Phe Asn Asn Leu Arg Tyr Asn Lys Gly Leu Leu Ala Ser Asp Gln Val
130 135 140
Leu Phe Thr Asp Arg Arg Ser Arg Pro Thr Val Asn Leu Phe Ala Ala
145 150 155 160
Asn Ala Thr Ala Phe Tyr Glu Ala Phe Val Ala Ala Met Ala Lys Leu
165 170 175
Gly Arg Ile Gly Leu Lys Thr Gly Ala Asp Gly Glu Ile Arg Arg Val
180 185 190
Cys Thr Ala Val Asn
195

(2) INFORMATION FOR SEQ ID NO:2887:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..140
(D) OTHER INFORMATION: / Ceres Seq. ID 1574704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2887:

Met	Ile	Ala	Leu	Ser	Gly	Ala	His	Thr	Ile	Gly	Val	Thr	His	Cys	Asp
1			5						10					15	
Lys	Phe	Val	Arg	Arg	Ile	Tyr	Thr	Phe	Lys	Gln	Arg	Leu	Ala	Trp	Asn
		20					25					30			
Pro	Pro	Met	Asn	Leu	Asp	Phe	Leu	Arg	Ser	Leu	Arg	Arg	Val	Cys	Pro
		35				40				45					
Leu	Ser	Tyr	Ser	Pro	Thr	Ala	Phe	Ala	Met	Leu	Asp	Val	Thr	Thr	Pro
	50					55				60					
Arg	Val	Phe	Asp	Asn	Ala	Tyr	Phe	Asn	Asn	Leu	Arg	Tyr	Asn	Lys	Gly
	65				70				75					80	
Leu	Leu	Ala	Ser	Asp	Gln	Val	Leu	Phe	Thr	Asp	Arg	Arg	Ser	Arg	Pro
			85					90						95	
Thr	Val	Asn	Leu	Phe	Ala	Ala	Asn	Ala	Thr	Ala	Phe	Tyr	Glu	Ala	Phe
		100					105						110		
Val	Ala	Ala	Met	Ala	Lys	Leu	Gly	Arg	Ile	Gly	Leu	Lys	Thr	Gly	Ala
		115					120					125			
Asp	Gly	Glu	Ile	Arg	Arg	Val	Cys	Thr	Ala	Val	Asn				
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:2888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..736
(D) OTHER INFORMATION: / Ceres Seq. ID 1574713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2888:

cccaaaatac	tcaccaccgc	caccactag	ggttccgca	ccgcattgca	gaacctcgcc	60
gcctccaccc	tcaccacacc	accggcgatg	tcacacgcgg	cggcgcaggg	cggcagcgac	120
aagccggcgc	tcgggaggcc	cgtcttcacc	aaggtcgacc	agctcaggcc	gggcaccaac	180
gggcacaccc	tcaccgtcaa	ggctgtcagc	gccacccccgc	tgcCtgGcg	cgccgcgccCa	240
ggcgaccccg	ccgcgcggcc	atcNccGcgc	gcgcgcgcatc	gccgagtgcc	tcgtcgggga	300
cgagaccggc	gccatcgctc	tcaccgcggc	caacgaccaa	gttgacttgc	tgaagcccaa	360
tgcgacagtg	atcttgcgca	atgcacaaat	agacatgttc	aaaggatcaa	tgaggcttgc	420
agtggaacaag	tgggggcgga	ttgagcgctg	agagccagcc	agtttcacgg	tgaaggaa	480
caacaacctg	tctctaatag	agtatgaatt	ggttaatgtg	gctgagtaac	tgtccaatcc	540
aagcgctttc	gcccccctta	tttcgtgcca	taagaaggaa	gtaccatgaa	tgaacattat	600
aaagcctctt	gaagcgaagc	gagtttattt	gtcacgggtg	ggtagataaa	ggatcaaggct	660
gtatggcctg	tggtagaact	ttggataaat	taagatgaat	tgcccttgca	tctatgagat	720
tggtatccat	ctttgt					

(2) INFORMATION FOR SEQ ID NO:2889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..175
(D) OTHER INFORMATION: / Ceres Seq. ID 1574714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2889:

Pro Lys Tyr Ser Thr Thr Ala Pro Thr Arg Val Ser Ala Pro His Cys

1				5						10					15
Arg	Thr	Ser	Pro	Pro	Pro	Pro	Ser	Pro	His	His	Arg	Arg	Cys	Pro	Gln
			20					25					30		
Arg	Arg	Arg	Arg	Ala	Ala	Ala	Thr	Ser	Arg	Arg	Ser	Gly	Gly	Pro	Ser
			35				40					45			
Ser	Pro	Arg	Ser	Thr	Ser	Ser	Gly	Arg	Ala	Pro	Thr	Gly	Thr	Pro	Ser
			50			55					60				
Pro	Ser	Arg	Ser	Ser	Ala	Pro	Pro	Pro	Cys	Leu	Gly	Ala	Arg	Ala	Gln
					70				75					80	
Ala	His	Pro	Pro	Pro	Pro	His	Xaa	Arg	Ala	Pro	Arg	Ile	Ala	Glu	Cys
				85					90					95	
Leu	Val	Gly	Asp	Glu	Thr	Gly	Ala	Ile	Val	Phe	Thr	Ala	Arg	Asn	Asp
			100				105						110		
Gln	Val	Asp	Leu	Leu	Lys	Pro	Asn	Ala	Thr	Val	Ile	Leu	Arg	Asn	Ala
			115				120						125		
Lys	Ile	Asp	Met	Phe	Lys	Gly	Ser	Met	Arg	Leu	Ala	Val	Asp	Lys	Trp
			130			135					140				
Gly	Arg	Ile	Glu	Ala	Val	Glu	Pro	Ala	Ser	Phe	Thr	Val	Lys	Glu	Asp
			145			150				155				160	
Asn	Asn	Leu	Ser	Leu	Ile	Glu	Tyr	Glu	Leu	Val	Asn	Val	Ala	Glu	
				165					170					175	

(2) INFORMATION FOR SEQ ID NO:2890:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1574715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2890:

Gln	Asn	Thr	Pro	Pro	His	Pro	Leu	Gly	Phe	Pro	His	Arg	Ile	Ala	
1			5					10					15		
Glu	Pro	Arg	Arg	Leu	His	Pro	His	His	Thr	Thr	Gly	Asp	Val	His	Ser
			20					25				30			
Gly	Gly	Ala	Gly	Arg	Gln	Arg	Gln	Ala	Gly	Ala	Pro	Glu	Ala	Arg	Leu
			35				40					45			
His	Gln	Gly	Arg	Pro	Ala	Gln	Ala	Gly	His	Gln	Arg	Ala	His	Pro	His
			50			55					60				
Arg	Gln	Gly	Arg	Gln	Arg	His	Pro	Arg	Ala	Trp	Ala	Arg	Ala	Pro	Arg
			65			70			75					80	
Arg	Thr	Arg	Arg	Arg	Pro	Ile	Xaa	Ala	Arg	Arg	Ala	Ser	Pro	Ser	Ala
				85					90				95		
Ser	Ser	Gly	Thr	Arg	Pro	Ala	Pro	Ser	Ser	Ser	Pro	Pro	Ala	Thr	Thr
			100					105					110		
Lys	Leu	Thr	Cys												
			115												

(2) INFORMATION FOR SEQ ID NO:2891:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 534 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..534

(D) OTHER INFORMATION: / Ceres Seq. ID 1574735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2891:

```

aaaaccattc cccgttctcg attccaattc caaccagccc atcccccttc gagcacagcg 60
gcagagcggg ggcggaaggca agagcaaaaca gactagccgc cgcgcgcgtc gccgtcgctcg 120
tcgtgtgtgt gtgtggagag gaaagaccgg gttttgtttt ttacggetta gcgttgagca 180
gctgagatgt tgcgagcgct ggcggcgagg tgctgcgccc actggcgccc gggcgccgcg 240
gcggcgctct gctcaccagg aacgtcgcca tcagctacaa cctgcgcccc gccaacccgc 300
tcggctactt caaggacgtg ccgctgcccc tctgcgcctc gctgctcaag cagttggact 360
cggacgacga cgacgatcag taatagcaca tcgtcgacga cgcgagactg gctggcacta 420
aaccacaatt cctcttcacc tggattacaa atatgtaact gagaaagaaa aggaatacaa 480
aatgtaact gcgtggctgt accaaattct gagtgctgga ttcttgctat tgctc

```

(2) INFORMATION FOR SEQ ID NO:2892:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1574736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2892:

```

Lys Pro Phe Pro Val Pro Asp Ser Asn Ser Asn Gln Pro Ile Pro Leu
1      5      10      15
Arg Ala His Ala Gln Ser Gly Gly Glu Gly Lys Ser Lys Gln Ser Ser
20     25     30
Arg Arg Arg Arg Arg Arg Arg Arg Val Cys Val Trp Arg Gly Lys
35     40     45
Thr Gly Phe Cys Phe Leu Arg Leu Ser Val Glu Gln Leu Arg Cys Cys
50     55     60
Glu Arg Trp Arg Arg Gly Ala Ala Ala Thr Gly Arg Arg Ala Pro Arg
65     70     75     80
Arg Arg Pro Ala His Gln Glu Arg Arg His Gln Leu Gln Pro Ala Pro
85     90     95
Arg Gln Pro Ala Arg Leu Leu Gln Gly Arg Ala Ala Ala His Leu Arg
100    105    110
Leu Ala Ala Gln Ala Val Gly Leu Gly Arg Arg Arg Ser Val Ile
115    120    125
Ala His Arg Arg Arg Pro Gln Thr Gly Trp His
130    135

```

(2) INFORMATION FOR SEQ ID NO:2893:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1574737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2893:

```

Met Leu Arg Ala Leu Ala Ala Arg Cys Cys Gly His Trp Pro Pro Gly
1      5      10      15
Ala Ala Ala Ala Ser Cys Ser Pro Gly Thr Ser Ala Ser Ala Thr Thr
20     25     30
Cys Ala Pro Pro Thr Arg Ser Ala Thr Ser Arg Thr Cys Arg Cys Pro
35     40     45
Ser Ala Pro Arg Cys Ser Ser Ser Trp Thr Arg Thr Thr Thr Thr Ile
50     55     60
Ser Asn Ser Thr Ser Thr Thr Thr Ala Asp Trp Leu Ala Leu Asn His
65     70     75     80

```

Lys Ser Ser Ser Pro Gly Leu Gln Ile Cys Asn
85 90

(2) INFORMATION FOR SEQ ID NO:2894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1185
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2894:

```
agctcgtgtac  cgccggcga  gcagtcggtt  tcttcctctt  ccttgattaa  accttcgcta  60
cccatatcca  cctgctgtcc  cgaccttcca  gtcttctccg  tagggggctc  gctccataga  120
tttcgcgcga  aggggcaacg  gcacacccac  caactgacct  gaccacagag  ggaaccgcag  180
atgaagatca  ttccggtccc  ttgcctggat  gacaaactat  cctacttaat  cgtggacgag  240
agcaccgaag  aggcagcgcc  cgttgacctt  gtggaaacgg  agaaggttct  caaggcggcc  300
ggcgaggtcg  ggcgctacgt  cgactgcgtt  ctacccaccc  atcaccactg  ggatcatgct  360
gggtggcaatg  agaagatgag  gctgcaggtg  ccagggataa  aggtatttgg  aggatccctg  420
gacaatgtga  aagcgtgcac  tgatcaggtg  gagaatggaa  tgaagttgtc  acttgggaag  480
gacattgaga  tactatgcct  acacacgcct  tgccacacta  aAggtcatat  cagctactat  540
gttactagta  aggaggtgaa  gatccagcgg  tcttcaccgg  agataccctg  ttcattgctg  600
gggtgtgggaa  gtttttttag  ggttctgcag  agcaaatgta  tcagtccctt  attgttacac  660
tgggttcgct  gccaaagtca  acccgagttt  actgtgggca  tgagtacact  gtgaagaacc  720
taaaattcat  gctgacactg  gagccagaga  atgagaagac  gaaacagaaa  ctggaattgg  780
ctgaaaagca  gcgcgaagcg  aatcagccaa  cagtgccttc  gactatagga  gatgagtttg  840
agataaatac  ttctatgcgt  gttgatctac  cagaaataca  ggccgaattc  agtgtcaact  900
ctccagttga  agcaatgata  gaggtcagga  agaccaagga  taattggaga  ggttgaggac  960
accatgggcc  gccactagtc  tgttgaaaca  cgattccaaa  gtgaactaat  gcagaaacct  1020
tgccctgtag  gtgggaatga  ggtttactgc  gctgaatgc  ttgagaaat  gtgttgttgt  1080
gaaggagaag  actcctacaa  taastcccg  ttaatgagta  gtaacaaatc  gctcctgtga  1140
acttgtggtc  tgtttgccaa  taataatgta  cgaactgtag  tgccct
```

(2) INFORMATION FOR SEQ ID NO:2895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..177
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2895:

```
Met Lys Ile Ile Pro Val Pro Cys Leu Asp Asn Tyr Ala Tyr Leu
1 5 10 15
Ile Val Asp Glu Ser Thr Lys Lys Ala Ala Val Asp Pro Val Glu
20 25 30
Pro Glu Lys Val Leu Lys Ala Ala Gly Glu Val Gly Ala Tyr Val Asp
35 40 45
Cys Val Leu Thr Thr His His His Trp Asp His Ala Gly Gly Asn Glu
50 55 60
Lys Met Arg Leu Gln Val Pro Gly Ile Lys Val Phe Gly Gly Ser Leu
65 70 75 80
Asp Asn Val Lys Gly Cys Thr Asp Gln Val Glu Asn Gly Met Lys Leu
85 90 95
Ser Leu Gly Lys Asp Ile Glu Ile Leu Cys Leu His Thr Pro Cys His
100 105 110
Thr Lys Gly His Ile Ser Tyr Tyr Val Thr Ser Lys Glu Val Lys Ile
```

(2) INFORMATION FOR SEQ ID NO:2896:

(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

```
(ix) FEATURE:
```

- (A) NAME/KEY: peptide
(B) LOCATION: 1..112
(D) OTHER INFORMATION: / Ceres Seq. ID 1574740

Met	Arg	Leu	Gln	Val	Pro	Gly	Ile	Lys	Val	Phe	Gly	Gly	Ser	Leu	Asp
1			5						10					15	
Asn	Val	Lys	Gly	Cys	Thr	Asp	Gln	Val	Glu	Asn	Gly	Met	Lys	Leu	Ser
		20						25					30		
Leu	Gly	Lys	Asp	Ile	Glu	Ile	Leu	Cys	Leu	His	Thr	Pro	Cys	His	Thr
		35					40					45			
Lys	Gly	His	Ile	Ser	Tyr	Tyr	Val	Thr	Ser	Lys	Glu	Val	Lys	Ile	Gln
		50				55					60				
Arg	Ser	Ser	Pro	Glu	Ile	Pro	Cys	Ser	Leu	Leu	Gly	Val	Gly	Ser	Phe
65					70					75					80
Leu	Arg	Val	Leu	Gln	Ser	Lys	Cys	Ile	Ser	Pro	Leu	Leu	Leu	His	Trp
			85						90					95	
Val	Arg	Cys	Gln	Ser	Gln	Pro	Glu	Phe	Thr	Val	Gly	Met	Ser	Thr	Leu
			100					105					110		

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..106
(D) OTHER INFORMATION: / Ceres Seq. ID 1574741

Met	Tyr	Gln	Ser	Leu	Ile	Val	Thr	Leu	Gly	Ser	Leu	Pro	Lys	Ser	Thr
1			5						10					15	
Arg	Val	Tyr	Cys	Gly	His	Glu	Tyr	Thr	Val	Lys	Asn	Leu	Lys	Phe	Met
			20					25					30		
Leu	Thr	Leu	Glu	Pro	Glu	Asn	Glu	Lys	Thr	Lys	Gln	Lys	Leu	Glu	Trp
			35				40					45			
Ala	Glu	Lys	Gln	Arg	Glu	Ala	Asn	Gln	Pro	Thr	Val	Pro	Ser	Thr	Ile
	50					55					60				
Gly	Asp	Glu	Phe	Glu	Ile	Asn	Thr	Phe	Met	Arg	Val	Asp	Leu	Pro	Glu
65					70					75					80
Ile	Gln	Ala	Lys	Phe	Ser	Val	Asn	Ser	Pro	Val	Glu	Ala	Met	Ile	Glu
			85						90					95	

Val Arg Lys Thr Lys Asp Asn Trp Arg Gly
100 105

(2) INFORMATION FOR SEQ ID NO:2898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..691
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2898:

atcactaggc	caccaccag	cggcgggctc	cagtcgcaac	tcgcaacaca	gtcacagagc	60
ccgcgcgccca	aagaagagac	tcaactccag	gagacaagac	agtgagaact	gaagagaagg	120
atgggcttcg	agaagcagat	cctgagatcc	ggcacccggc	ccaagccgat	aaagggccag	180
aaggctcaccc	ttaactgcac	cggctacggg	aaggatcgtg	atcttccaag	aaattttgga	240
gcaccaagga	ccctgggcag	cagccattca	gtttcagcat	tggtcagggt	tcagtgatca	300
aaggatggga	cgagggaatt	atgaccatgc	aagtgggtga	agttgctcgt	atccagtgcg	360
cgcttgattg	tgccttatgga	gccggcgggt	tcccagcctg	gggaattcaa	ccaaactcag	420
tgcttgtgtt	tcgagattga	agtctctcag	gccacagta	tcgcatctgt	cagctatgga	480
aacgttggcc	atgctttctc	agtAaatgaa	ataattccgt	gtcacctcca	tgctacatac	540
agcagattgg	tgttacgagb	baaatcctgt	gamactttag	cattctgtaa	cogtggatgt	600
cgagtttatg	gagttccctg	tgtggcgcc	caagtaagt	tctcgtaaaa	gattgtaata	660
tgatggcttc	cattgtgact	tgtaggcsc	t			

(2) INFORMATION FOR SEQ ID NO:2899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2899:

Met Gly Phe Glu Lys Lys Val Thr Val His Cys Thr Gly Tyr Gly Lys Asp	10	15
Ile Lys Gly Glu Lys Val Thr Val His Cys Thr Gly Tyr Gly Lys Asp	20	30
Arg Asp Leu Pro Arg Asn Phe Gly Ala Pro Arg Thr Leu Gly Ser Ser	35	45
His Ser Val Ser Ala Leu Val Arg Val Gln	50	55

(2) INFORMATION FOR SEQ ID NO:2900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2900:

Met Thr Met Gln Val Gly Glu Val Ala Arg Ile Gln Cys Thr Pro Asp	5	10	15
Tyr Ala Tyr Gly Ala Gly Gly Phe Pro Ala Trp Gly Ile Gln Pro Asn			

20 25 30
Ser Val Leu Val Phe Arg Asp
35
(2) INFORMATION FOR SEQ ID NO:2901:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..37
(D) OTHER INFORMATION: / Ceres Seq. ID 1574757
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2901:
Met Gln Val Gly Glu Val Ala Arg Ile Gln Cys Thr Pro Asp Tyr Ala
1 5 10 15
Tyr Gly Ala Gly Gly Phe Pro Ala Trp Gly Ile Gln Pro Asn Ser Val
20 25 30
Leu Val Phe Arg Asp
35

(2) INFORMATION FOR SEQ ID NO:2902:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 600 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..600
(D) OTHER INFORMATION: / Ceres Seq. ID 1574758
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2902:
tcattacaag caaaagcaac aaggcagcag cacaagcaaag aaccacacct cctcccttcg 60
cctgtgatca tgtcgtcttg ctgcggcgcc aagtgcgggt gcgctccag ctgctccctgc 120
ggcagcggtat gcaacggctg cggtatgtac cctgacgttg agaccgcgc caccagcagc 180
gtcaagacca cggctctcgc cgcgccgacc accaaggcca gcgccggcgg cttccgaggcg 240
gccaccgagg gcggcggtcg cgaactgcaac acctgcaagt gcggcaccag ctgcggctgc 300
tcctgctgca gctgcaactg agccggcccg gcccgcgcat ggcgcacgag agtcgagagg 360
aggaggacga cgacgaggcg dtdtaaatat aatagcgcg tccagtaaat aagatcctgt 420
caactgcacc cgccattatc catggtcgct cgtcccNtcg cctgcgtctc ctggtcctcg 480
ggttcgtctg aacgtctcgc cggtcttcac acgcgatgcc gcctccgtcg atcctgtccg 540
tctcgtgccg grbtkaatat tagatctata tgcgtgtttt tctgcgttat tactacatct 600

(2) INFORMATION FOR SEQ ID NO:2903:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..106
(D) OTHER INFORMATION: / Ceres Seq. ID 1574759
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2903:
Ser Ser Gln Ala Lys Ala Thr Arg Gln Gln His Lys Gln Glu Pro His
1 5 10 15
Leu Leu Pro Ser Pro Val Ile Met Ser Ser Cys Cys Gly Gly Lys Cys
20 25 30
Gly Cys Gly Ser Ser Cys Ser Cys Gly Ser Gly Cys Asn Gly Cys Gly

35 40 45
Met Tyr Pro Asp Val Glu Thr Ala Ala Thr Ser Ser Val Lys Thr Thr
50 55 60
Val Leu Ala Ala Pro Thr Thr Lys Ala Ser Ala Gly Gly Phe Glu Ala
65 70 75
Ala Thr Glu Gly Gly Gly Cys Asp Cys Asn Thr Cys Lys Cys Gly Thr
85 90 95
Ser Cys Gly Cys Ser Cys Cys Ser Cys Asn
100 105

(2) INFORMATION FOR SEQ ID NO:2904:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1574760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2904:

Met Ser Ser Cys Cys Gly Gly Lys Cys Gly Cys Gly Ser Ser Cys Ser
1 5 10 15
Cys Gly Ser Gly Cys Asn Gly Cys Gly Met Tyr Pro Asp Val Glu Thr
20 25 30
Ala Ala Thr Ser Ser Val Lys Thr Thr Val Leu Ala Ala Pro Thr Thr
35 40 45
Lys Ala Ser Ala Gly Gly Phe Glu Ala Ala Thr Glu Gly Gly Cys
50 55 60
Asp Cys Asn Thr Cys Lys Cys Gly Thr Ser Cys Gly Cys Ser Cys Cys
65 70 75 80
Ser Cys Asn

(2) INFORMATION FOR SEQ ID NO:2905:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1574761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2905:

Met Tyr Pro Asp Val Glu Thr Ala Ala Thr Ser Ser Val Lys Thr Thr
1 5 10 15
Val Leu Ala Ala Pro Thr Thr Lys Ala Ser Ala Gly Gly Phe Glu Ala
20 25 30
Ala Thr Glu Gly Gly Gly Cys Asp Cys Asn Thr Cys Lys Cys Gly Thr
35 40 45
Ser Cys Gly Cys Ser Cys Cys Ser Cys Asn
50 55

(2) INFORMATION FOR SEQ ID NO:2906:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 842 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..842

(D) OTHER INFORMATION: / Ceres Seq. ID 1574762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2906:

ctcgaaatct	cgcccccctg	tcgagttgtc	catatccctt	cctctcttcc	tcgccaggcc	60
aaccgctgat	tgttgttcag	acagaggaag	gaaggaagga	aggaggagat	cagaagcatc	120
agccatgtcg	aactcggcgt	cggaatggc	cgtttgtgac	gaatgcaaac	tcaagtcttc	180
ggaaactcaag	gcgaagagga	gcttccgttt	catcgtgttc	aagatcaacg	agaacgtgca	240
gcaggtgggtg	gtggacaggc	ttgggggacc	aggtgaaagc	tacgatgcgt	tcagggcctg	300
ctttcccgcc	aacgagTgyc	gctacgcggt	gtttgatttt	gactttgtca	ctgatgagaa	360
ctgcgaagaag	agcaagatct	tcttcacatc	ttggggccca	gatgcatcga	gggtgagaag	420
caagatgttg	tacgcaagct	ccaaggaccg	gttcaagagg	gagctogacg	gcattcaggt	480
ggagctacaa	gcaactgagc	cgagcgaaat	gagcatggac	atcatcaagt	cgcgagccct	540
ctgaaacagc	ccggcgcatg	ctcctgcatg	cccgtcgatt	cttcggtgtt	ggtaacggtc	600
atccggttttc	gtgtcccttgt	ttttcctgga	agcaaaagcc	ttgcgttctg	tatgagactt	660
ctgtatacca	tttccctctc	ctnknntttc	ccaatctctg	ccgtagtcct	gcactcctgc	720
tactgctgta	aactagwact	tatttgcgtg	ttgtctcgt	ggcattgtcg	agtcgcttat	780
gtgtctatgc	aatgctagtt	gtgagaagcc	taatgtacct	tagcttaatc	accgaattgc	840

(2) INFORMATION FOR SEQ ID NO:2907:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1574763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2907:

Ser	Lys	Ser	Arg	Pro	Ser	Leu	Gln	Leu	Ser	Ile	Ser	Leu	Pro	Leu	Phe
1				5					10					15	
Leu	Ala	Arg	Pro	Thr	Ala	Asp	Cys	Cys	Ser	Asp	Arg	Gly	Arg	Lys	Glu
			20					25					30		
Gly	Arg	Arg	Arg	Ser	Glu	Ala	Ser	Ala	Met	Ser	Asn	Ser	Ala	Ser	Gly
			35				40					45			
Met	Ala	Val	Cys	Asp	Glu	Cys	Lys	Leu	Lys	Phe	Leu	Glu	Leu	Lys	Ala
			50			55					60				
Lys	Arg	Ser	Phe	Arg	Phe	Ile	Val	Phe	Lys	Ile	Asn	Glu	Asn	Val	Gln
65				70					75					80	
Gln	Val	Val	Val	Asp	Arg	Leu	Gly	Gly	Pro	Gly	Glu	Ser	Tyr	Asp	Ala
				85					90				95		
Phe	Arg	Ala	Cys	Phe	Pro	Ala	Asn	Glu	Xaa	Arg	Tyr	Ala	Val	Phe	Asp
			100					105				110			
Phe	Asp	Phe	Val	Thr	Asp	Glu	Asn	Cys	Gln	Lys	Ser	Lys	Ile	Phe	Phe
			115				120					125			
Ile	Ser	Trp	Ala	Pro	Asp	Ala	Ser	Arg	Val	Arg	Ser	Lys	Met	Leu	Tyr
			130			135					140				
Ala	Ser	Ser	Lys	Asp	Arg	Phe	Lys	Arg	Glu	Leu	Asp	Gly	Ile	Gln	Val
145				150					155					160	
Glu	Leu	Gln	Ala	Thr	Glu	Pro	Ser	Glu	Met	Ser	Met	Asp	Ile	Ile	Lys
				165				170					175		
Ser	Arg	Ala	Leu												
			180												

(2) INFORMATION FOR SEQ ID NO:2908:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1574764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2908:

Arg	Asn	Leu	Ala	Pro	Arg	Cys	Ser	Cys	Pro	Tyr	Pro	Phe	Leu	Ser	Ser
1				5					10					15	
Ser	Pro	Gly	Gln	Pro	Leu	Ile	Val	Val	Gln	Thr	Glu	Glu	Gly	Arg	Lys
			20					25					30		
Glu	Gly	Gly	Asp	Gln	Lys	His	Gln	Pro	Cys	Arg	Thr	Arg	Arg	Arg	Glu
		35					40					45			
Trp	Pro	Phe	Val	Thr	Asn	Ala	Asn	Ser	Ser	Ser	Trp	Asn	Ser	Arg	Arg
	50				55					60					
Arg	Gly	Ala	Ser	Val	Ser	Ser	Cys	Ser	Arg	Ser	Thr	Arg	Thr	Cys	Ser
	65				70					75				80	
Arg	Trp	Trp	Trp	Thr	Gly	Leu	Gly	Asp	Gln	Val	Lys	Ala	Thr	Met	Arg
			85					90						95	
Ser	Gly	Pro	Ala	Phe	Pro	Pro	Thr	Ser	Xaa	Ala	Thr	Arg	Cys	Leu	Ile
			100					105					110		
Leu	Thr	Leu	Ser	Leu	Met	Arg	Thr	Ala	Arg	Arg	Ala	Arg	Ser	Ser	Ser
		115				120							125		
Ser	Leu	Gly	Pro	Gln	Met	His	Arg	Gly							
	130					135									

(2) INFORMATION FOR SEQ ID NO:2909:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1574765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2909:

Met	Ser	Asn	Ser	Ala	Ser	Gly	Met	Ala	Val	Cys	Asp	Glu	Cys	Lys	Leu
1				5					10					15	
Lys	Phe	Leu	Glu	Leu	Lys	Ala	Lys	Arg	Ser	Phe	Arg	Phe	Ile	Val	Phe
			20					25					30		
Lys	Ile	Asn	Glu	Asn	Val	Gln	Gln	Val	Val	Val	Asp	Arg	Leu	Gly	Gly
		35				40					45				
Pro	Gly	Glu	Ser	Tyr	Asp	Ala	Phe	Arg	Ala	Cys	Phe	Pro	Ala	Asn	Glu
	50				55					60					
Xaa	Arg	Tyr	Ala	Val	Phe	Asp	Phe	Asp	Phe	Val	Thr	Asp	Glu	Asn	Cys
	65				70				75					80	
Gln	Lys	Ser	Lys	Ile	Phe	Phe	Ile	Ser	Trp	Ala	Pro	Asp	Ala	Ser	Arg
			85					90						95	
Val	Arg	Ser	Lys	Met	Leu	Tyr	Ala	Ser	Ser	Lys	Asp	Arg	Phe	Lys	Arg
			100					105					110		
Glu	Leu	Asp	Gly	Ile	Gln	Val	Glu	Leu	Gln	Ala	Thr	Glu	Pro	Ser	Glu
		115				120							125		
Met	Ser	Met	Asp	Ile	Ile	Lys	Ser	Arg	Ala	Leu					
	130					135									

(2) INFORMATION FOR SEQ ID NO:2910:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 672 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..672

(D) OTHER INFORMATION: / Ceres Seq. ID 1574769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2910:

acagccgtca	cgcacttcaa	tccagcagcc	tctgctctgc	ctgcgtcgca	gccagtggct	60
cagcgggtgc	gcccggtgct	gtcacgtctt	gtcctcaatc	tctctctctc	tcaatcctca	120
ctctctccgc	tctctttctc	ctccccagtc	cccaacggtg	aggccccccg	cgtgcagccc	180
atcgacgcat	tgccgctgca	agcgsgggac	accgagggct	agaagcgcg	gcggtgccag	240
ggctcggcgc	tgggttgcca	atggcgaggc	ggcttatgct	ggcgctccct	gtgctcctct	300
tctttattgc	cgtcgggcgc	ccgggattct	tccgtgctaa	tggggaatgg	gtcacatgct	360
tctgttcagt	gcactggcac	ggtggatctg	aagtttactt	cgggaaagat	cgtgcagctg	420
aagaacgtgc	atcatgtccc	kkctatacac	aagaatctcg	ttagcggaac	ccttctatgt	480
agagatgggt	tcaaggtagt	tttagagctc	aataaattag	ttgtgtccaa	gtctggacaa	540
tttattggta	aaggctatga	ttggcgaggc	ttgttccgct	tttcttttgt	agatttcaat	600
aataagctcg	tgaaccatat	ttgtgcta	gttgatgatc	ttgcgagtat	ttggcattct	660
cgtttggctc	at					

(2) INFORMATION FOR SEQ ID NO:2911:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..73

(D) OTHER INFORMATION: / Ceres Seq. ID 1574770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2911:

Thr	Ala	Val	Thr	His	Phe	Asn	Pro	Ala	Ala	Leu	Pro	Ala	Ser
1				5				10				15	
Gln	Pro	Val	Ala	Gln	Arg	Leu	Arg	Pro	Cys	Leu	Ser	Arg	Leu
				20				25				30	Val
Asn	Leu	Ser	Leu	Ser	Gln	Ser	Ser	Pro	Leu	Arg	Leu	Ser	Phe
				35				40				45	Ser
Pro	Val	Pro	Asn	Gly	Glu	Ala	Pro	Ala	Val	Gln	Pro	Ile	Asp
				50				55				60	Ala
Pro	Leu	Gln	Gly	Xaa	Asp	Thr	Glu	Gly					Leu
65				70									

(2) INFORMATION FOR SEQ ID NO:2912:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1574771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2912:

Gln	Pro	Ser	Arg	Thr	Ser	Ile	Gln	Gln	Pro	Leu	Leu	Cys	Leu	Arg	Arg
1				5				10				15			
Ser	Gln	Trp	Leu	Ser	Gly	Cys	Ala	Arg	Ala	Cys	His	Val	Leu	Ser	Ser
				20				25				30			
Ile	Ser	Leu	Ser	Leu	Asn	Pro	His	Leu	Ser	Gly	Ser	Leu	Ser	Pro	Pro
				35				40				45			
Gln	Ser	Pro	Thr	Val	Arg	Pro	Pro	Pro	Cys	Ser	Pro	Ser	Thr	His	Cys
				50				55				60			
Arg	Cys	Lys	Ala	Xaa	Thr	Pro	Arg	Ala	Arg	Ser	Gly	Gly	Gly	Ala	Arg
65				70				75				80			

Ala	Arg	Arg	Ser	Val	Gly	Asn	Gly	Glu	Ala	Ala	Tyr	Ala	Gly	Ala	Pro
			85					90					95		
Cys	Ala	Pro	Leu	Leu	Ile	Ala	Arg	Arg	Ala	Pro	Gly	Ile	Leu	Pro	Cys
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:2913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1574772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2913:

Met	Gly	Asn	Gly	Ser	His	Ala	Ser	Val	His	Gly	Thr	Gly	Thr	Val	Asp
1			5					10						15	
Leu	Lys	Phe	Thr	Ser	Gly	Lys	Ile	Val	Gln	Leu	Lys	Asn	Val	His	His
			20				25					30			
Val	Xaa	Xaa	Ile	His	Lys	Asn	Leu	Val	Ser	Gly	Thr	Leu	Leu	Cys	Arg
		35				40						45			
Asp	Gly	Phe	Lys	Val	Val	Leu	Glu	Ser	Asn	Lys	Leu	Val	Val	Ser	Lys
	50					55					60				
Ser	Gly	Gln	Phe	Ile	Gly	Lys	Gly	Tyr	Asp	Cys	Gly	Gly	Leu	Phe	Arg
	65			70				75						80	
Phe	Ser	Leu	Leu	Asp	Phe	Asn	Asn	Lys	Ser	Val	Asn	His	Ile	Cys	Ala
			85					90					95		
Asn	Val	Asp	Asp	Leu	Ala	Ser	Ile	Trp	His	Ser	Arg	Leu	Cys	His	
			100				105						110		

(2) INFORMATION FOR SEQ ID NO:2914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..588

(D) OTHER INFORMATION: / Ceres Seq. ID 1574773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2914:

aacctactga	cgagctcgcc	atggcctccc	tctctctgc	cgccgtcacc	gccccttccct	60
tcgcgcgacc	agcgccacccc	gogccgtggt	cagaaggagg	tccttcaccg	tgccgcgcctc	120
ttctcgcgaag	gccaccgcga	ccgcgcccg	ggcaatggct	gccagcgccc	tgcttgccgg	180
cggtgccatg	gccaggagg	tgctgtggg	cgcaggcgac	ggcgggctcg	tcttcgagcc	240
cgagcagttc	accgtcaagg	ccggcgacac	catcTacatt	caagaacaac	gcccgccttc	300
cgacacaagt	ctctttcgac	gaagacgagg	tgccgagcgg	cgtcgacacc	accaagatct	360
cgcaggaggga	gtacctcaac	gcgcgagcgg	agacctactc	cgtcaccctc	accgtgccgg	420
gaacctacgg	cttctactgc	gagccgcac	aaggagccgg	aatggtcggc	aagatcacccg	480
tcaactaat	aagctagcta	tcgatcgata	tcattcatg	tattagctgt	tgcttctctg	540
ttgtactcc	gcgcgtctgt	ccatctctwc	atgttttcgk	cttcacac		

(2) INFORMATION FOR SEQ ID NO:2915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1574774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2915:

```
Asn Leu Leu Thr Ser Ser Pro Trp Pro Pro Ser Pro Leu Pro Pro Ser
1      5      10      15
Pro Pro Leu Pro Ser Pro His Gln Arg His Pro Arg Arg Gly Gln Lys
20      25      30
Glu Val Leu His Arg Ala Arg Leu Ser Pro Gln Gly His Arg His Arg
35      40      45
Arg Arg Gly Asn Gly Cys Gln Arg Pro Ala Cys Arg Arg Cys His Gly
50      55      60
Pro Gly Gly Ala Ala Gly Arg Arg Arg Arg Ala Arg Leu Arg Ala
65      70      75      80
Gln Pro Val His Arg Gln Gly Arg Arg His His Leu His Ser Arg Thr
85      90      95
Thr Pro Ala Ser Arg Thr Thr Xaa Ser Ser Thr Lys Thr Arg Cys Arg
100     105     110
Ala Ala Ser Thr Pro Pro Arg Ser Arg Arg Arg Ser Thr Ser Thr Arg
115     120     125
Gln Ala Arg Pro Thr Pro Ser Pro Ser Pro Cys Arg Glu Pro Thr Ala
130     135     140
Ser Thr Ala Ser Arg Ile Lys Glu Pro Glu Trp Ser Ala Arg Ser Pro
145     150     155     160
Ser Thr Asn
```

(2) INFORMATION FOR SEQ ID NO:2916:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1574775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2916:

```
Pro Thr Asp Glu Leu Ala Met Ala Ser Leu Ser Ser Ala Ala Val Thr
1      5      10      15
Ala Pro Ser Phe Ala Ala Pro Ala Pro Pro Ala Pro Trp Ser Glu Gly
20      25      30
Gly Pro Ser Pro Cys Ala Pro Leu Ser Ala Arg Pro Pro Ala Pro Pro
35      40      45
Pro Trp Gln Trp Leu Pro Ala Pro Cys Leu Pro Ala Val Pro Trp Pro
50      55      60
Arg Arg Cys Cys Trp Ala Gln Ala Thr Ala Gly Ser Ser Ser Ser Pro
65      70      75      80
Ala Ser Ser Pro Ser Arg Pro Ala Thr Pro Ser Thr Phe Lys Asn Asn
85      90      95
Ala Gly Phe Pro His Asn Val Xaa Phe Asp Glu Asp Glu Val Pro Ser
100     105     110
Gly Val Asp Thr Thr Lys Ile Ser Gln Glu Glu Tyr Leu Asn Ala Pro
115     120     125
Gly Glu Thr Tyr Ser Val Thr Leu Thr Val Pro Gly Thr Tyr Gly Phe
130     135     140
Tyr Cys Glu Pro His Gln Gly Ala Gly Met Val Gly Lys Ile Thr Val
145     150     155     160
Asn
```

(2) INFORMATION FOR SEQ ID NO:2917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2917:

```
Met Ala Ser Leu Ser Ser Ala Ala Val Thr Ala Pro Ser Phe Ala Ala
1      5      10      15
Pro Ala Pro Pro Ala Pro Trp Ser Glu Gly Gly Pro Ser Pro Cys Ala
20      25      30
Pro Leu Ser Ala Arg Pro Pro Ala Pro Pro Trp Gln Trp Leu Pro
35      40      45
Ala Pro Cys Leu Pro Ala Val Pro Trp Pro Arg Arg Cys Cys Trp Ala
50      55      60
Gln Ala Thr Ala Gly Ser Ser Ser Pro Ala Ser Ser Pro Ser Arg
65      70      75      80
Pro Ala Thr Pro Ser Thr Phe Lys Asn Asn Ala Gly Phe Pro His Asn
85      90      95
Val Xaa Phe Asp Glu Asp Glu Val Pro Ser Gly Val Asp Thr Thr Lys
100      105      110
Ile Ser Gln Glu Glu Tyr Leu Asn Ala Pro Gly Glu Thr Tyr Ser Val
115      120      125
Thr Leu Thr Val Pro Gly Thr Tyr Gly Phe Tyr Cys Glu Pro His Gln
130      135      140
Gly Ala Gly Met Val Gly Lys Ile Thr Val Asn
145      150      155
```

(2) INFORMATION FOR SEQ ID NO:2918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..466
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2918:

```
gataaatctc tccatcagcg agcacctagc tagcagcagc caatgacgaa gccttcgcgag      60
gtgctgttgg cggcgctcgc cgytggggcg gtggtcctgc tgetgtgtgt cgccgcgcgcg      120
ccgcggggcg cCgacgcggc gacggcgtgc gacgccacgc agctgacgcc gtggccggcg      180
gccatcatca tcgggaggtc gccacgcgcg cgtgtgtgca gtaggctcaa ggagcagcag      240
ccgtgcctgt gcacgtacgc gcgcgacccc aatcttcagc gctacgtcaa ctgcgccaaac      300
ggcaagaagg ccatggccgc gtgcaagggt cccgtrccgt cgtgctagt aacttctgtt      360
tgcrcgcgcg ccgcgtacgt gtctgttgtt gcctgtgtca gtacgacgaa gcccactgg      420
acagggacag agtatggcgt cactttctgt ttccgtacat acgtac
```

(2) INFORMATION FOR SEQ ID NO:2919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..101
(D) OTHER INFORMATION: / Ceres Seq. ID 1574798
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2919:
Met Thr Lys Pro Ser Gln Val Leu Leu Ala Ala Leu Ala Xaa Trp Ala
1 5 10 15
Val Val Leu Leu Leu Cys Ala Ala Ala Pro Arg Gly Ala Asp Ala
20 25 30
Ala Thr Ala Cys Asp Ala Thr Gln Leu Thr Pro Cys Ala Gly Ala Ile
35 40 45
Ile Ile Gly Arg Ser Pro Ser Ala Ala Cys Cys Ser Arg Leu Lys Glu
50 55 60
Gln Gln Pro Cys Leu Cys Thr Tyr Ala Arg Asp Pro Asn Leu Gln Arg
65 70 75 80
Tyr Val Asn Ser Pro Asn Gly Lys Lys Ala Met Ala Ala Cys Lys Val
85 90 95
Pro Xaa Pro Ser Cys
100

(2) INFORMATION FOR SEQ ID NO:2920:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 743 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..743

(D) OTHER INFORMATION: / Ceres Seq. ID 1574803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2920:

aggatcctct	cggcgcgagg	ctccgagttg	ccgtctccgc	ctctctgagt	tagcgttctc	60
caccaagagc	agcatggagt	ccgacgtgta	cagctacggc	gtggtgtctg	tggagctgct	120
cacgaggagg	ggcgcggtgg	atccctcgtt	tcccacggc	acggacatag	tcagctgggc	180
gtcgtccgcc	ctgaacSggc	accgacaaaa	tcgaggccgt	ctgcgacccg	gctctcatgt	240
aggaagtctt	cggcacgggt	gagatggagg	aggtgagtaa	ggctctgtca	gtggcgctgc	300
ggtgcgcggc	cagggaggcg	agccaaagc	ctccatgac	gcgcgtctgt	aaggagctga	360
cgatgacacg	gcctgccact	ggcgcgcgcc	ggctcgtgtc	caagtccga	caggggaaac	420
caggatcgca	atccaacagc	agcgccctacc	ggcagtagga	tctctgactc	tgccgagctg	480
tttggggaca	ccaactttac	tcaacttgta	gtctctactc	tatagTacc	ctcgtttggt	540
gtacatcctg	attggttagt	tggcaaaagt	tagttgtagt	tcaaatgaaa	cggagagatg	600
ctggactTcg	tgctagtgcg	agtgaagcaa	gctgcttggt	ctgaaatctg	tggactgtgtg	660
cttgctcgtg	gcttcacagg	acgggaccag	gagagaatgg	gtattcgaaa	ttgtactaaa	720
ggaaaaaaaa	attagatggt	ctg				

(2) INFORMATION FOR SEQ ID NO:2921:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1574804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2921:

Gly Ser Ser Arg Pro Arg Ala Pro Ser Cys Arg Leu Arg Leu Ser Glu	
1 5 10 15	
Leu Ala Phe Ser Thr Lys Ser Ser Met Glu Ser Asp Val Tyr Ser Tyr	
20 25 30	
Gly Val Val Leu Leu Glu Leu Leu Thr Arg Arg Ala Ala Val Asp Pro	
35 40 45	
Ser Phe Pro Asp Gly Thr Asp Ile Val Ser Trp Ala Ser Ser Ala Leu	

50 55 60
Asn Xaa His Arg Gln Asn Arg Gly Arg Leu Arg Pro Gly Ser His Gly
65 70 75 80
Gly Ser Leu Arg His Gly Gly Asp Gly Gly Gly Glu
85 90

(2) INFORMATION FOR SEQ ID NO:2922:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1574805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2922:

Met Glu Ser Asp Val Tyr Ser Tyr Gly Val Val Leu Leu Glu Leu Leu
1 5 10 15
Thr Arg Arg Ala Ala Val Asp Pro Ser Phe Pro Asp Gly Thr Asp Ile
20 25 30
Val Ser Trp Ala Ser Ser Ala Leu Asn Xaa His Arg Gln Asn Arg Gly
35 40 45
Arg Leu Arg Pro Gly Ser His Gly Gly Ser Leu Arg His Gly Gly Asp
50 55 60
Gly Gly Gly Glu
65

(2) INFORMATION FOR SEQ ID NO:2923:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..73

(D) OTHER INFORMATION: / Ceres Seq. ID 1574806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2923:

Met Glu Glu Val Phe Gly Thr Val Glu Met Glu Glu Val Ser Lys Val
1 5 10 15
Leu Ser Val Ala Leu Arg Cys Ala Ala Arg Glu Ala Ser Gln Arg Pro
20 25 30
Ser Met Thr Ala Val Val Lys Glu Leu Thr Asp Ala Arg Pro Ala Thr
35 40 45
Gly Gly Gly Arg Ser Leu Ser Lys Ser Lys Gln Gly Lys Pro Gly Ser
50 55 60
Gln Ser Asn Ser Ser Ala Tyr Arg Gln
65 70

(2) INFORMATION FOR SEQ ID NO:2924:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 582 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..582

(D) OTHER INFORMATION: / Ceres Seq. ID 1574814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2924:

```

aaaacttctg  tgcgaagaag  ctcaagaacg  aagccatcaa  aagcggagct  gcgagagcgg  60
agagagagag  tgaRgggagg  cgcgcagccc  gagtcctttc  ttcctcctgc  atctgccgct  120
gtttccgaca  ggaagtgttt  cactgaggac  gactacgacc  gtggggtgaa  caccttctct  180
cgcgaggggc  ggcgtgttcc  ggtcgagtac  gccatcgagg  ccatcaagtt  gggatccact  240
gcgatcggtt  tgaagacaaa  ggaatgtgtt  gtctcgcgcg  ttgagaaaac  tgtgacctca  300
ccactgctgg  aaccaagcag  tgtggaaaaa  ataattgaaa  ttgatgagca  cataggctgt  360
gccatgagtg  gacttatgtc  tgatgctaga  acactagtgg  aacatgctcg  tgttgaactc  420
cagaatcata  ggttctcata  cggagagcca  atgactgtag  aatcttcgac  acaagctatc  480
tgtgacttag  ctctgcgttt  tggcgaaggt  gacgaagagt  caatgtcacg  gccatttggg  540
gtctctctcc  taattgctgg  acatgatgag  aatggacctc  gc

```

(2) INFORMATION FOR SEQ ID NO:2925:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..194

(D) OTHER INFORMATION: / Ceres Seq. ID 1574815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2925:

```

Lys Thr Ser Phe Ala Arg Ser Ser Glu Gln Lys Pro Ser Lys Ala Arg
1      5      10      15
Leu Arg Glu Arg Arg Glu Arg Val Xaa Gly Gly Ala Asp Ala Glu Ser
20     25     30
Phe Leu His Pro Ala Ser Ala Ala Val Ser Asp Arg Met Phe Leu Thr
35     40     45
Arg Thr Glu Tyr Asp Arg Gly Val Asn Thr Phe Ser Pro Glu Gly Arg
50     55     60
Leu Phe Gln Val Glu Tyr Ala Ile Glu Ala Ile Lys Leu Gly Ser Thr
65     70     75     80
Ala Ile Gly Leu Lys Thr Lys Asp Gly Val Val Leu Ala Val Glu Lys
85     90     95
Arg Val Thr Ser Pro Leu Leu Glu Pro Ser Ser Val Glu Lys Ile Met
100    105    110
Glu Ile Asp Glu His Ile Gly Cys Ala Met Ser Gly Leu Ile Ala Asp
115    120    125
Ala Arg Thr Leu Val Glu His Ala Arg Val Glu Thr Gln Asn His Arg
130    135    140
Phe Ser Tyr Gly Glu Pro Met Thr Val Glu Ser Ser Thr Gln Ala Ile
145    150    155    160
Cys Asp Leu Ala Leu Arg Phe Gly Glu Gly Asp Glu Glu Ser Met Ser
165    170    175
Arg Pro Phe Gly Val Ser Leu Leu Ile Ala Gly His Asp Glu Asn Gly
180    185    190
Pro Ser

```

(2) INFORMATION FOR SEQ ID NO:2926:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1574816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2926:

```

Met Phe Leu Thr Arg Thr Glu Tyr Asp Arg Gly Val Asn Thr Phe Ser

```


1	5	10	15
Pro Glu Gly Arg Leu Phe Gln Val Glu Tyr Ala Ile Glu Ala Ile Lys			
20	25	30	
Leu Gly Ser Thr Ala Ile Gly Leu Lys Thr Lys Asp Gly Val Val Leu			
35	40	45	
Ala Val Glu Lys Arg Val Thr Ser Pro Leu Leu Glu Pro Ser Ser Val			
50	55	60	
Glu Lys Ile Met Glu Ile Asp Glu His Ile Gly Cys Ala Met Ser Gly			
65	70	75	80
Leu Ile Ala Asp Ala Arg Thr Leu Val Glu His Ala Arg Val Glu Thr			
85	90	95	
Gln Asn His Arg Phe Ser Tyr Gly Glu Pro Met Thr Val Glu Ser Ser			
100	105	110	
Thr Gln Ala Ile Cys Asp Leu Ala Leu Arg Phe Gly Glu Gly Asp Glu			
115	120	125	
Glu Ser Met Ser Arg Pro Phe Gly Val Ser Leu Ile Ala Gly His			
130	135	140	
Asp Glu Asn Gly Pro Ser			
145	150		

(2) INFORMATION FOR SEQ ID NO:2927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 905 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..905
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2927:

aaaccctttc	gactgtctca	actaccaaac	ctgtctcttc	tcacgcgaga	60
gcactccact	ccCacgcgaa	Accctagcag	tggtttctcc	tcggggcccc	120
ttggttccaa	gctgtagaag	catctccgat	cccatccgcg	gcgggttgag	180
ccggtttctg	cagccggatt	tgggatccgc	gagatgtctt	ggctccgcgc	240
ctctctctcca	ctctccctgc	cggcttcttg	gacaagaaac	ttattgtctt	300
ggacggaaac	tgcttggcac	ctctgctca	tttgatcagt	ttgcaaatgt	360
ggtgctgtgt	aacgagtgat	tgtgggggaa	caatatttgt	atgttctctt	420
gtaatccggg	gagagaacct	tggttttaac	ggagaattgg	atcgcgaaaa	480
ctctgtcaca	tgacctgtgt	ttcagaagca	gaaataagaa	aggctgaaaa	540
gaagccagag	atctgaaagg	gacgatgagg	aaacggatgg	agttctcgga	600
caccgtcaac	Ygcggcgctt	gcgcgtcccc	attgtggcgg	aatctttagt	660
gtgccataca	tgccctgtga	ccgcgcgcgc	gcaccttgga	ttgctggagg	720
cagtttcttt	ttaaactaga	gtgctgtttt	atactctcgt	ggccacacag	780
gcctctgat	acagctttgt	caccactctg	atcattgcct	cgatgaattt	840
acgttttgga	ttggatctgc	gccaaaaacg	catttctatg	gagagagtct	900
agctc					

(2) INFORMATION FOR SEQ ID NO:2928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2928:

Met Ser Trp Ser Ala Pro Asp Asp Ile Leu Leu Ser Thr Ser Leu Ala		
1	5	10
		15

```

Gly Phe Leu Asp Lys Lys Leu Ile Val Leu Leu Arg Asp Gly Arg Lys
      20      25      30
Leu Leu Gly Thr Leu Cys Ser Phe Asp Gln Phe Ala Asn Val Val Leu
      35      40      45
Gln Gly Ala Cys Glu Arg Val Ile Val Gly Glu Gln Tyr Cys Asp Val
      50      55      60
Pro Leu Gly Leu Tyr Val Ile Arg Gly Glu Asn Val Val Leu Ile Gly
      65      70      75      80
Glu Leu Asp Arg Glu Lys Asp Glu Leu Pro Ala His Met Thr Cys Val
      85      90      95
Ser Glu Ala Glu Ile Arg Lys Ala Glu Lys Ala Glu Arg Glu Ala Arg
      100      105      110
Asp Leu Lys Gly Thr Met Arg Lys Arg Met Glu Phe Leu Asp Phe Asp
      115      120      125

```

(2) INFORMATION FOR SEQ ID NO:2929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..666
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2929:

```

gtaacgaggc atcgacactg acagagtcca cggcaccggt tgtttaccac caaccatccg      60
gcccttcccc gaccCatggc ggccggcacc cctcgctggt ggccgctcct cctgcagctc      120
gcaatcgccc ttggcatcct gctcgcdgcg gccgaggctt ggacggggga gatccgcggc      180
cgcgctgctt cgcgagctct cggcgacgca gccatcggcc cgaggagcca cgccctcgaa      240
ggtgcggagg ttgctgtcct ctgcacaca aaatctggtg aggttatcaa ctatcaagcc      300
ttcacaaact ccaaggcgct gtatactgtc gccgagacta tgcggagag cgacaggtgg      360
gactcgtgct tggcgaggcc tatgagcagc ttccatctac attgcacacg gcggggtgat      420
gctcactctg ggggtgaagt cacttacaac aaatcgtctg ggaacccaca cacogtcaag      480
cctttcctct acaagccggc caccatccct ctgtattgta gttaaacaac acatcttgct      540
ggaacgcaga agatagaaca tacaggaaga aaatatgtat tcgtgccccg acctcatata      600
taagtaaaac cttttgatgt aaatcaaaga ttacgctgtc tatgggagct gttctagtgt      660
ctggtc

```

(2) INFORMATION FOR SEQ ID NO:2930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2930:

```

Asn Glu Ala Ser Thr Leu Thr Glu Ser Thr Ala Arg Leu Val Tyr His
1      5      10      15
Gln Pro Ser Gly Pro Ser Pro Thr His Gly Gly Gly Thr Pro Ser Leu
      20      25      30
Val Ala Ala Pro Pro Ala Ala Arg Asn Arg Pro Trp His Pro Ala Arg
      35      40      45
Xaa Gly Arg Gly Leu Asp Gly Gly Asp Pro Arg Pro Arg Arg Leu Arg
      50      55      60
Arg Leu Arg Arg Arg Ser His Arg Pro Gly Gly Pro Arg Pro Arg Arg

```

65 70 75 80
Cys Gly Gly Cys Cys Pro Leu His His Lys Ile Trp
85 90

(2) INFORMATION FOR SEQ ID NO:2931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2931:

Met	Ala	Ala	Ala	Pro	Pro	Arg	Trp	Trp	Pro	Leu	Leu	Leu	Gln	Leu	Ala
1				5					10					15	
Ile	Ala	Leu	Gly	Ile	Leu	Leu	Xaa	Ala	Ala	Glu	Ala	Trp	Thr	Gly	Glu
			20					25				30			
Ile	Arg	Gly	Arg	Val	Val	Cys	Asp	Val	Cys	Gly	Asp	Ala	Ala	Ile	Gly
		35					40				45				
Pro	Glu	Asp	His	Ala	Leu	Glu	Gly	Ala	Glu	Val	Ala	Val	Leu	Cys	Ile
		50				55					60				
Thr	Lys	Ser	Gly	Glu	Val	Ile	Asn	Tyr	Gln	Ala	Phe	Thr	Asn	Ser	Lys
65					70				75					80	
Gly	Val	Tyr	Thr	Val	Ala	Glu	Thr	Met	Pro	Glu	Ser	Asp	Arg	Trp	Asp
				85				90						95	
Ser	Cys	Leu	Ala	Arg	Pro	Met	Ser	Ser	Phe	His	Leu	His	Cys	Thr	Arg
			100					105					110		
Arg	Gly	Asp	Ala	His	Ser	Gly	Val	Lys	Phe	Thr	Tyr	Asn	Lys	Ser	Ser
			115				120					125			
Gly	Asn	Pro	His	Thr	Val	Lys	Pro	Phe	Leu	Tyr	Lys	Pro	Ala	Thr	Ile
		130				135					140				
Pro	Leu	Tyr	Cys	Ser											

(2) INFORMATION FOR SEQ ID NO:2932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..816
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2932:

aaattccatt	ccaaatccgc	agtcgcgcaga	cgagagtggga	agcgggggcac	agacaggagaag	60
agaagccaat	ggcgctgtcc	Ctctccctcg	cgcgcccgcgc	gcccCtcgcc	gtttccgcgcg	120
gcgcaggagc	caggaagcta	ccgcgcagcca	gcctcgcatt	cccggcgaaa	tccttcttcg	180
gcgcgcgcgt	ggcgcgccac	cgccgcctcgc	tgcgctgcgc	gtcccccgcgc	aaGccggcca	240
ctctccaccac	ctcgcctcgc	gtcgtgcgcg	cggggaagaa	gggctacaag	atgaagacgc	300
acaaagcgctc	ggcgaaacgg	tcgggtgtgac	ggggagggggc	aagatcgtgc	ggcggtgcgcg	360
cgggaaagcag	cacttgctcg	ccaagaagaa	caccaagcgc	aagaagagcg	ctctgaagat	420
ggtgcaagtc	aacaagagtg	actacgacaa	tgttacgggt	gcactgccct	acctcaaaagt	480
gaataggaaa	gc aaactgat	agctacgtgg	ttctcaaaaa	atcattaagt	ttcgttccac	540
caaatgttaa	ttttgtgtat	cttccactgt	atttccttct	caaaaatact	gaggcatcat	600
ttcaaaagca	gc aaaaaaaca	acctctggta	tcaacagtat	agcgatattt	cagaataggg	660
tgcaactgctt	gctatagttg	ttatttagtc	gcaaatatgt	gcaagtaaga	gtggcaacttg	720
agccattagc	tcctcttagg	atatggccag	cagatcgtgt	atatggctgt	gcaagacact	780
gttttgccac	attttatata	tagactgcac	tgttttg			

(2) INFORMATION FOR SEQ ID NO:2933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2933:

Lys Phe His Ser Lys Ser Ala Val Arg Arg Arg Glu Trp Lys Arg Gly
1 5 10 15
Thr Asp Arg Lys Arg Ser Gln Trp Arg Cys Pro Ser Pro Ser Arg Ala
20 25 30
Pro Arg Pro Ser Pro Phe Pro Pro Ala Gln Glu Pro Gly Ser Tyr Pro
35 40 45
Gln Pro Ala Ser His Ser Arg Arg Asn Pro Ser Ser Ala Arg Arg Trp
50 55 60
Pro Pro Pro Arg Pro Pro Ser Arg Arg Arg Ser Arg Ala Ser Arg Pro
65 70 75 80
Pro Pro Pro Pro Arg Ser Arg Ser Ser Arg Arg Gly Arg Arg Ala Thr
85 90 95
Arg

(2) INFORMATION FOR SEQ ID NO:2934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2934:

Asn Ser Ile Pro Asn Pro Gln Ser Ala Asp Glu Ser Gly Ser Gly Ala
1 5 10 15
Gln Thr Gly Arg Glu Ala Asn Gly Ala Val Pro Leu Pro Arg Ala Pro
20 25 30
Arg Ala Pro Arg Arg Phe Arg Arg Arg Ser Gln Glu Ala Thr Arg
35 40 45
Ser Gln Pro Arg Ile Pro Gly Glu Ile Leu Leu Arg Arg Ala Ala Gly
50 55 60
Arg His Arg Gly Leu Arg Arg Val Ala Ala Pro Ala Gln Ala Gly His
65 70 75 80
Leu His His Leu Ala Arg Gly Arg Arg Gly Gly Glu Glu Gly Leu Gln
85 90 95
Asp Glu Asp Ala Gln Gly Val Gly Glu Arg Phe Arg Val Thr Gly Arg
100 105 110
Gly Lys Ile Val Arg Arg Cys Ala Gly Lys Gln His Leu Leu Ala Lys
115 120 125
Lys Asn Thr Lys Arg Lys Lys Arg Leu Ser Lys Met Val Gln Val Asn
130 135 140
Lys Ser Asp Tyr Asp Asn Val Thr Gly Ala Leu Pro Tyr Leu Lys Val
145 150 155 160
Asn Arg Lys Ala Asn
165

(2) INFORMATION FOR SEQ ID NO:2935:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..108
(D) OTHER INFORMATION: / Ceres Seq. ID 1574841
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2935:
Ile Pro Phe Gln Ile Arg Ser Pro Gln Thr Arg Val Glu Ala Gly His
1 5 10 15
Arg Gln Glu Glu Lys Pro Met Ala Leu Ser Leu Ser Leu Ala Arg Pro
20 25 30
Ala Pro Leu Ala Val Ser Ala Gly Ala Arg Lys Leu Pro Ala
35 40 45
Ala Ser Leu Ala Phe Pro Ala Lys Ser Phe Phe Gly Ala Pro Leu Ala
50 55 60
Ala Thr Ala Ala Ser Val Ala Ser Pro Leu Pro Arg Lys Pro Ala Thr
65 70 75 80
Ser Thr Thr Ser Leu Glu Val Val Ala Ala Gly Lys Lys Gly Tyr Lys
85 90 95
Met Lys Thr His Lys Ala Ser Ala Asn Gly Ser Gly
100 105

(2) INFORMATION FOR SEQ ID NO:2936:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 743 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..743
(D) OTHER INFORMATION: / Ceres Seq. ID 1574842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2936:

acaggcgaaaa aaaaaaactg ttgttagcgc tgacgtgcgt raggagctcg gactcggaagc 60
gaatcgaaaaa ggcgaaaaact cagtgtctcg agtttctctg gwnccnaggc gatggctggg 120
aaggggaggga aagcgttgct cgccgcgaag actacggcgg ccaagtcgcc cgagaaggac 180
aagggggaaga aggccccaat ctcaagctcc tcccgcgccg gectccagtt ccctgttggg 240
cgtatccacc gtcagctgaa gcaaaaggact caggcaaatg gtccgcttgg tgccaccgca 300
gcgcgttaact cgcgtgccat cctggagtac ttgactgccg aggttctKgg agctggcgaa 360
tgctagcaag gatctgaagk tgaagcgtat cacccttcgc catttgcaac tagccattcg 420
tgagagcgag gagctggaca cctcatcaa gggcaccatc gcaggcgag gtgtcatccc 480
gcacattcac aagtcctcga tcaacaagtc ctccaaggag tgaagactag gggatgtgca 540
tctttagttt aaactagact tctgtgcgct cctcggcgag tccttgcgat cctgtaggtt 600
ttagttgagc tgtcagttg tgctcctct gtgtaacgt tgccctggta tgcttcatca 660
gttatttgggt tattgtgttt gtgttgagtt gttaacttca ggggtgcгаа cctggatgct 720
tatttagtta tgtgactact gct

(2) INFORMATION FOR SEQ ID NO:2937:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..124
(D) OTHER INFORMATION: / Ceres Seq. ID 1574843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2937:

Arg	Arg	Lys	Lys	Lys	Leu	Phe	Val	Ser	Val	Thr	Cys	Xaa	Arg	Ser	Leu
1			5						10					15	
Glu	Ser	Asp	Gly	Ile	Glu	Lys	Ala	Lys	Thr	Gln	Cys	Leu	Glu	Phe	Pro
			20					25					30		
Arg	Xaa	Xaa	Gly	Asp	Gly	Trp	Glu	Gly	Arg	Glu	Arg	Leu	Ala	Arg	Arg
			35				40					45			
Glu	Asp	Trp	Gly	Gly	Gln	Val	Arg	Arg	Glu	Gly	Gln	Gly	Glu	Glu	Gly
			50			55					60				
Pro	Asn	Leu	Thr	Leu	Leu	Pro	Arg	Arg	Pro	Pro	Val	Pro	Cys	Trp	Ala
				70					75					80	
Tyr	Pro	Pro	Ser	Ala	Glu	Ala	Lys	Asp	Ser	Gly	Lys	Trp	Ser	Arg	Trp
			85					90						95	
Cys	His	Arg	Ser	Arg	Leu	Leu	Arg	Cys	His	Pro	Gly	Val	Leu	Asp	Cys
			100					105					110		
Arg	Gly	Ser	Xaa	Ser	Trp	Arg	Met	Leu	Ala	Arg	Ile				
			115				120								

(2) INFORMATION FOR SEQ ID NO:2938:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2938:

Met	Ala	Gly	Lys	Gly	Gly	Lys	Gly	Leu	Leu	Ala	Ala	Lys	Thr	Thr	Ala
1			5					10						15	
Ala	Lys	Ser	Ala	Glu	Lys	Asp	Lys	Gly	Lys	Lys	Ala	Pro	Ile	Ser	Arg
			20					25					30		
Ser	Ser	Arg	Ala	Gly	Leu	Gln	Phe	Pro	Val	Gly	Arg	Ile	His	Arg	Gln
			35				40					45			
Leu	Lys	Gln	Arg	Thr	Gln	Ala	Asn	Gly	Arg	Val	Gly	Ala	Thr	Ala	Ala
			50			55					60				
Val	Tyr	Ser	Ala	Ala	Ile	Leu	Glu	Tyr	Leu	Thr	Ala	Glu	Val	Xaa	Gly
			65		70				75					80	
Ala	Gly	Glu	Cys												

(2) INFORMATION FOR SEQ ID NO:2939:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..739
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2939:

atgttctctgtg	gcaaacacac	acacacacac	acacacacac	acacacacac	acacacacac	acacacacac	60
acacacacac	ttgtctgttgc	aacaaagctc	tacacgggaa	gacaggctgc	ttctttcttg		120
cagtcctctgg	tccagaagcc	tgaagaatg	gcgtcaccca	acgtcacatt	octtgcttc		180
ttcgtggccc	tcgcactatc	ggcgcttcac	accgacgcag	cgccggcggt	cagaaacctt		240
gcacacatag	agcgacacat	ggtgcgtggc	caagccgtgc	acgcaggagg	cgccgctgcg		300
gggcaacctg	gagttcgctc	gctccgagag	cgactcggcg	gccatccagg	gcacccggctg		360
ggcggccagc	cgacagcctg	ctgtcgcggg	cgctcggtgc	catgaacgcc	tactaccagg		420
ccggggggag	gaactcgtgg	aactgcttct	tcaacggcac	cggcataatc	accatcactg		480

(2) INFORMATION FOR SEQ ID NO:2940:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: lin

(1x) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1 83

(B) LOCATION: 1..82
(B) OTHER INFORMATION:

(D) OTHER INFORMATION: / Ceres Seq. ID 1574850
SEQUENCE DESCRIPTION: SEQ ID NO:2040:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:2940:
 Phe Ser Gly Leu His Met His Thr His Thr His

(2) INFORMATION FOR SEQ ID NO:2941:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1574852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2941:

Cys 1	Ser 1	Leu 1	Ala 1	Asn 5	Thr 5	His 5	Thr 10	His 10	Thr 10	His 10	Thr 10	His 10	Thr 15	His 15	Thr 15
His 1	Thr 1	His 1	Thr 1	His 1	Ile 1	Val 1	Leu 1	Leu 1	Leu 1	Gln 1	Gln 1	Ser 1	Ser 1	Thr 1	Arg 1
Glu 20	Asp 20	Arg 20	Leu 20	Leu 20	Ser 20	Cys 20	Ser 20	Leu 20	Trp 20	Ser 20	Arg 20	Ser 20	Leu 20	Lys 20	
Lys 35	Trp 35	Arg 35	His 35	Pro 35	Thr 35	Ser 35	His 35	Ser 35	Leu 35	Pro 35	Ser 35	Ser 35	Trp 35	Pro 35	Ser 35
His 50	Tyr 50	Arg 50	Arg 50	Phe 50	Thr 50	Pro 50	Thr 50	Gln 50	Arg 50	Arg 50	Arg 50	Ser 50	Glu 50	Thr 50	Leu 50
His 65	Xaa 65	Arg 65	Ser 65	Asp 65	Thr 65	Trp 65	Cys 65	Val 65	Ala 65	Lys 65	Pro 65	Ser 65	Thr 65	Gln 65	Glu 65
Ala 85	Ala 85	Leu 85	Arg 85	Gly 85	Asn 85	Leu 85	Glu 85	Phe 85	Ala 85	Cys 85	Ser 85	Ser 85	Asp 85	Cys 85	
Gly 100	Ala 100	Ile 100	Gln 100	Gly 100	Thr 100	Gly 100	Val 100	Arg 100	Pro 100	Ala 100	Arg 100	Gln 100	Pro 100	Ala 100	Val 100
Ala 115	Gly 115	Val 115	Gly 115	Gly 115	His 115	Glu 115	Arg 115	Leu 115	Pro 115	Gly 115	Pro 115	Gly 115	Glu 115	Glu 115	
Leu 130	Val 130	Glu 130	Leu 130	Leu 130	Gln 130	Arg 130	His 130	Arg 130	His 130	Asn 130	His 130	His 130	His 130	His 130	
Leu 145	Val 145	Glu 145	Leu 145	Leu 145	Gln 145	Arg 145	His 145	Arg 145	His 145	Asn 145	His 145	His 145	His 145	His 145	

(2) INFORMATION FOR SEQ ID NO:2942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2942:

agctcaccgc	cacctccacg	ctcgaagctc	ctcccgaaacc	ggccgcacatcg	tcgccatggc	60
agccgcgcgt	tctgcaagct	ccgtgaagga	agtgtgcgcg	tctccctcga	cctccgcctc	120
cgagccccct	Ccccttttct	gatggcaacca	ccaggttgta	cgtggccctat	ctttgcccggt	180
tcgcgcagcg	cttggattgc	tagaaactac	aagggctctgc	aggacaaagt	taagatagtt	240
gcacatgcac	tcgctgacag	gccagcgtgg	tacaaggaga	aggtttatcc	agaaaaacaag	300
gtgcctcttc	tagagcacga	caaccagggtg	aaaggagaga	gcttggtattt	ggttaagtac	360
atcgacaaca	acttcgaagg	tccatcgttg	ctccccgagg	atcatgcaaa	gcagcagttc	420
gctgaggagc	tgctcggata	cactgacgca	tccaacaaag	catttttactc	atgttttagtc	480
gacagggaag	atgtgtctga	ggaagccgtt	gctgccttgg	acaaaataga	agacgcccgt	540
gggaaattca	acgacggccc	gttcttccct	ggccagttca	gtctggtgga	cgttgcgat	600
gtaccggtca	tcgagaggtt	tcagatactc	tattccaata	taaaagaacta	tgacatcaca	660
aaggggcagc	ccagcccttca	gaattcctac	gaggaaagtga	acaagatcga	tcggtacaca	720
cacagctaac	tggaaccgca	gtttttgctt	gagcaaacaa	agaagcggct	tgggattgct	780
taaaagcctgt	gaccaaggag	gagactttgc	ccagaagcac	cagcgtagta	gatcggagct	840
cgtttttagta	ggttgtgtgc	ttggaatata	cgctcgtgtc	tcaataaaggc	atggccttct	900
ttaatggctg	tgcttctgaa	aataaataaa	ctagttgtcc	aggtattatc	gttgcttttg	960
tgacgtgtcg	atgtcactgt	atatatatga	atgggtggga	aaGaatatgc	gatgtgcagt	1020
gtgttctgtg	caaatattgc	cgagatgaag	gatacgtatc	catgtagaca	ttcatatatt	1080
gctcatattg	tgacacggcg	catgaagac	atggtttcgg	ccctaccacg	gc	

(2) INFORMATION FOR SEQ ID NO:2943:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..260
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2943:

Ser	Ser	Pro	Pro	Pro	Pro	Arg	Ser	Lys	Leu	Leu	Pro	Asn	Arg	Pro	His
1				5				10						15	
Arg	Arg	His	Gly	Ser	Arg	Arg	Phe	Cys	Lys	Leu	Arg	Glu	Gly	Ser	Ala
			20					25					30		
Ala	Val	Ser	Pro	Asp	Leu	Arg	Leu	Arg	Ala	Pro	Ser	Pro	Phe	Ser	Met
			35				40				45				
Ala	Pro	Pro	Gly	Cys	Thr	Trp	Pro	Ile	Phe	Ala	Arg	Ser	Arg	Ser	Ala
			50			55					60				
Trp	Ile	Ala	Arg	Asn	Tyr	Lys	Gly	Leu	Gln	Asp	Lys	Ile	Lys	Ile	Val
				70				75						80	
Ala	Ile	Asp	Leu	Ala	Asp	Arg	Pro	Ala	Trp	Tyr	Lys	Glu	Lys	Val	Tyr
			85					90						95	
Pro	Glu	Asn	Lys	Val	Pro	Ser	Leu	Glu	His	Asp	Asn	Gln	Val	Lys	Gly
			100					105					110		
Glu	Ser	Leu	Asp	Leu	Val	Lys	Tyr	Ile	Asp	Asn	Asn	Phe	Glu	Gly	Pro
			115				120					125			
Ser	Leu	Leu	Pro	Glu	Asp	His	Ala	Lys	Gln	Gln	Phe	Ala	Glu	Glu	Leu
			130				135					140			

Leu Gly Tyr Thr Asp Ala Phe Asn Lys Ala Phe Tyr Ser Cys Leu Val
145 150 155 160
Asp Arg Glu Asp Val Ser Glu Glu Ala Val Ala Ala Leu Asp Lys Ile
165 170 175
Glu Asp Ala Leu Gly Lys Phe Asn Asp Gly Pro Phe Phe Leu Gly Gln
180 185 190
Phe Ser Leu Val Asp Val Ala Tyr Val Pro Phe Ile Glu Arg Phe Gln
195 200 205
Ile Leu Tyr Ser Asn Ile Lys Asn Tyr Asp Ile Thr Lys Gly Arg Pro
210 215 220
Ser Leu Gln Lys Phe Ile Glu Glu Val Asn Lys Ile Asp Ala Tyr Thr
225 230 235 240
Gln Thr Lys Leu Asp Pro Gln Phe Leu Leu Glu Gln Thr Lys Lys Arg
245 250 255
Leu Gly Ile Ala
260

(2) INFORMATION FOR SEQ ID NO:2944:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..213

(D) OTHER INFORMATION: / Ceres Seq. ID 1574855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2944:

Met Ala Pro Pro Gly Cys Thr Trp Pro Ile Phe Ala Arg Ser Arg Ser
1 5 10 15
Ala Trp Ile Ala Arg Asn Tyr Lys Gly Leu Gln Asp Lys Ile Lys Ile
20 25 30
Val Ala Ile Asp Leu Ala Asp Arg Pro Ala Trp Tyr Lys Glu Lys Val
35 40 45
Tyr Pro Glu Asn Lys Val Pro Ser Leu Glu His Asp Asn Gln Val Lys
50 55 60
Gly Glu Ser Leu Asp Leu Val Lys Tyr Ile Asp Asn Asn Phe Glu Gly
65 70 75 80
Pro Ser Leu Leu Pro Glu Asp His Ala Lys Gln Phe Ala Glu Glu
85 90 95
Leu Leu Gly Tyr Thr Asp Ala Phe Asn Lys Ala Phe Tyr Ser Cys Leu
100 105 110
Val Asp Arg Glu Asp Val Ser Glu Glu Ala Val Ala Leu Asp Lys
115 120 125
Ile Glu Asp Ala Leu Gly Lys Phe Asn Asp Gly Pro Phe Phe Leu Gly
130 135 140
Gln Phe Ser Leu Val Asp Val Ala Tyr Val Pro Phe Ile Glu Arg Phe
145 150 155 160
Gln Ile Leu Tyr Ser Asn Ile Lys Asn Tyr Asp Ile Thr Lys Gly Arg
165 170 175
Pro Ser Leu Gln Lys Phe Ile Glu Glu Val Asn Lys Ile Asp Ala Tyr
180 185 190
Thr Gln Thr Lys Leu Asp Pro Gln Phe Leu Leu Glu Gln Thr Lys Lys
195 200 205
Arg Leu Gly Ile Ala
210

(2) INFORMATION FOR SEQ ID NO:2945:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 747 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..747
(D) OTHER INFORMATION: / Ceres Seq. ID 1574868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2945:

aaaaaaccaa	aagcagaggg	gaaagtgcg	tcggctctga	ctctggggca	cttggctgac	60
gaccgcgtct	ctctctgcaa	ctgcaactgc	aacgcaccaa	gaaactgcgc	gcgatcgatc	120
ggggaaggag	ataaacatgg	tgcaacggaa	gctggargtc	ctcctcgctc	ccgccaaggg	180
actcgaggag	accgatttcc	tcaataacat	ggacccttcc	gtgatcetta	cctgcgcgac	240
ccaagacgag	aaaagcagcg	tcgcaaatgg	agcaggaagc	gagcccgaa	ggaacgagac	300
cttcgtcttc	accgtcttcc	acgacacccc	gcagctgcac	ctcaagatca	tggacagcga	360
cctcaccaac	gacgatttgc	tcggcgaagc	aaacatcccc	ctggaggccg	tggttcagg	420
aggcagcctt	ccccggcg	ttcacccggt	cgtaaggag	gagaagtact	gcggagaggt	480
caagctcgct	caacttcaat	ccagcagcgg	aaactgcgcg	ccttgatgac	aacgaggagg	540
ggcgccctta	cagcagctgg	agttgatcta	tctgccatgg	gatgcatgca	tcatatatat	600
ccaccaagag	aagcagaggt	aattaatata	tctactcaag	agaagaatca	gtgttgctgt	660
tatgcgaccc	tctatctatc	tatatatatg	tgcttaattt	gtcataacga	ctgccaatat	720
aaaataaact	attcagagtt	gtttgcc				

(2) INFORMATION FOR SEQ ID NO:2946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..129
(D) OTHER INFORMATION: / Ceres Seq. ID 1574869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2946:

Met	Val	His	Gly	Lys	Leu	Xaa	Val	Leu	Leu	Val	Ser	Ala	Lys	Gly	Leu
1			5						10				15		
Glu	Asp	Thr	Asp	Phe	Leu	Asn	Asn	Met	Asp	Pro	Phe	Val	Ile	Leu	Thr
			20					25					30		
Cys	Arg	Thr	Gln	Glu	Gln	Lys	Ser	Ser	Val	Ala	Asn	Gly	Ala	Gly	Ser
			35				40					45			
Glu	Pro	Glu	Trp	Asn	Glu	Thr	Phe	Val	Phe	Thr	Val	Ser	Asp	Asp	Thr
			50			55					60				
Pro	Gln	Leu	His	Leu	Lys	Ile	Met	Asp	Ser	Asp	Leu	Thr	Asn	Asp	Asp
65			70					75					80		
Phe	Val	Gly	Glu	Ala	Thr	Ile	Pro	Leu	Glu	Ala	Val	Phe	Gln	Glu	Gly
			85					90					95		
Ser	Leu	Pro	Pro	Ala	Val	His	Pro	Val	Val	Lys	Glu	Glu	Lys	Tyr	Cys
			100				105						110		
Gly	Glu	Val	Lys	Leu	Ala	His	Leu	His	Ser	Ser	Ser	Gly	Asn	Ser	Pro
			115				120						125		

Pro

(2) INFORMATION FOR SEQ ID NO:2947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..105
(D) OTHER INFORMATION: / Ceres Seq. ID 1574870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2947:

Met	Asp	Pro	Phe	Val	Ile	Leu	Thr	Cys	Arg	Thr	Gln	Glu	Gln	Lys	Ser
1			5						10					15	
Ser	Val	Ala	Asn	Gly	Ala	Gly	Ser	Glu	Pro	Glu	Trp	Asn	Glu	Thr	Phe
			20					25					30		
Val	Phe	Thr	Val	Ser	Asp	Asp	Thr	Pro	Gln	Leu	His	Leu	Lys	Ile	Met
			35				40					45			
Asp	Ser	Asp	Leu	Thr	Asn	Asp	Asp	Phe	Val	Gly	Glu	Ala	Thr	Ile	Pro
			50			55					60				
Leu	Glu	Ala	Val	Phe	Gln	Glu	Gly	Ser	Leu	Pro	Pro	Ala	Val	His	Pro
				70						75				80	
Val	Val	Lys	Glu	Glu	Lys	Tyr	Cys	Gly	Glu	Val	Lys	Leu	Ala	His	Leu
			85						90					95	
His	Ser	Ser	Ser	Gly	Asn	Ser	Pro	Pro							
			100				105								

(2) INFORMATION FOR SEQ ID NO:2948:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1574871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2948:

Met	Glu	Arg	Asp	Leu	Arg	Leu	His	Arg	Leu	Arg	Arg	His	Pro	Ala	Ala
1			5						10					15	
Ala	Pro	Gln	Asp	His	Gly	Gln	Arg	Pro	His	Gln	Arg	Arg	Phe	Arg	Arg
			20					25					30		
Arg	Ser	Asn	His	Pro	Pro	Gly	Gly	Arg	Val	Ser	Gly	Arg	Gln	Pro	Ser
			35				40					45			
Pro	Gly	Gly	Ser	Pro	Gly	Arg	Gln	Gly	Gly	Glu	Val	Leu	Arg	Arg	Gly
			50			55					60				
Gln	Ala	Arg	Ser	Pro	Ser	Leu	Gln	Gln	Arg	Lys	Leu	Ala	Ala	Leu	Met
			65		70				75					80	
Thr	Thr	Arg	Arg	Gly	Arg	Leu	Thr	Ala	Ala	Gly	Val	Asp	Leu	Ser	Ala
			85					90						95	
Met	Gly	Cys	Met	His	His	Ile	Tyr	Pro	Pro	Arg	Glu	Glu	Arg	Ile	Ile
			100					105						110	
Asn															

(2) INFORMATION FOR SEQ ID NO:2949:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 935 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..935

(D) OTHER INFORMATION: / Ceres Seq. ID 1574880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2949:

agt	tta	tggg	ctg	gaat	tggg	cgc	tcaaac	tgg	cccgtta	cgt	gaatttr	gcg	ggggctgc	60
cgct	ggg	gac	cgag	acgtg	tgg	ctgcaca	gcg	acgtccg	trg	gagcrgg	cg	ggcgactg	120	
cagg	cagag	gttt	cgctcg	aacct	agtg	tct	ccacac	gcc	gtgcaca	tgg	ccgcgcg	180		
cgcg	cgccgc	ctcc	gcctgc	agc	gccagtg	cct	gcgcgc	aac	cccttc	tct	ctccg	240		
gcat	ggcctc	cgct	accgca	agct	ttaggt	cat	ctccacc	acg	actattg	ata	agctggg	300		
gaa	agcagg	gaggt	gtgtca	aggt	ggcgcc	tgg	ccacttc	cg	caaccacc	ttat	gcccaa	360		

gatgctcgca gtccccgaacc tggacaaaatt cgccatacta atccgagagc agcgcaagCt 420
ctatcaacgc gaagaggagg tccgggtgaa acaagtcacg gagaagaatg atgatgcacg 480
gtacacaggaa gaagaatatga agcagtagca aacggcagca aagcggctag ataacgcact 540
ctctgggtgtg aggagggttca tctcgactgg aaacgagctg cgtactccgt taacaaaaaga 600
cgaaaattgtt tccgagggtgg cgaggcagct caacatcaac atccatccgg agaacctgca 660
tctgcagtcga cctttggcgt cgctcggcga atttgagttg cccctccgggt taccgcagaa 720
cataccgtgc ccagaaggtta agctccagtg gactctgaag gtgaagatca ggagaaaaatg 780
agcgacaggaa ctgggggaagt ttcttttggc ccccccacaa ctggtgtatg gtacccaaacc 840
attgttagct ccgaacaat ggtaccaaac catgtgttat gcaagtttag ctccgaaaaa 900
tttttttctg atgtataata aaagagtaag gttgc

(2) INFORMATION FOR SEQ ID NO:2950:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..203

(D) OTHER INFORMATION: / Ceres Seq. ID 1574881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2950:

Met Ala Ala Ala Arg Ala Ala Leu Arg Leu Gln Arg Gln Cys Leu Ala
1 5 10 15
Ala Asn Pro Phe Leu Phe Ser Gly His Gly Leu Arg Tyr Arg Lys Leu
20 25 30
Glu Val Ile Leu Thr Thr Thr Ile Asp Lys Leu Gly Lys Ala Gly Glu
35 40 45
Val Val Lys Val Ala Pro Gly His Phe Arg Asn His Leu Met Pro Lys
50 55 60
Met Leu Ala Val Pro Asn Leu Asp Lys Phe Ala Ile Leu Ile Arg Glu
65 70 75 80
Gln Arg Lys Leu Tyr Gln Arg Glu Glu Glu Val Ala Val Lys Gln Val
85 90 95
Thr Glu Lys Asp Asp Asp Ala Arg Leu Gln Glu Glu Arg Met Lys Gln
100 105 110
Tyr Gln Thr Ala Ala Lys Arg Leu Asp Asn Ala Leu Leu Val Leu Arg
115 120 125
Arg Phe Ile Ser Thr Gly Asn Glu Leu Arg Thr Pro Val Thr Lys Asp
130 135 140
Glu Ile Val Ser Glu Val Ala Arg Gln Leu Asn Ile Asn Ile His Pro
145 150 155 160
Glu Asn Leu His Leu Gln Ser Pro Leu Ala Ser Leu Gly Glu Phe Glu
165 170 175
Leu Pro Leu Arg Leu Pro Gln Asn Ile Pro Cys Pro Glu Gly Lys Leu
180 185 190
Gln Trp Thr Leu Lys Val Lys Ile Arg Arg Lys
195 200

(2) INFORMATION FOR SEQ ID NO:2951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1574882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2951:

Met Pro Lys Met Leu Ala Val Pro Asn Leu Asp Lys Phe Ala Ile Leu

1 5 10 15
Ile Arg Glu Gln Arg Lys Leu Tyr Gln Arg Glu Glu Glu Val Ala Val
20 25 30
Lys Gln Val Thr Glu Lys Asp Asp Asp Ala Arg Leu Gln Glu Glu Arg
35 40 45
Met Lys Gln Tyr Gln Thr Ala Ala Lys Arg Leu Asp Asn Ala Leu Leu
50 55 60
Val Leu Arg Arg Phe Ile Ser Thr Gly Asn Glu Leu Arg Thr Pro Val
65 70 75 80
Thr Lys Asp Glu Ile Val Ser Glu Val Ala Arg Gln Leu Asn Ile Asn
85 90 95
Ile His Pro Glu Asn Leu His Leu Gln Ser Pro Leu Ala Ser Leu Gly
100 105 110
Glu Phe Glu Leu Pro Leu Arg Leu Pro Gln Asn Ile Pro Cys Pro Glu
115 120 125
Gly Lys Leu Gln Trp Thr Leu Lys Val Lys Ile Arg Arg Lys
130 135 140

(2) INFORMATION FOR SEQ ID NO:2952:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1574883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2952:

Met Leu Ala Val Pro Asn Leu Asp Lys Phe Ala Ile Leu Ile Arg Glu
1 5 10 15
Gln Arg Lys Leu Tyr Gln Arg Glu Glu Val Ala Val Lys Gln Val
20 25 30
Thr Glu Lys Asp Asp Asp Ala Arg Leu Gln Glu Glu Arg Met Lys Gln
35 40 45
Tyr Gln Thr Ala Ala Lys Arg Leu Asp Asn Ala Leu Leu Val Leu Arg
50 55 60
Arg Phe Ile Ser Thr Gly Asn Glu Leu Arg Thr Pro Val Thr Lys Asp
65 70 75 80
Glu Ile Val Ser Glu Val Ala Arg Gln Leu Asn Ile Asn Ile His Pro
85 90 95
Glu Asn Leu His Leu Gln Ser Pro Leu Ala Ser Leu Gly Glu Phe Glu
100 105 110
Leu Pro Leu Arg Leu Pro Gln Asn Ile Pro Cys Pro Glu Gly Lys Leu
115 120 125
Gln Trp Thr Leu Lys Val Lys Ile Arg Arg Lys
130 135

(2) INFORMATION FOR SEQ ID NO:2953:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 938 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..938

(D) OTHER INFORMATION: / Ceres Seq. ID 1574896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2953:

gcacgaggtc caggacatca ggcacccagaa aaaagtccga acgcatctct tctttctact
tctttgtaac ccaagacgaa ctggtgaac tctttctcct cgcgcasacc ggagcacaat

60

120

caaggattcc	agtcacgtcc	tgccaatgga	gtgcgttttg	ggcttggttg	gccgcgactt	180
cgcgggtggt	gccggccgaca	cctccgcgt	gcagagtatc	ctcgtccaca	agactgacga	240
ggacaaagta	atggtctctg	actcgcacaa	gctgttggtg	gcttcarggg	agcctggtga	300
cgcgggtgcag	ttttacggag	tcatacagaa	gaacctccac	ctgtaccagt	tcgcacaacac	360
catcccgctg	tcaaccgcgc	Ctgccgccaa	cttcacacgc	ggcgagctcg	ccacagccct	420
tcgtaagaat	ccatacatgg	tcaatgttat	tctcggtggt	tacgataagg	atggtggcgc	480
ctcactgtac	tacatcgact	acattgcgac	cttcgacaag	atcgacaagg	gcgcttttgg	540
gtacggatcg	tatttctgcc	tgctctgat	ggacaagctg	taccgcccgc	acatgaccgt	600
tgaggaascg	gtagacctcg	ttgataagtg	cattaaggag	atccggctgc	ggctggttgt	660
ggcgccocag	aactctgtga	tcaagatcgt	cgacaaggac	ggggccaggg	agtacgcgag	720
gcgtgaactc	gtcggcgaca	gtgcacctcg	tgaagctgca	gctacggttg	cgcctgagg	780
catgaaactt	gtttgtgtta	gttgtttgtt	tctcagcgag	gctactatgt	aatcaaatgg	840
atactggtgg	gggtcccaac	gctgtttttt	aatcaatttt	agccccagaca	tgtaattctg	900
ttcttgact	aattcatgtc	ttcgccgagt	acaagttg			

(2) INFORMATION FOR SEQ ID NO:2954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..210
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2954:

Met	Glu	Cys	Val	Leu	Gly	Leu	Val	Gly	Arg	Asp	Phe	Ala	Val	Ala	
1			5						10				15		
Ala	Asp	Thr	Ser	Ala	Val	Gln	Ser	Ile	Leu	Val	His	Lys	Thr	Asp	Glu
			20					25					30		
Asp	Lys	Val	Met	Val	Leu	Asp	Ser	His	Lys	Leu	Leu	Gly	Ala	Ser	Xaa
			35					40				45			
Glu	Pro	Gly	Asp	Arg	Val	Gln	Phe	Thr	Glu	Phe	Ile	Gln	Lys	Asn	Leu
			50				55				60				
His	Leu	Tyr	Gln	Phe	Arg	Asn	Thr	Ile	Pro	Leu	Ser	Thr	Ala	Ala	Ala
			65			70				75			80		
Ala	Asn	Phe	Thr	Arg	Gly	Glu	Leu	Ala	Thr	Ala	Leu	Arg	Lys	Asn	Pro
			85					90					95		
Tyr	Met	Val	Asn	Val	Ile	Leu	Gly	Gly	Tyr	Asp	Lys	Asp	Val	Gly	Ala
			100				105						110		
Ser	Leu	Tyr	Tyr	Ile	Asp	Tyr	Ile	Ala	Thr	Leu	His	Lys	Ile	Asp	Lys
			115				120					125			
Gly	Ala	Phe	Gly	Tyr	Gly	Ser	Tyr	Phe	Cys	Leu	Ser	Leu	Met	Asp	Lys
			130				135					140			
Leu	Tyr	Arg	Pro	Asp	Met	Thr	Val	Glu	Glu	Xaa	Val	Asp	Leu	Val	Asp
			145			150				155					160
Lys	Cys	Ile	Lys	Glu	Ile	Arg	Leu	Arg	Leu	Val	Val	Ala	Pro	Glu	Asn
			165						170					175	
Phe	Val	Ile	Lys	Ile	Val	Asp	Lys	Asp	Gly	Ala	Arg	Glu	Tyr	Ala	Arg
			180					185					190		
Arg	Glu	Leu	Val	Gly	Asp	Ser	Ala	Pro	Ala	Glu	Ala	Ala	Ala	Thr	Val
			195				200						205		
Ala	Ala														

(2) INFORMATION FOR SEQ ID NO:2955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1574898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2955:

```
Met Val Leu Asp Ser His Lys Leu Leu Gly Ala Ser Xaa Glu Pro Gly
1      5      10      15
Asp Arg Val Gln Phe Thr Glu Phe Ile Gln Lys Asn Leu His Leu Tyr
20      25      30
Gln Phe Arg Asn Thr Ile Pro Leu Ser Thr Ala Ala Ala Asn Phe
35      40      45
Thr Arg Gly Glu Leu Ala Thr Ala Leu Arg Lys Asn Pro Tyr Met Val
50      55      60
Asn Val Ile Leu Gly Gly Tyr Asp Lys Asp Val Gly Ala Ser Leu Tyr
65      70      75
Tyr Ile Asp Tyr Ile Ala Thr Leu His Lys Ile Asp Lys Gly Ala Phe
85      90      95
Gly Tyr Gly Ser Tyr Phe Cys Leu Ser Leu Met Asp Lys Leu Tyr Arg
100     105     110
Pro Asp Met Thr Val Glu Glu Xaa Val Asp Leu Val Asp Lys Cys Ile
115     120     125
Lys Glu Ile Arg Leu Arg Leu Val Val Ala Pro Gln Asn Phe Val Ile
130     135     140
Lys Ile Val Asp Lys Asp Gly Ala Arg Glu Tyr Ala Arg Arg Glu Leu
145     150     155
Val Gly Asp Ser Ala Pro Ala Glu Ala Ala Thr Val Ala Ala
165     170     175
```

(2) INFORMATION FOR SEQ ID NO:2956:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1574899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2956:

```
Met Val Asn Val Ile Leu Gly Gly Tyr Asp Lys Asp Val Gly Ala Ser
1      5      10      15
Leu Tyr Tyr Ile Asp Tyr Ile Ala Thr Leu His Lys Ile Asp Lys Gly
20      25      30
Ala Phe Gly Tyr Gly Ser Tyr Phe Cys Leu Ser Leu Met Asp Lys Leu
35      40      45
Tyr Arg Pro Asp Met Thr Val Glu Glu Xaa Val Asp Leu Val Asp Lys
50      55      60
Cys Ile Lys Glu Ile Arg Leu Arg Leu Val Val Ala Pro Gln Asn Phe
65      70      75
Val Ile Lys Ile Val Asp Lys Asp Gly Ala Arg Glu Tyr Ala Arg Arg
85      90      95
Glu Leu Val Gly Asp Ser Ala Pro Ala Glu Ala Ala Ala Thr Val Ala
100     105     110
Ala
```

(2) INFORMATION FOR SEQ ID NO:2957:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 907 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..907

(D) OTHER INFORMATION: / Ceres Seq. ID 1574910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2957:

atccatccaa	ctcttcataa	caggcgacct	gagagcagag	cagacagaga	gcgttctggc	60
agccgtttcg	gasttgaacc	tctgcaacca	ccaacagcta	aactaaaagc	agcrgcggac	120
ggcgcgcggt	actggacagc	cgccgcagca	tggctacgcc	ggcgcasagc	agggtgacca	180
gcaccagccg	aggctgcaga	agggtgatgt	ggctgtagac	gagagcgagt	gcagccggca	240
cgcgctggag	tgggcgctgc	ggaacctggc	gcccacgctg	gccccaccgc	tactggtgct	300
caocgtgcag	cgcacttccc	cgtcgggata	cgtctccgcc	gcgtcCttcg	gcgcaccocct	360
gggcaccgctc	cctccgggtg	ctccggagct	catcaggctcg	atgcaggagc	agcagaggga	420
gCtcacgcag	gagctcctcg	acaaggccag	ggccatctgc	gccgagcacg	gggttgcgtg	480
agaggcaatt	gtcgaggtgc	gagatgcaaa	ggaggtgata	tgtgaagtgg	ctgagaagaa	540
aaatgtcgat	ctgctgggttc	tgggaagcca	cagtcgtggg	ccaatacaga	ggttgttcc	600
tgggagcgct	agtaactact	gtgtacatca	ttctaagtgt	ccagttcttg	tgtgaaagaa	660
ccaagcgctga	tgaaggattc	aactccagc	tgctagtctc	aatcatgttc	gggtatttgt	720
caacgtattt	gtaattgcta	gtacttgc	tagccaaacg	cattggccaa	taaagttagct	780
tgctttgctt	cttgggaagg	cagaggctgg	actggaggag	agttcttttt	ctttttcttt	840
ttcttcgtca	gtgtgccttc	gctccggaat	ggcagagttg	taaataagaa	ctacgaacct	900

tgctgcgc

(2) INFORMATION FOR SEQ ID NO:2958:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1574911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2958:

Met	Val	Ala	Val	Asp	Glu	Ser	Glu	Cys	Ser	Arg	His	Ala	Leu	Glu	Trp
1				5					10					15	
Ala	Leu	Arg	Asn	Leu	Ala	Pro	Thr	Leu	Ala	Pro	Pro	Leu	Leu	Val	Leu
				20				25					30		
Thr	Val	Gln	Pro	His	Phe	Pro	Leu	Gly	Tyr	Val	Ser	Ala	Ala	Ser	Phe
		35				40				45					
Gly	Ala	Pro	Leu	Gly	Thr	Val	Pro	Val	Ala	Pro	Gly	Leu	Ile	Arg	
		50				55				60					
Ser	Met	Gln	Glu	Gln	Arg	Glu	Leu	Thr	Gln	Glu	Leu	Leu	Asp	Lys	
		65				70				75				80	
Ala	Arg	Ala	Ile	Cys	Ala	Glu	His	Gly	Val	Ala	Val	Glu	Ala	Ile	Val
			85					90						95	
Glu	Val	Gly	Asp	Ala	Lys	Glu	Val	Ile	Cys	Glu	Val	Ala	Glu	Lys	Lys
			100					105						110	
Asn	Val	Asp	Leu	Leu	Val	Leu	Gly	Ser	His	Ser	Arg	Gly	Pro	Ile	Gln
			115					120						125	
Arg	Leu	Phe	Leu	Gly	Ser	Val	Ser	Asn	Tyr	Cys	Val	His	His	Ser	Lys
			130					135						140	
Cys	Pro	Val	Leu	Val	Val	Lys	Asn	Gln	Gly						
			145					150							

(2) INFORMATION FOR SEQ ID NO:2959:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1574912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2959:

```
Met Gln Gln Gln Gln Arg Glu Leu Thr Gln Gln Leu Leu Asp Lys Ala
1           5           10           15
Arg Ala Ile Cys Ala Glu His Gly Val Ala Val Glu Ala Ile Val Glu
20           25           30
Val Gly Asp Ala Lys Glu Val Ile Cys Glu Val Ala Glu Lys Lys Asn
35           40           45
Val Asp Leu Leu Val Leu Gly Ser His Ser Arg Gly Pro Ile Gln Arg
50           55           60
Leu Phe Leu Gly Ser Val Ser Asn Tyr Cys Val His His Ser Lys Cys
65           70           75           80
Pro Val Leu Val Val Lys Asn Gln Gly
85
```

(2) INFORMATION FOR SEQ ID NO:2960:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..846

(D) OTHER INFORMATION: / Ceres Seq. ID 1574947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2960:

```
gccatcggttc cctcctctgc accccccatc ctccgacatc ctgcctcgca gcagaccctc 60
ctctggtgcg cgtgcgccac cgcgagatg tcgaagaaaa tcgtggtgaa gctgcacctg 120
caggacaaca aggacaagca gaaggccatg aaggctgtct cgcgctcac cggcctgcac 180
gagatatccg cggacatggc gtcgcacaag atgacggtgg ccgcatggtt ggaccccgct 240
agcgtgttga gcaagctgcg caaggcgctg tggtcggcga ccategatc cgtcggccct 300
gccaccgcgc cgccgcgcgc gccgcataca ctgtcacctg cgctatggcc cgtatcaagg 360
tgcacgagct ccgggggaag agcaagacgg acctgcaggc gcaGctcaag gagctgaagt 420
ctgagctctc cctcctccgc gtaGccaagg tcaccggcgg cgacccaac aagctctcca 480
agatcaagggt ggtgcgcacc tcgatcgcgc gcgtgtctac agtgcctcgc cagaagcaga 540
agtcggcggtt gcgggaggcg tacaagaaga agaacctgct cccctcgac ctccgcccta 600
agaagaccgc tgccatccgc cgccgtctga ccaagcacca gctttctctg aagaccgaga 660
gggaaagaaa gcgtgagaag tacttcccca tgaggaahta tgctatcaag gcctaggcta 720
gaactgtgag atgctgtgct tagcatatca tcggctgtgt ttttaattttt ggtttgatg 780
gacatttgtt gaagtacgat gtattcctct gtttccatat aaatggctag attggtttga 840
ctggct
```

(2) INFORMATION FOR SEQ ID NO:2961:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1574948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2961:

```
Ala Ile Val Pro Ser Ser Ala Pro Pro Ile Leu Gly His Pro Arg Leu
1           5           10           15
Gln Gln Thr Leu Leu Trp Cys Ala Cys Ala Thr Gly Glu Met Ser Lys
20           25           30
Lys Ile Val Val Lys Leu His Leu Asp Asn Lys Asp Lys Gln Lys
```

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..123
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574950
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2963:
Met Ala Arg Ile Lys Val His Glu Leu Arg Gly Lys Ser Lys Thr Asp
1 5 10 15
Leu Gln Ala Gln Leu Lys Glu Leu Lys Ser Glu Leu Ser Leu Leu Arg
 20 25 30
Val Ala Lys Val Thr Gly Gly Ala Pro Asn Lys Leu Ser Lys Ile Lys
 35 40 45
Val Val Arg Thr Ser Ile Ala Arg Val Leu Thr Val Ile Ser Gln Lys
 50 55 60
Gln Lys Ser Ala Leu Arg Glu Ala Tyr Lys Lys Lys Asn Leu Leu Pro
65 70 75 80
Leu Asp Leu Arg Pro Lys Lys Thr Arg Ala Ile Arg Arg Arg Leu Thr
 85 90 95
Lys His Gln Leu Ser Leu Lys Thr Glu Arg Glu Lys Lys Arg Glu Lys
 100 105 110
Tyr Phe Pro Met Arg Lys Tyr Ala Ile Lys Ala
 115 120
(2) INFORMATION FOR SEQ ID NO:2964:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1052 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1052
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574981
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2964:
taagaatgat gtgatcaaat ttgtccaaga gaacaatttt cattctgggt tctttgatgg 60
aactgaaaac aacatggtag ctgatgccta tgaattgaag gtgcgtctttg aacacatcat 120
tgaaaggata gcccttgattt ctgatgctgc aaatacagaa cgacctcttc ttgttgtcaa 180
caacttgctc ataggtgggg ctctggctgc aaggtctaag tacaccctac agcatttggg 240
cattaccact gtactctgtt tgtgttcaaa tgagattggt caatccgatt cccaatttcc 300
cgatcttttt gaatacaaga acttttcaat tagcgatgat gatgatgcaa acatcagtga 360
tctttttgag gaagcatcag acttcattga tcatgtggat catgttgggg gcaaggttct 420
agttcattgc tttgaaggga aaagtgcgag tgccacagtc gtacttgccct atctttatgt 480
tagagagggc tttactcttg caaaagccctg gaacttactg aagaagatca accgtcgagc 540
gcaGccaaac aagggcttcgc aaaggtctctc ctggcccttg acaagaggct gcattggcaag 600
gtatctatgg actggcaaca caagcggcca gaaatgaagg ttgtgtccaat ctgcagcaag 660
aatgttggtc taagtacgag ttcaactcaag ctgcacctgc agaagggcaca caagcgtcta 720
ctctcgaggc gtgtcgacag cgccatgacc atgaagatcc aaaaaatcgat cgagtcactc 780
cagatcagcc gaggaggaag cctgagcccg tcccagaagc tgaccaaggt gttagcaaat 840
gagctgagct tctgatctgt tttcctgtac tatagatgag gcaatgtact tggctcacat 900
tgtaataact tgtactatca gactgaactt gtgaactgtag gtttagttca cagccctata 960
tgattagcac acgaatgttc aggtgtgaag ggtgcaacac taaagaatgt tcaggttctt 1020
tatttgttgc ctgcagtatg cagttttctt ct
(2) INFORMATION FOR SEQ ID NO:2965:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 211 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide

(B) LOCATION: 1..211

(D) OTHER INFORMATION: / Ceres Seq. ID 1574982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2965:

Lys Asn Asp Val Ile Lys Phe Cys Gln Glu Asn Asn Phe His Ser Gly
1 5 10 15
Phe Phe Asp Gly Thr Glu Asn Asn Met Val Ala Asp Ala Tyr Glu Leu
20 25 30
Lys Val Arg Leu Glu His Ile Ile Glu Arg Ile Ala Leu Ile Ser Asp
35 40 45
Ala Ala Asn Thr Glu Arg Pro Ser Leu Val Val Asn Asn Leu Phe Ile
50 55 60
Gly Gly Ala Leu Ala Ala Arg Ser Lys Tyr Thr Leu Gln His Leu Gly
65 70 75 80
Ile Thr His Val Leu Cys Leu Cys Ser Asn Glu Ile Gly Gln Ser Asp
85 90 95
Ser Gln Phe Pro Asp Leu Phe Glu Tyr Lys Asn Phe Ser Ile Ser Asp
100 105 110
Asp Asp Asp Ala Asn Ile Ser Asp Leu Phe Glu Glu Ala Ser Asp Phe
115 120 125
Ile Asp His Val Asp His Val Gly Gly Lys Val Leu Val His Cys Phe
130 135 140
Glu Gly Lys Ser Arg Ser Ala Thr Val Val Leu Ala Tyr Leu Met Leu
145 150 155 160
Arg Glu Gly Phe Thr Leu Ala Lys Ala Trp Asn Leu Leu Lys Lys Val
165 170 175
His Arg Arg Ala Gln Pro Asn Asp Gly Ser Gln Arg Leu Ser Trp Pro
180 185 190
Leu Thr Arg Gly Cys Met Ala Arg Tyr Leu Trp Thr Gly Asn Thr Ser
195 200 205
Gly Gln Lys
210

(2) INFORMATION FOR SEQ ID NO:2966:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1574983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2966:

Met Val Ala Asp Ala Tyr Glu Leu Lys Val Arg Leu Glu His Ile Ile
1 5 10 15
Glu Arg Ile Ala Leu Ile Ser Asp Ala Ala Asn Thr Glu Arg Pro Ser
20 25 30
Leu Val Val Asn Asn Leu Phe Ile Gly Gly Ala Leu Ala Arg Ser
35 40 45
Lys Tyr Thr Leu Gln His Leu Gly Ile Thr His Val Leu Cys Leu Cys
50 55 60
Ser Asn Glu Ile Gly Gln Ser Asp Ser Gln Phe Pro Asp Leu Phe Glu
65 70 75 80
Tyr Lys Asn Phe Ser Ile Ser Asp Asp Asp Ala Asn Ile Ser Asp
85 90 95
Leu Phe Glu Glu Ala Ser Asp Phe Ile Asp His Val Asp His Val Gly
100 105 110
Gly Lys Val Leu Val His Cys Phe Glu Gly Lys Ser Arg Ser Ala Thr
115 120 125
Val Val Leu Ala Tyr Leu Met Leu Arg Glu Gly Phe Thr Leu Ala Lys
130 135 140

Ala Trp Asn Leu Leu Lys Lys Val His Arg Arg Ala Gln Pro Asn Asp
145 150 155 160
Gly Ser Gln Arg Leu Ser Trp Pro Leu Thr Arg Gly Cys Met Ala Arg
165 170 175
Tyr Leu Trp Thr Gly Asn Thr Ser Gly Gln Lys
180 185

(2) INFORMATION FOR SEQ ID NO:2967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..948
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2967:

ctycgtgcc	ctctcgvct	ctcgcgcatc	cttctttact	gcccgagagt	tctgactagc	60
cacatccagt	caagcagtaa	aggcgaccca	tggaggcggc	ggcgagagaat	aaggaggccg	120
agcaggagga	gcagcagcta	cgcgcgcgcg	agaaggataa	cgcgcccgcc	gccgccgagg	180
aagacgaagg	ggattccggag	gagaccgagc	gccgcaaccg	cgacctcaag	tcgccctctc	240
acccocttag	gcacaaactc	gtgctctggt	acactgcgcg	gacgcctgga	gcgaggtcgc	300
agtcgtacga	ggacaacatc	aagaagatca	tcgatttcag	cacagtcgaa	tcgttctggt	360
tttgcactag	ccaccttgcg	cgcccttctt	ccctgcggag	ccccactgac	cttcatctct	420
tcaaggatgg	catccgtccc	ctctgggagg	atctctcaaa	ccagaatggt	ggcaagtgga	480
taattagatt	caaaaaagca	gtttcaggct	gattttggga	ggatttggtg	ctagtggtag	540
taggcgacca	gcttgagtat	agcgatgatg	tctgtggtgt	tgtgcttagt	gtccgtttca	600
atgaagacat	tctgagcgct	tggaaacgga	acgcacacaga	ccatcaggct	gtgatggcat	660
tgagggtatc	tatacaagagg	cacctcaagc	tgccgcacag	ctatctgatg	gagtacaaac	720
cccatgatst	tcgcggcggtg	acaactogtc	ctacaggaaac	acatgggtga	gaggatagat	780
aaacctcatg	atactcggca	gcttcaactgc	gacggttctg	aagcaaaagag	actcttttat	840
gtaccaagaa	cgcagacatat	tatgcaatgt	agtactacta	ctactactac	tcaaaagccc	900
ctacaatgtg	acgcgcaaca	attttactat	ctaatgtgtt	ttttttgc		

(2) INFORMATION FOR SEQ ID NO:2968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2968:

Xaa Arg Xaa Pro Pro Xaa Leu Leu Ala Ile Leu Leu Tyr Cys Pro Arg	
1 5 10 15	
Val Leu Thr Ser His Ile Gln Ser Ser Ser Lys Gly Ala Pro Trp Arg	
20 25 30	
Arg Arg Arg Arg Ile Arg Arg Pro Ser Arg Arg Ser Ser Tyr Arg	
35 40 45	
Thr Arg Arg Arg Ile Thr Arg Pro Pro Pro Arg Lys Thr Lys Arg	
50 55 60	
Ile Arg Arg Arg Pro Ser Ala Ala Thr Ala Thr Ser Ser Pro Ala Phe	
65 70 75 80	
Thr Pro Leu Gly Thr Asn Ser Cys Ser Gly Thr Leu Ala Gly Arg Leu	
85 90 95	
Glu Arg Gly Arg Ser Arg Thr Arg Thr Thr Ser Arg Arg Ser Ser Ile	
100 105 110	
Ser Ala Gln Ser Asn Arg Ser Gly Phe Ala Thr Ala Thr Leu Arg Ala	

115	120	125	
Leu Leu Pro Cys Arg Ala Pro Leu Thr Phe Ile Ser Ser Arg Met Ala			
130	135	140	
Ser Val Pro Ser Gly Arg Ile Leu Gln Thr Arg Met Val Ala Ser Gly			
145	150	155	160

(2) INFORMATION FOR SEQ ID NO:2969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..226
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2969:

Met	Glu	Ala	Ala	Ala	Glu	Asn	Lys	Glu	Ala	Glu	Gln	Glu	Glu	Gln	Gln
1			5					10						15	
Leu	Pro	His	Ala	Gln	Lys	Asp	Asn	Ala	Pro	Ala	Ala	Ala	Glu	Glu	Asp
			20				25						30		
Glu	Ala	Asp	Ser	Glu	Glu	Thr	Glu	Arg	Arg	Asn	Arg	Asp	Leu	Lys	Ser
		35				40						45			
Gly	Leu	His	Pro	Leu	Arg	His	Lys	Leu	Val	Leu	Trp	Tyr	Thr	Arg	Arg
	50				55					60					
Thr	Pro	Gly	Ala	Arg	Ser	Gln	Ser	Tyr	Glu	Asp	Asn	Ile	Lys	Lys	Ile
65				70				75						80	
Ile	Asp	Phe	Ser	Thr	Val	Glu	Ser	Phe	Trp	Val	Cys	Tyr	Cys	His	Leu
			85					90					95		
Ala	Arg	Pro	Ser	Leu	Pro	Ser	Pro	Thr	Asp	Leu	His	Leu	Phe	Lys	
		100				105						110			
Asp	Gly	Ile	Arg	Pro	Leu	Trp	Glu	Asp	Pro	Ala	Asn	Gln	Asn	Gly	Gly
	115					120						125			
Lys	Trp	Ile	Ile	Arg	Phe	Lys	Lys	Ala	Val	Ser	Gly	Arg	Phe	Trp	Glu
	130					135					140				
Asp	Leu	Val	Leu	Val	Val	Gly	Asp	Gln	Leu	Glu	Tyr	Ser	Asp	Asp	
145			150					155						160	
Val	Cys	Gly	Val	Val	Leu	Ser	Val	Arg	Phe	Asn	Glu	Asp	Ile	Leu	Ser
			165					170					175		
Val	Trp	Asn	Arg	Asn	Ala	Ser	Asp	His	Gln	Ala	Val	Met	Ala	Leu	Arg
		180						185					190		
Asp	Ser	Ile	Lys	Arg	His	Leu	Lys	Leu	Pro	His	Ser	Tyr	Leu	Met	Glu
	195					200						205			
Tyr	Lys	Pro	His	Asp	Xaa	Arg	Gly	Val	Thr	Thr	Arg	Pro	Thr	Gly	Thr
	210					215					220				
His	Gly														
225															

(2) INFORMATION FOR SEQ ID NO:2970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 965 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..965
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2970:

agaccagcaa	tcaacattca	agccatggca	ctgttcaagt	gcattgtgcat	cttcttagtc	60
togctttcac	tcgcctccac	cttcaccaat	gcccaggaag	aatcttcaca	tgggactctc	120
ccaccgttcc	cttgcattcc	agggccagca	cgcccccgcg	ggttgccacc	ttgcccgcgc	180
gcaccaaccc	agtgctacac	gtcgtgtgct	ggaatgatgc	cgtgcgcgga	cttctcacc	240
cacaacgagg	tgccaccgat	gcccaccacg	gtcgcctgtt	gtGgatggtc	tcagggtcac	300
cgtaaccaac	cggtccatct	gtctatgcca	tatcgtcaac	ggtaacatca	acaagctcct	360
accggcgccc	atgataccgc	tgccgatggt	ggcgctcccc	cgctttttgt	ttgtccgctt	420
cccacgagcc	atacttgcgc	gggtgatcag	agggcatttg	ccaccgatga	accctccgcg	480
tcacaccag	gcataccgct	cgggaaccac	atctacatcg	ccagcagcat	caccatcgga	540
atcaccacca	gcagcatcgc	caccagaatc	gcgctcgaca	ccaccaccag	agtcgctcga	600
ctacaccgcc	gacaccagca	gcagcaccac	cgaaatcacc	gtctgatcca	ccaccagcta	660
cgtaaccagca	atcatcatct	gatccaccgt	cgaccaccag	agctacacca	accggcgact	720
catcccccac	atcttaatac	cgaaagatat	ttcaaaagca	gtagttagtt	agtcacaaata	780
gatatgcgtt	ttaggattct	agttgatgat	cgctcattat	tttgttcac	tcgaatgcag	840
tagtgtgtta	gctatgtagt	tgcatacctc	tcataactaa	gtctattaga	agtatctcta	900
ataatattta	ggatctgtca	tcaataaaat	gtatgcaaca	atacagcat	tgtattattt	960

(2) INFORMATION FOR SEQ ID NO:2971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1575000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2971:

Arg	Pro	Ala	Ile	Asn	Ile	Gln	Ala	Met	Ala	Leu	Phe	Lys	Cys	Met	Cys
1			5					10						15	
Ile	Phe	Leu	Val	Ser	Leu	Leu	Leu	Ala	Leu	Thr	Phe	Thr	Asn	Ala	Gln
			20					25					30		
Glu	Glu	Ser	Ser	His	Arg	Thr	Leu	Pro	Pro	Phe	Pro	Cys	Ile	Pro	Gly
			35				40					45			
Gln	Pro	Arg	Pro	Pro	Arg	Leu	Pro	Pro	Cys	Pro	Pro	Ala	Pro	Thr	Glu
			50			55					60				
Cys	Tyr	Thr	Ser	Leu	Ser	Gly	Met	Met	Pro	Cys	Ala	Asp	Phe	Leu	Thr
65				70					75					80	
His	Asn	Glu	Val	Pro	Pro	Met	Pro	Pro	Thr	Val	Ala	Cys	Cys	Gly	Trp
			85						90				95		
Ser	Gln	Val	Thr	Arg	His	Gln	Arg	Val	His	Leu	Ser	Met	Pro	Tyr	Arg
			100				105						110		
Gln	Arg														

(2) INFORMATION FOR SEQ ID NO:2972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1575001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2972:

Thr	Ser	Asn	Gln	His	Ser	Ser	His	Gly	Thr	Val	Gln	Val	His	Val	His
1			5					10					15		
Leu	Leu	Ser	Leu	Ala	Ser	Thr	Arg	Pro	His	Leu	His	Gln	Cys	Pro	Gly
			20				25					30			

Arg Ile Phe Thr Ser Asp Ser Pro Thr Val Pro Leu His Pro Arg Pro
35 40 45
Ala Thr Ala Pro Ala Val Ala Thr Leu Pro Ala Gly Thr Asn Arg Val
50 55 60
Leu His Val Ala Val Gly Asn Asp Ala Val Arg Gly Leu Pro His Pro
65 70 75 80
Gln Arg Gly Ala Thr Asp Ala Thr His Gly Arg Leu Leu Trp Met Val
85 90 95
Ser Gly His Ser Ser Pro Thr Arg Pro Ser Val Tyr Ala Ile Ser Ser
100 105 110
Thr Val Thr Ser Thr Ser Ser Thr Arg Arg Pro
115 120

(2) INFORMATION FOR SEQ ID NO:2973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2973:

Met Ala Leu Phe Lys Cys Met Cys Ile Phe Leu Val Ser Leu Leu Leu
1 5 10 15
Ala Leu Thr Phe Thr Asn Ala Gln Glu Glu Ser Ser His Arg Thr Leu
20 25 30
Pro Pro Phe Pro Cys Ile Pro Gly Gln Pro Arg Pro Pro Arg Leu Pro
35 40 45
Pro Cys Pro Pro Ala Pro Thr Glu Cys Tyr Thr Ser Leu Ser Gly Met
50 55 60
Met Pro Cys Ala Asp Phe Leu Thr His Asn Glu Val Pro Pro Met Pro
65 70 75 80
Pro Thr Val Ala Cys Cys Gly Trp Ser Gln Val Thr Arg His Gln Arg
85 90 95
Val His Leu Ser Met Pro Tyr Arg Gln Arg
100 105

(2) INFORMATION FOR SEQ ID NO:2974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..660
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2974:

aagaagaact	cggtgcgggt	catcctgcc	aacctggagg	tgaagtctgt	cgaccccgac	60
acgggcccgt	cgctgcccac	gaacaacgcc	ggggagatct	cgctccggag	tcaggccgtg	120
atgcagggct	actacaggaa	gaaggaggag	acggagcgca	ccatcgatgc	caagggggtg	180
ctccataccg	gcgacgtcgg	ctacatcgac	gacgacggcg	acgtgttcat	cgtcgaccgg	240
atcaaggagc	tcatacaagta	caagggcctc	caggtcgctc	ctgcccgagct	ggaggccatt	300
ctcctgtccc	accgctcggt	ccaagatgcg	gccgtcttcg	gcttcgccga	cgaggaggct	360
ggcgagatcc	cggtgtcggt	cggtgtcgcg	cggtgtggcg	cgtcggagag	cgaaGCgaN	420
catcatggcg	tacgtggcgg	gccgcgtggc	gtcgtacaag	aagctccggc	tgctgcagtt	480
cggtgacgtc	atccacaagt	cggtgtcagg	caagatcctg	cggcggcagc	tcgggggacga	540
gttcgttagc	aggacccaaa	cggcggcagc	ctagctctag	cgagagctag	acagtccaat	600
atgccagtta	catacttaca	ttgcacacgt	acatcaaacg	aataaatgtc	aagctattct	660

(2) INFORMATION FOR SEQ ID NO:2975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2975:

Lys Lys Asn Ser Val Gly Phe Ile Leu Pro Asn Leu Glu Val Lys Phe
1 5 10 15
Val Asp Pro Asp Thr Gly Arg Ser Leu Pro Lys Asn Thr Pro Gly Glu
20 25 30
Ile Cys Val Arg Ser Gln Ala Val Met Gln Gly Tyr Tyr Arg Lys Lys
35 40 45
Glu Glu Thr Glu Arg Thr Ile Asp Ala Lys Gly Trp Leu His Thr Gly
50 55 60
Asp Val Gly Tyr Ile Asp Asp Asp Gly Asp Val Phe Ile Val Asp Arg
65 70 75 80
Ile Lys Glu Leu Ile Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala Glu
85 90 95
Leu Glu Ala Ile Leu Leu Ser His Pro Ser Val Gln Asp Ala Ala Val
100 105 110
Phe Gly Leu Pro Asp Glu Glu Ala Gly Glu Ile Pro Val Ser Cys Val
115 120 125
Val Arg Arg Cys Gly Ala Ser Glu Ser Glu Ala Xaa His His Gly Val
130 135 140
Arg Gly Gly Pro Arg Gly Val Val Gln Glu Ala Pro Ala Ala Val
145 150 155 160
Arg Gly Arg His Pro Gln Val Gly Val Arg Gln Asp Pro Ala Ala Ala
165 170 175
Ala Pro Gly Arg Val Arg
180

(2) INFORMATION FOR SEQ ID NO:2976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..195
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2976:

Glu Glu Leu Gly Arg Val His Pro Ala Gln Pro Gly Gly Glu Val Arg
1 5 10 15
Arg Pro Arg His Gly Pro Val Ala Ala Gln Glu His Ala Arg Gly Asp
20 25 30
Leu Arg Pro Glu Ser Gly Arg Asp Ala Gly Leu Leu Gln Glu Glu Gly
35 40 45
Gly Asp Gly Ala His His Arg Cys Gln Gly Val Ala Pro Tyr Arg Arg
50 55 60
Arg Arg Leu His Arg Arg Arg Arg Arg Val His Arg Arg Pro Asp
65 70 75 80
Gln Gly Ala His Gln Val Gln Gly Leu Pro Gly Arg Ser Cys Arg Ala
85 90 95

Gly Gly His Ser Pro Val Pro Pro Val Gly Pro Arg Cys Gly Arg Leu
100 105 110
Arg Pro Ala Gly Arg Gly Gly Trp Arg Asp Pro Gly Val Val Arg Gly
115 120 125
Ala Ala Val Trp Arg Val Gly Glu Arg Ser Gly Xaa Ser Trp Arg Thr
130 135 140
Trp Arg Ala Ala Trp Arg Arg Thr Arg Ser Ser Gly Cys Cys Ser Ser
145 150 155 160
Trp Thr Ser Ser Thr Ser Arg Cys Gln Ala Arg Ser Cys Gly Gly Ser
165 170 175
Ser Gly Thr Ser Ser Leu Ala Gly Pro Lys Arg Arg Gln Pro Ser Ser
180 185 190
Ser Glu Ser
195

(2) INFORMATION FOR SEQ ID NO:2977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1575006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2977:

Met Gln Gly Tyr Tyr Arg Lys Lys Glu Glu Thr Glu Arg Thr Ile Asp
1 5 10 15
Ala Lys Gly Trp Leu His Thr Gly Asp Val Gly Tyr Ile Asp Asp Asp
20 25 30
Gly Asp Val Phe Ile Val Asp Arg Ile Lys Glu Leu Ile Lys Tyr Lys
35 40 45
Gly Phe Gln Val Ala Pro Ala Glu Leu Glu Ala Ile Leu Leu Ser His
50 55 60
Pro Ser Val Gln Asp Ala Ala Val Phe Gly Leu Pro Asp Glu Glu Ala
65 70 75 80
Gly Glu Ile Pro Val Ser Cys Val Val Arg Arg Cys Gly Ala Ser Glu
85 90 95
Ser Glu Ala Xaa His His Gly Val Arg Gly Gly Pro Arg Gly Val Val
100 105 110
Gln Glu Ala Pro Ala Ala Val Arg Gly Arg His Pro Gln Val Gly
115 120 125
Val Arg Gln Asp Pro Ala Ala Ala Pro Gly Arg Val Arg
130 135 140

(2) INFORMATION FOR SEQ ID NO:2978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..487

(D) OTHER INFORMATION: / Ceres Seq. ID 1575013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2978:

gactccacgc	cgccagtcac	gaccacgccg	cgctccgcgc	tggaaccctt	tagccgagcg	60
gagCaaggga	agaaatgggg	aagggtacgg	gcagcttcgg	caagcgccgg	aacaagacgc	120
acacgctctg	catccgctgc	ggccgcgcga	gcttccacct	ccagaagagc	acctgctctt	180
ctcgcggtta	ccccgccgcc	cgcatccgca	agtataactg	gagtggtgaa	gccatcagcg	240
gtaagacaac	tggtaccgga	aggatgaggt	acatgcgaca	cgttcctcgc	cgtttcaaga	300

gcaacttcag agaaggagact gaggtgccc caaagaaggg tgtgtgtgct gccaaactaag 360
tgtggtcttg ctgcatcaaa gaagtgtgact aacttgagac ttttgattg aattgtactt 420
ctgaactctt tagcaccataa tactatgctt gaattaattt cagacgcctt ggagaggtat 480
gatatgt

(2) INFORMATION FOR SEQ ID NO:2979:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1575014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2979:

Asp Ser Thr Pro Pro Val Thr Thr Thr Pro Arg Leu Arg Leu Glu Pro
1 5 10 15
Phe Ser Arg Ala Glu Gln Gly Lys Lys Trp Gly Arg Val Arg Ala Ala
20 25 30
Ser Ala Ser Ala Gly Thr Arg Arg Thr Arg Ser Ala Ser Ala Ala Ala
35 40 45
Ala Ala Ala Ser Thr Ser Arg Arg Ala Pro Ala Pro Ala Ala Thr
50 55 60
Pro Pro Pro Ala Ser Ala Ser Ile Thr Gly Val
65 70 75

(2) INFORMATION FOR SEQ ID NO:2980:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1575015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2980:

Thr Pro Arg Arg Gln Ser Arg Pro Arg Arg Ala Ser Ala Trp Asn Pro
1 5 10 15
Leu Ala Glu Arg Ser Lys Gly Arg Asn Gly Glu Gly Tyr Gly Gln Leu
20 25 30
Arg Gln Ala Pro Glu Gln Asp Ala His Ala Leu His Pro Leu Arg Pro
35 40 45
Pro Gln Leu Pro Pro Pro Glu Glu His Leu Leu Leu Arg Leu Pro
50 55 60
Arg Arg Pro His Pro Gln Val
65 70

(2) INFORMATION FOR SEQ ID NO:2981:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1575016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2981:

Met Gly Lys Gly Thr Gly Ser Phe Gly Lys Arg Arg Asn Lys Thr His

1	5	10	15
Thr Leu Cys Ile Arg Cys Gly Arg Arg Ser Phe His Leu Gln Lys Ser			
	20	25	30
Thr Cys Ser Ser Cys Gly Tyr Pro Ala Ala Arg Ile Arg Lys Tyr Asn			
	35	40	45
Trp Ser Val Lys Ala Ile Arg Arg Lys Thr Thr Gly Thr Gly Arg Met			
	50	55	60
Arg Tyr Met Arg His Val Pro Arg Arg Phe Lys Ser Asn Phe Arg Glu			
	65	70	75
Gly Thr Glu Ala Ala Pro Lys Lys Gly Val Ala Ala Asn			
	85	90	

(2) INFORMATION FOR SEQ ID NO:2982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..670
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2982:

gagcctcgaa	ccctaacc	caccacgtaa	ctccttgaa	ttaccgaaat	gccactcttc	60
ttctccaaat	tgcaccatt	ggtccccgc	gtccgcgcgc	tttccatcgc	cgcgccgaca	120
gcggcgcgang	sgaccctaag	ctgtctcgaa	tcggcgatga	gtctctcgcc	ctatcccccg	180
ccgagctgga	cgactatgcg	gcgctcctgc	gCctcaagct	ccgcctgtcg	ctcactctca	240
gcgcagbent	Tggagcctct	ccggcccggg	ccggggagcg	cgcggtgcga	gcgtggagg	300
Cgcgcgcgc	kgtgaagacg	gcgttcgact	tgaagatcga	gaagtacgag	gccgcgcgca	360
agattaaagat	catcaaggag	gtgcgcgcga	tgacggacct	gggtctgaag	gaggcgaaag	420
agctcgtgga	gaaggcgccc	atagtgtgtg	gcgcgggggt	gcctaaagag	gagggccgag	480
cgctcgcgcg	taagctcaag	gccgcgcgtg	ccgctgttgc	actcgagtga	tcccacgaag	540
gtgtgcgcctc	tttttttttt	gttctagtgt	ttcttagacg	atgcaacgta	tctttgcgcc	600
ttaatttgtt	tgtaatggaa	ttcaatagat	tggtataggg	tataaagagg	atgcaacgtc	660
taagaacact						

(2) INFORMATION FOR SEQ ID NO:2983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2983:

Ala Ser Asn Pro Asn Pro His His Val Thr Pro Trp Asn Tyr Arg Asn							
	5	10	15				
Ala Thr Leu Leu Leu Gln Ile Arg Thr Ile Gly Pro Pro Arg Pro Pro							
	20	25	30				
Pro Phe His Arg Arg Gly Asp Ser Arg Arg Xaa Asp Pro Lys Leu Ser							
	35	40	45				
Arg Ile Ala Asp Glu Leu Leu Ala Leu Ser Pro Ala Glu Leu Asp Asp							
	50	55	60				
Tyr Ala Ala Leu Leu Arg Leu Lys Leu Arg Leu Ser Leu Thr Ser Ser							
	65	70	75				
Ala Xaa Xaa Gly Ala Ser Pro Ala Gly Ala Gly Asp Ala Ala Ala Ala							
	85	90	95				
Ala Val Glu Ala Ala Ala Xaa Val Lys Thr Ala Phe Asp Leu Lys Ile							
	100	105	110				

Glu Lys Tyr Glu Ala Ala Ala Lys Ile Lys Ile Ile Lys Glu Val Arg
115 120 125
Ala Met Thr Asp Leu Gly Leu Lys Glu Ala Lys Glu Leu Val Glu Lys
130 135 140
Ala Pro Ile Val Val Arg Ala Gly Leu Pro Lys Glu Glu Ala Glu Ala
145 150 155 160
Leu Ala Ala Lys Leu Lys Ala Ala Gly Ala Val Ala Leu Glu
165 170 175

(2) INFORMATION FOR SEQ ID NO:2984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1575019

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2984:

Met Pro Leu Phe Phe Ser Lys Phe Ala Pro Leu Val Pro Arg Val Arg
1 5 10 15
Arg Leu Ser Ile Ala Ala Ala Thr Ala Gly Xaa Xaa Thr Leu Ser Cys
20 25 30
Leu Glu Ser Arg Met Ser Ser Ser Pro Tyr Pro Pro Pro Ser Trp Thr
35 40 45
Thr Met Arg Arg Ser Cys Ala Ser Ser Ser Ala Cys Arg Ser Pro Pro
50 55 60
Ala Gln Xaa Leu Glu Pro Leu Arg Pro Gly Pro Gly Thr Pro Arg Leu
65 70 75 80
Gln Pro Trp Arg Pro Pro Arg Xaa
85

(2) INFORMATION FOR SEQ ID NO:2985:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1109

(D) OTHER INFORMATION: / Ceres Seq. ID 1575027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2985:

gttcggttcc ttctcgtacc gagccgagg tagccagcca accgcccagc cakycacaa 60
cgatgaagcg cttcttccag ccagtgccca aggaacggct ccggtccaa aagcggctag 120
cgngtgctcg ctgaaccggg cgacggcccc acatcagcgc gtgcccgccac cgGccgttg 180
cggggatgta gaggggaggg ccaccaggga gccgttccaa ttctcgacgt ggaacgccc 240
cagcgtcgtc ctccggatga agagcgactg gccgtcttcc tcgacgtcgc tcgcccgcc 300
tgaccgcagc gtcatttggt tccaggaagt gcggatgcgc gcagctgggt ccaaaaggcc 360
acctaaaaac ccagtgtaac taaaagatga cacaagcttg tcacgggatg aaaagcaggt 420
agttctacgt gctttgtcag cttcaccttt caaagactac cgtgtctggt ggtctctttc 480
agattcaaaa tatgctggga castatgttt ataaagaaaa agtttgagcc taagaaggtg 540
tctttcaact tggatagaac atcttctaag catgaagcgc atggcggtgt tataattgcg 600
gaatttgat cattctcttt tactgaacac ttattctcca aacaattggt ggaaggagga 660
ggaaaatgca tttaaaagaa gacgtaagt ggacaagagg atgctagaat ttgttcaaca 720
cgtggataaa cccttaactc ggtgtgggga cttgaatgct agtcatgaag aatcgacgt 780
cagccatcct gatcttctta gcagcgctaa gctgaatgga tacacccac ccaataaaga 840
ggactgtgga cagccagatg tcaccccagc agagagacgg cgttttgcca acatattatt 900
ccaaggaaa cgtgtagatg cttacaggca cctgcacaaa gaaaaggaca tagacggtg 960
cttctcttg tccggtcatc caattggcaa gtaccgagga aagagaatga ggtatcgacta 1020

cttcctgtgt tcggaacagt taaaggacag aatgatttca tgtgaaatgc atggccgtgg 1080
cattgaattg gatggatttt atggaagtg

(2) INFORMATION FOR SEQ ID NO:2986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2986:

Phe	Gly	Ser	Phe	Ser	Tyr	Arg	Ala	Ala	Gly	Ser	Gln	Pro	Thr	Ala	Asp	
1				5					10					15		
Ala	Xaa	Thr	Ser	Asp	Glu	Ala	Leu	Leu	Pro	Ala	Ser	Ala	Gln	Gly	Arg	
			20					25					30			
Leu	Pro	Val	Gln	Glu	Ala	Ala	Ser	Xaa	Val	Leu	Leu	Asn	Arg	Ala	Thr	
		35					40					45				
Ala	Pro	His	Gln	Pro	Val	Pro	Pro	Pro	Ala	Pro	Gly	Gly	Asp	Val	Glu	
		50				55					60					
Gly	Arg	Pro	Thr	Glu	Glu	Pro	Phe	Lys	Phe	Leu	Thr	Trp	Asn	Ala	Asn	
		65			70					75				80		
Ser	Leu	Leu	Leu	Arg	Met	Lys	Ser	Asp	Trp	Pro	Ala	Phe	Ser	Gln	Leu	
			85					90					95			
Val	Ala	Arg	Leu	Asp	Pro	Asp	Val	Ile	Cys	Val	Gln	Glu	Val	Arg	Met	
			100					105					110			
Pro	Ala	Ala	Gly	Ser	Lys	Gly	Ala	Pro	Lys	Asn	Pro	Ser	Glu	Leu	Lys	
			115				120					125				
Asp	Asp	Thr	Ser	Leu	Ser	Arg	Asp	Glu	Lys	Gln	Val	Val	Leu	Arg	Ala	
		130					135				140					
Leu	Ser	Ala	Ser	Pro	Phe	Lys	Asp	Tyr	Arg	Val	Trp	Trp	Ser	Leu	Ser	
		145			150					155				160		
Asp	Ser	Lys	Tyr	Ala	Gly	Thr	Xaa	Cys	Leu							
				165					170							

(2) INFORMATION FOR SEQ ID NO:2987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2987:

Met	Lys	Ser	Asp	Trp	Pro	Ala	Phe	Ser	Gln	Leu	Val	Ala	Arg	Leu	Asp	
1				5					10					15		
Pro	Asp	Val	Ile	Cys	Val	Gln	Glu	Val	Arg	Met	Pro	Ala	Ala	Gly	Ser	
			20					25					30			
Lys	Gly	Ala	Pro	Lys	Asn	Pro	Ser	Glu	Leu	Lys	Asp	Asp	Thr	Ser	Leu	
		35					40					45				
Ser	Arg	Asp	Glu	Lys	Gln	Val	Val	Leu	Arg	Ala	Leu	Ser	Ala	Ser	Pro	
		50				55					60					
Phe	Lys	Asp	Tyr	Arg	Val	Trp	Trp	Ser	Leu	Ser	Asp	Ser	Lys	Tyr	Ala	
		65			70					75				80		
Gly	Thr	Xaa	Cys	Leu												
				85												

(2) INFORMATION FOR SEQ ID NO:2988:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..136
(D) OTHER INFORMATION: / Ceres Seq. ID 1575030
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2988:
Met Leu Glu Phe Val Gln His Val Asp Lys Pro Leu Ile Trp Cys Gly
1 5 10 15
Asp Leu Asn Val Ser His Glu Glu Ile Asp Val Ser His Pro Asp Phe
20 25 30
Phe Ser Ser Ala Lys Leu Asn Gly Tyr Thr Pro Pro Asn Lys Glu Asp
35 40 45
Cys Gly Gln Pro Gly Phe Thr Pro Ala Glu Arg Arg Phe Gly Asn
50 55 60
Ile Leu Phe Gln Gly Lys Leu Val Asp Ala Tyr Arg His Leu His Lys
65 70 75 80
Glu Lys Asp Ile Asp Gly Gly Phe Ser Trp Ser Gly His Pro Ile Gly
85 90 95
Lys Tyr Arg Gly Lys Arg Met Arg Ile Asp Tyr Phe Leu Val Ser Glu
100 105 110
Gln Leu Lys Asp Arg Ile Val Ser Cys Glu Met His Gly Arg Gly Ile
115 120 125
Glu Leu Asp Gly Phe Tyr Gly Ser
130 135
(2) INFORMATION FOR SEQ ID NO:2989:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..316
(D) OTHER INFORMATION: / Ceres Seq. ID 1575038
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2989:
atctctcact caaccgcgcg cgaagCacac gagatagagc tgctagaggc tagagcagta 60
gagctagaag aggaggacaa caaccatgga tgcgcggcgc gcgcgcgcgc cgaggggaga 120
tacgaagaag aagaagatgc ttgccaccct ggtgggctgc aactacgcgc gcacgcgcta 180
cgagctgcag ggctgcatca acgacgtcca cgcctgcgc gccgtactcc tcgcccgctt 240
cggCttcgcg cctgcgcagc tcaccgtgct caccgcacgc cagcacgggc gcggcggcgc 300
cggcggcgtg ctcccg
(2) INFORMATION FOR SEQ ID NO:2990:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..105
(D) OTHER INFORMATION: / Ceres Seq. ID 1575039
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2990:
Ile Ser His Ser Thr Ala Arg Glu Ala His Glu Ile Glu Leu Leu Glu
1 5 10 15

Ala Arg Ala Val Glu Leu Glu Glu Glu Asp Asn Asn His Gly Cys Gly
20 25 30
Gly Gly Gly Gly Glu Gly Arg Tyr Glu Glu Glu Glu Asp Ala Cys
35 40 45
His Pro Gly Gly Leu Gln Leu Arg Arg His Ala Val Arg Ala Ala Gly
50 55 60
Leu His Gln Arg Arg Pro Arg His Ala Arg Pro Pro Arg Pro Leu
65 70 75 80
Arg Leu Arg Ala Cys Arg Arg His Arg Ala His Arg Arg Pro Ala Arg
85 90 95
Ala Arg Arg Arg Arg Arg Ala Pro
100 105

(2) INFORMATION FOR SEQ ID NO:2991:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..77
(D) OTHER INFORMATION: / Ceres Seq. ID 1575040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2991:

Met Asp Ala Ala Ala Ala Ala Ala Arg Gly Asp Thr Lys Lys Lys
1 5 10 15
Lys Met Leu Ala Thr Leu Val Gly Cys Asn Tyr Ala Gly Thr Pro Tyr
20 25 30
Glu Leu Gln Gly Cys Ile Asn Asp Val His Ala Met Arg Ala Val Leu
35 40 45
Leu Ala Arg Phe Gly Phe Ala Pro Ala Asp Val Thr Val Leu Thr Asp
50 55 60
Asp Gln His Gly Arg Gly Gly Gly Gly Val Leu Pro
65 70 75

(2) INFORMATION FOR SEQ ID NO:2992:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..75
(D) OTHER INFORMATION: / Ceres Seq. ID 1575041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2992:

Met Arg Arg Arg Arg Arg Arg Gly Glu Ile Arg Arg Arg Arg
1 5 10 15
Cys Leu Pro Pro Trp Trp Ala Ala Thr Thr Pro Ala Arg Arg Thr Ser
20 25 30
Cys Arg Ala Ala Ser Thr Thr Ser Thr Pro Cys Ala Pro Ser Ser Ser
35 40 45
Pro Ala Ser Ala Ser Arg Leu Pro Thr Ser Pro Cys Ser Pro Thr Thr
50 55 60
Ser Thr Gly Ala Ala Ala Ala Ala Cys Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:2993:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 928 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..928
(D) OTHER INFORMATION: / Ceres Seq. ID 1575056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2993:

agggccttgc	attttttctc	cgcgtttg	tcctccgatt	acgttccctc	gctactcgct	60
agtcgccact	tctcccggtt	cccccccg	tctctcttct	cgttgcgacg	actcggcgat	120
ccctgcgcgc	ccccgtctcc	cgcctccgc	cgcagggtgc	ccagggtgtc	gcggggccct	180
tcgcgcggca	tgagcaccac	acaggagggt	actgagaact	acgcaaatcc	taagacatgc	240
ttcttccatg	ttctcttcaa	ggcatcggca	ttggcggtct	acatactgtc	caactgttct	300
gtgaacaact	tcgtcatcat	ctttgtcatc	actgtgctcc	tcgcagcact	tgactctctg	360
gtcgtgaaga	atgtcagcgg	aaggatactg	gttgggctgc	gggtgtggaa	tgagattaac	420
gatgaggggg	agagtgtctg	gaagtttgag	tgccttgatg	gagagctccc	tggttaggat	480
gaataagaag	gactcatggc	tgctctgggt	gactctatat	ttgactcgcg	ctgcactggat	540
tatacttggg	atattctcgc	tcatacagact	tcaagctgat	tacottctcg	ttgttggagt	600
ttgcttgagc	ctcagcattg	caaatawat	kgstrwcwsc	rwwtgcawtm	wagatkcsc	660
gaagaacatc	caggattgga	caaggaaatg	actctatca	ggtagtgtca	gacgcactct	720
gcagtcagca	tttggtgtct	gaacaataac	ctatgacctt	gttatcagtg	tagtgctgta	780
taattttcac	ataacatgat	tggttactag	agtgcgctcg	tttttttttt	tggtggctat	840
gtgcactctt	ctaggcagag	tcggaagaac	atcttcagag	ccgtgtatca	actcgaatga	900
taatgcagtt	tgaataaaat	ctctcttt				

(2) INFORMATION FOR SEQ ID NO:2994:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..158
(D) OTHER INFORMATION: / Ceres Seq. ID 1575057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2994:

Arg	Ala	Leu	His	Phe	Phe	Leu	Arg	Phe	Ala	Phe	Pro	Asp	Tyr	Val	Pro
1			5						10				15		
Ser	Leu	Leu	Ala	Ser	Arg	His	Phe	Ser	Arg	Cys	Pro	Pro	Ala	Ser	Leu
			20					25					30		
Phe	Ser	Leu	Arg	Arg	Leu	Gly	Asp	Pro	Cys	Arg	Pro	Pro	Ser	Pro	Ala
			35				40					45			
Pro	Arg	Arg	Gln	Val	Pro	Arg	Leu	Ser	Pro	Gly	Pro	Ser	Pro	Ala	Met
			50				55				60				
Ser	Thr	Gln	Gln	Glu	Val	Thr	Glu	Asn	Tyr	Ala	Asn	Pro	Lys	Thr	Cys
65					70				75						80
Phe	Phe	His	Val	Leu	Phe	Lys	Ala	Ser	Ala	Leu	Ala	Phe	Tyr	Ile	Leu
			85				90						95		
Ser	Thr	Leu	Phe	Val	Asn	Asn	Phe	Val	Ile	Phe	Val	Ile	Thr	Val	
			100				105						110		
Leu	Leu	Ala	Ala	Leu	Asp	Phe	Trp	Val	Val	Lys	Asn	Val	Ser	Gly	Arg
			115				120					125			
Ile	Leu	Val	Gly	Leu	Arg	Trp	Trp	Asn	Glu	Ile	Asn	Asp	Glu	Gly	Glu
			130				135					140			
Ser	Val	Trp	Lys	Phe	Glu	Cys	Leu	Asp	Gly	Glu	Ser	Pro	Gly		
145					150					155					

(2) INFORMATION FOR SEQ ID NO:2995:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..123
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575058
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2995:
Met Ser Ala Glu Gly Tyr Trp Leu Gly Cys Gly Gly Gly Met Arg Leu
1 5 10 15
Thr Met Arg Glu Arg Val Ser Gly Ser Leu Ser Ala Leu Met Glu Ser
 20 25 30
Pro Leu Ala Arg Met Asn Lys Lys Asp Ser Trp Leu Phe Trp Trp Thr
 35 40 45
Leu Tyr Leu Thr Ala Ala Ala Trp Ile Ile Leu Gly Ile Phe Ser Leu
50 55 60
Ile Arg Leu Gln Ala Asp Tyr Leu Leu Val Val Gly Val Cys Leu Ser
65 70 75 80
Leu Ser Ile Ala Asn Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Asp Xaa
 85 90 95
Lys Lys Asn Ile Gln Asp Trp Thr Arg Asn Ala Leu Leu Ser Gly Ser
100 105 110
Val Arg Ser His Leu Gln Ser Ala Phe Gly Val
115 120

(2) INFORMATION FOR SEQ ID NO:2996:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..110
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575059
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2996:
Met Arg Leu Thr Met Arg Glu Arg Val Ser Gly Ser Leu Ser Ala Leu
1 5 10 15
Met Glu Ser Pro Leu Ala Arg Met Asn Lys Lys Asp Ser Trp Leu Phe
 20 25 30
Trp Trp Thr Leu Tyr Leu Thr Ala Ala Ala Trp Ile Ile Leu Gly Ile
 35 40 45
Phe Ser Leu Ile Arg Leu Gln Ala Asp Tyr Leu Leu Val Val Gly Val
50 55 60
Cys Leu Ser Leu Ser Ile Ala Asn Xaa Xaa Xaa Xaa Xaa Cys Xaa
65 70 75 80
Xaa Asp Xaa Lys Lys Asn Ile Gln Asp Trp Thr Arg Asn Ala Leu Leu
 85 90 95
Ser Gly Ser Val Arg Ser His Leu Gln Ser Ala Phe Gly Val
100 105 110

(2) INFORMATION FOR SEQ ID NO:2997:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 887 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..887
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575067
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2997:
ataaataact tatgaggcca aactaaagar ggcagggcag gcgaatcgaa ggaaaagtag

tcaggagagg cgtttccctc gcaatcgacc atcacagatc aaatcgctgc aactagctag 120
ggtttcgctc cctcatctct cgtcgatcca tcatggcggt ccgaggggcga aaacaagagg 180
atgatcacgc tcaggagctc cgacttagag gagttcgagg tggaggaaagc ggtggccatg 240
gagtcgcaga ctctccgcga catgatcgag gacgactgcd ccgacaaagg catcccgctc 300
cccaacgtca actccaggat cctctctaa gtcacgaGg tactgcaaca gtacagctcca 360
cgccgcccgc aaaccgcgtg actccgctgc ctccgagggc ggcgaggacc tcaagagctg 420
ggacgcgaag tctgtcaagg tggaccaGgc tacgctcttc gacctcatcc tgggtgccaa 480
ctatctgaac atcaagggat tgctggacct gacctgccag acggttgctg acatgatcaa 540
gggcaagact ccggaggaga tccgcaagac attcagcatc aagaacgact tcaccaagaa 600
ggaggaggat gagatcgca tggagaacca gtgggccttc gagtgattgt tctcttctct 660
tccctgggtga tgggtgggtg tcttttaciaa gaacagatgg atgtctgcac tgcactctac 720
aatgctagt c tatctactta cgaataagta gtgaataagt agtataatg tctgtatggt 780
tgtatccctt tttgattgg atgtatgtca agctgggtgg tgctagtctg tctgtctgga 840
ctgttacta gttaatatct cataatacat atataaagt ggaatctt

(2) INFORMATION FOR SEQ ID NO:2998:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1575068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2998:

Met Ala Ser Glu Gly Glu Asn Lys Arg Met Ile Thr Leu Arg Ser Ser
1 5 10 15
Asp Leu Glu Glu Phe Glu Val Glu Glu Ala Val Ala Met Glu Ser Gln
20 25 30
Thr Leu Arg His Met Ile Glu Asp Asp Cys Xaa Asp Asn Gly Ile Pro
35 40 45
Leu Pro Asn Val Asn Ser Arg Ile Leu Ser Lys Val Ile Glu Val Leu
50 55 60
Gln Gln Ser Arg Pro Arg Arg Arg Gln Thr Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:2999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1575069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2999:

Met Ile Thr Leu Arg Ser Ser Asp Leu Glu Glu Phe Glu Val Glu Glu
1 5 10 15
Ala Val Ala Met Glu Ser Gln Thr Leu Arg His Met Ile Glu Asp Asp
20 25 30
Cys Xaa Asp Asn Gly Ile Pro Leu Pro Asn Val Asn Ser Arg Ile Leu
35 40 45
Ser Lys Val Ile Glu Val Leu Gln Gln Ser Arg Pro Arg Arg Arg Gln
50 55 60
Thr Arg
65

(2) INFORMATION FOR SEQ ID NO:3000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..47
(D) OTHER INFORMATION: / Ceres Seq. ID 1575070
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3000:
Met Glu Ser Gln Thr Leu Arg His Met Ile Glu Asp Asp Cys Xaa Asp
1 5 10 15
Asn Gly Ile Pro Leu Pro Asn Val Asn Ser Arg Ile Leu Ser Lys Val
20 25 30
Ile Glu Val Leu Gln Gln Ser Arg Pro Arg Arg Arg Gln Thr Arg
35 40 45

(2) INFORMATION FOR SEQ ID NO:3001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..723
(D) OTHER INFORMATION: / Ceres Seq. ID 1575105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3001:

gcgggtttgcm ggcactvrca ggargagaga ccganarcrc ggcgcaggarg gcgtcgagca 60
ctgavgwqcn ghircggcgg cgccgagctg gacggaggag gggaccacaa gaagcggcgg 120
ctgaccgacg agcaggtaga gatgctggar ctgagcttcc gggaggagcg gaagctggag 180
accggccgga aggtgcacct ggccgcccag ctccggctcg accccaagca ggtcgcgctc 240
tggttcacga accgcggcgc ccgccacaag agcaagctgc tcgaggagga gttcgcccaag 300
ctcaagcagg cacacgacgc cgccatcctc cacaatgcc accttgagaa cgaggtgatg 360
agRgctgaag gacaagctgg tgctcgccga ggaggagGct gacgcgttcc agatccgcgg 420
gcaaccacgc ggtctccggt gacggcggag acgtcatggc ccgtgccctc tgcagcggga 480
gcccagctc atcgttctcg actggcactc gccagcagcc cggaggaggc ggccggcggc 540
gcgatcactc gggggacgac gacctgctct atgttctcga ctatgcctac gctgacagca 600
gcgtggctga gtggtttagc ctgtatggac tgatgtaatc gatggtatgg tatgccatcg 660
tcgtcggcag attaattcta gctagctact catcgtagcg tgctattgct gtgsgaatt 720
gct

(2) INFORMATION FOR SEQ ID NO:3002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..133
(D) OTHER INFORMATION: / Ceres Seq. ID 1575106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3002:

Ala Val Cys Xaa His Xaa Gln Xaa Glu Arg Pro Xaa Xaa Arg Arg Arg
1 5 10 15
Xaa Arg Arg Ala Ala Xaa Xaa Xaa Xaa Gly Gly Gly Glu Leu Asp Gly
20 25 30
Gly Gly Asp His Lys Lys Arg Arg Leu Thr Asp Glu Gln Val Glu Met
35 40 45
Leu Xaa Leu Ser Phe Arg Glu Glu Arg Lys Leu Glu Thr Gly Arg Lys
50 55 60
Val His Leu Ala Ala Glu Leu Gly Leu Asp Pro Lys Gln Val Ala Val

65 70 75 80
Trp Phe Gln Asn Arg Arg Ala Arg His Lys Ser Lys Leu Leu Glu Glu
85 90 95
Glu Phe Ala Lys Leu Lys Gln Ala His Asp Ala Ala Ile Leu His Lys
100 105 110
Cys His Leu Glu Asn Glu Val Met Xaa Ala Glu Gly Gln Ala Gly Ala
115 120 125
Arg Arg Gly Gly Gly
130

(2) INFORMATION FOR SEQ ID NO:3003:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1575107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3003:

Gly Leu Xaa Ala Xaa Xaa Gly Xaa Glu Thr Xaa Xaa Xaa Ala Gln Xaa
1 5 10 15
Ala Ser Ser Ser Xaa Xaa Xaa Xaa Arg Arg Arg Arg Ala Gly Arg Arg
20 25 30
Arg Gly Pro Gln Glu Ala Ala Ala Asp Arg Arg Ala Gly Arg Asp Ala
35 40 45
Gly Xaa Glu Leu Pro Gly Gly Ala Glu Ala Gly Asp Arg Pro Glu Gly
50 55 60
Ala Pro Gly Arg Arg Ala Arg Ala Arg Pro Gln Ala Gly Arg Arg Leu
65 70 75 80
Val Pro Glu Pro Pro Arg Pro Pro Gln Glu Gln Ala Ala Arg Gly Gly
85 90 95
Val Arg Gln Ala Gln Ala Gly Thr Arg Arg Arg His Pro Pro Gln Met
100 105 110
Pro Pro

(2) INFORMATION FOR SEQ ID NO:3004:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1575108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3004:

Met Leu Xaa Leu Ser Phe Arg Glu Glu Arg Lys Leu Glu Thr Gly Arg
1 5 10 15
Lys Val His Leu Ala Ala Glu Leu Gly Leu Asp Pro Lys Gln Val Ala
20 25 30
Val Trp Phe Gln Asn Arg Arg Ala Arg His Lys Ser Lys Leu Leu Glu
35 40 45
Glu Glu Phe Ala Lys Leu Lys Gln Ala His Asp Ala Ala Ile Leu His
50 55 60
Lys Cys His Leu Glu Asn Glu Val Met Xaa Ala Glu Gly Gln Ala Gly
65 70 75 80
Ala Arg Arg Gly Gly Gly
85

(2) INFORMATION FOR SEQ ID NO:3005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 770 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..770
(D) OTHER INFORMATION: / Ceres Seq. ID 1575124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3005:

aatctccaggt	cgtgtttgtg	cgggaagaga	cagacacgca	aacgagaga	ctctgagagag	60
attccgcgcg	caccacgcgcg	ctcagatcgc	cgcgcgcagt	cgcgcagatc	ctctcgcgcg	120
cttcccaagg	caacaccttg	ccttccctct	tctctccctt	ctttgtotata	tctgtccacgc	180
ctgtccctcg	cgcgcactcg	caccacagggc	gtctccgcga	gggcctcttc	ctctctctca	240
ctcccgagct	ctctctctgg	ttccgcgatt	gaggattctg	ctcaagaagc	ggtgtccgat	300
aaccctcggtg	ctcatctact	taagtcatgt	tgtctcattt	ccatcggaagt	gaagtcacac	360
ttcaacggag	tctgtgtgca	ggcccacatg	atctgagctg	caactctcgg	agctcaagaa	420
ccacaactac	aaaaagttatt	agaaagatcg	actggcagct	ctactctgtc	taacgttttt	480
atcgtgtgaa	acactgcgttg	acgcgtgcac	gataccgtga	agctgtgtac	gaacggggga	540
ctctgctatg	atgtctctgcg	actcggatat	caacattgac	aactcatgac	aagctatgtt	600
gtccaaagat	tggcgcagag	ttggcgacga	ctgtattgag	ttctcttttt	taacctgtgc	660
gatgacaaac	actgtgtgtca	ttttcacatt	ttcgtttgtg	actccgatta	aatcattgaa	720
tttgaccacc	gtatatatga	attattcgtg	aaaaaagaag	gaaccagctc		

(2) INFORMATION FOR SEQ ID NO:3006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..182
(D) OTHER INFORMATION: / Ceres Seq. ID 1575125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3006:

[illegible]

(2) INFORMATION FOR SEQ ID NO:3007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3007:

Met Pro Pro Pro Gln Ser Gly Met Thr Leu Cys Arg Leu Pro Lys Ala
1 5 10 15
Thr Leu Gly Leu Pro Leu Ser Leu Pro Ser Leu Leu Tyr Arg Pro Ser
20 25 30
Leu Ser Leu Ala Ala Arg Arg Thr Lys Ala Val Ser Ala Arg Ala Ser
35 40 45
Ser Ser Ser Pro Ser Pro Asp Ser Ser Phe Gly Ser Arg Met Glu Asp
50 55 60
Ser Val Lys Lys Thr Val Ala Asp Asn Pro Val Val Ile Tyr Ser Lys
65 70 75 80
Ser Trp Cys Ser Tyr Ser Met Glu Val Lys Ser Leu Phe Lys Arg Ile
85 90 95
Gly Val Gln Pro His Val Ile Glu Leu Asp Asn Leu Gly Ala Gln Gly
100 105 110
Pro Gln Leu Gln Lys Val Leu Glu Arg Leu Thr Gly Gln Ser Thr Val
115 120 125
Pro Asn Val Phe Ile Gly Gly Lys His Val Gly Arg Cys Thr Asp Thr
130 135 140
Val Lys Ala Val Ser Gln Gly Gly Ala Ser
145 150

(2) INFORMATION FOR SEQ ID NO:3008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3008:

Met Thr Leu Cys Arg Leu Pro Lys Ala Thr Leu Gly Leu Pro Leu Ser
1 5 10 15
Leu Pro Ser Leu Leu Tyr Arg Pro Ser Leu Ser Leu Ala Ala Arg Arg
20 25 30
Thr Lys Ala Val Ser Ala Arg Ala Ser Ser Ser Ser Pro Ser Pro Asp
35 40 45
Ser Ser Phe Gly Ser Arg Met Glu Asp Ser Val Lys Lys Thr Val Ala
50 55 60
Asp Asn Pro Val Val Ile Tyr Ser Lys Ser Trp Cys Ser Tyr Ser Met
65 70 75 80
Glu Val Lys Ser Leu Phe Lys Arg Ile Gly Val Gln Pro His Val Ile
85 90 95
Glu Leu Asp Asn Leu Gly Ala Gln Gly Pro Gln Leu Gln Lys Val Leu
100 105 110
Glu Arg Leu Thr Gly Gln Ser Thr Val Pro Asn Val Phe Ile Gly Gly
115 120 125
Lys His Val Gly Arg Cys Thr Asp Thr Val Lys Ala Val Ser Gln Gly

130 135 140
Gly Ala Ser
145

(2) INFORMATION FOR SEQ ID NO:3009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..685

(D) OTHER INFORMATION: / Ceres Seq. ID 1575143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3009:

ccatcatcatg	ctccaggacg	cagcgaccgg	tattatttat	gtgctgggtt	agctagtcac	60
cattatagca	aacttagcta	gctagctacc	tgcctataat	ggagcgggag	caggagttgg	120
accttgagct	caccctcctc	ccctccgcct	gggctacgca	ggaagaggcg	cccggtctct	180
tcctctgcac	gtactgcggc	cgcaagttct	gcacctccca	ggcgctcggc	ggccaccaga	240
acgcgcacaa	gtacgagcgc	gccctagcca	agcgcccgcc	ggacatcgcc	gctgccttgc	300
gtaagCacgg	tggtcccggtg	acgcgcgctg	gccagttcca	cgccggggcc	agccccagcg	360
ccaggggcac	tgccggagtc	gctggatctg	aacgacctga	tgctgggagg	gagagggcac	420
tgccgggtgga	cgagctgcaa	ggtgctccgg	cgccctggca	atctggcgcc	cCtgcctcac	480
caggtcgagc	gcacagagga	gctggatttg	tcctctggcc	tgtgattatt	gcgtttctcc	540
gatccatgta	ccacttccat	ctccttggtc	ttgcgtattt	aaattgctat	atacatgcac	600
gtatatataa	tgtgattgct	ttctctcccc	agaggccaga	gcgcccttaa	attcgctcagt	660
gtgtgctact	tgacggttac	tggtgc				

(2) INFORMATION FOR SEQ ID NO:3010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..183

(D) OTHER INFORMATION: / Ceres Seq. ID 1575144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3010:

Met	Glu	Arg	Glu	Gln	Glu	Leu	Asp	Leu	Glu	Leu	Thr	Leu	Leu	Pro	Ser
1			5					10				15			
Ala	Trp	Ala	Thr	Gln	Glu	Glu	Ala	Pro	Gly	Phe	Phe	Leu	Cys	Thr	Tyr
			20					25					30		
Cys	Gly	Arg	Lys	Phe	Cys	Thr	Ser	Gln	Ala	Leu	Gly	Gly	His	Gln	Asn
			35					40				45			
Ala	His	Lys	Tyr	Glu	Arg	Ala	Leu	Ala	Lys	Arg	Arg	Arg	Asp	Ile	Ala
			50					55				60			
Ala	Ala	Leu	Arg	Lys	His	Gly	Val	Pro	Val	Thr	Arg	Ala	Gly	Gln	Phe
			65					70				75			80
His	Ala	Gly	Ala	Ser	Pro	Ser	Ala	Arg	Ala	Thr	Ala	Gly	Val	Ala	Gly
			85					90					95		
Ser	Glu	Arg	Pro	Asp	Gly	Arg	Glu	Arg	Pro	Val	Ala	Val	Asp	Glu	
			100					105				110			
Leu	Gln	Gly	Ala	Pro	Ala	Pro	Trp	Gln	Ser	Gly	Gly	Pro	Ala	Pro	Pro
			115					120				125			
Gly	Arg	Ala	His	Arg	Gly	Ala	Gly	Phe	Val	Pro	Arg	Pro	Val	Ile	Ile
			130					135				140			
Ala	Phe	Ser	Arg	Ser	Met	Tyr	His	Phe	His	Leu	Gly	Phe	Ala	Tyr	
			145					150				155			160
Leu	Asn	Cys	Tyr	Ile	His	Ala	Cys	Ile	Tyr	Asn	Val	Ile	Ala	Phe	Leu
			165					170					175		

Pro Gln Arg Pro Glu Arg Leu
180

(2) INFORMATION FOR SEQ ID NO:3011:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 788 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..788
(D) OTHER INFORMATION: / Ceres Seq. ID 1575163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3011:

atctccgaaa	aaaaaacgcg	aacgcagAAC	gccgccggcc	cgctcgtgac	tcgtgtttcc	60
cttcctccac	ttgccttcgt	gttcgtgatt	cgtgatttcc	ccgccggaaa	gccgagggag	120
agggagcgat	atgggggttcg	tcggagacac	gatggagtcg	atccgctcca	tcagatCcg	180
ccaagtgtc	atgcagatca	tcagcctcgg	tatgattgtt	acctctgcat	taatcatatg	240
gaagggtttg	atagttttca	cggggagcga	gtcaccagtt	gtagtgtgtc	tctcgggtag	300
catggagcct	ggatttaaaa	ggggtgatat	cctgtttttg	catatgagca	aagatcccat	360
tcgcacagga	gaaatagtgt	ttttcaatat	cgatggctgt	gagattccaa	ttgtccaccg	420
agtgattaa	gtccatgaac	gtcaggacac	tcagaagtgt	gacatcctca	ccaaaggtga	480
caataatttt	ggggatgacc	gactattata	tgacatggc	cagctttggc	tcacagcaaa	540
ccacattatg	gggcgtgcgg	tgggctaact	tccatagtgt	ggctgggtta	caattatcat	600
gactgagaaa	ccatttatta	agtaacctgt	gattggcgca	ctgggcttgc	tggtcataaac	660
gtcgaaagat	tagtgcgtgc	aaacttcagg	gccatgtaga	tttgtctctt	atggcgcaac	720
agcagagatc	actggctttg	tggcgtttga	gagatgccgc	tatgttgcgc	catgtatcaa	780
acgagrag						

(2) INFORMATION FOR SEQ ID NO:3012:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..180
(D) OTHER INFORMATION: / Ceres Seq. ID 1575164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3012:

Met	Gly	Phe	Val	Gly	Asp	Thr	Met	Glu	Ser	Ile	Arg	Ser	Met	Gln	Ile
1				5					10					15	
Arg	Gln	Val	Leu	Met	Gln	Ile	Ile	Ser	Leu	Gly	Met	Ile	Val	Thr	Ser
			20					25					30		
Ala	Leu	Ile	Ile	Trp	Lys	Gly	Leu	Ile	Val	Phe	Thr	Gly	Ser	Glu	Ser
			35				40					45			
Pro	Val	Val	Val	Val	Leu	Ser	Gly	Ser	Met	Glu	Pro	Gly	Phe	Lys	Arg
			50			55					60				
Gly	Asp	Ile	Leu	Phe	Leu	His	Met	Ser	Lys	Asp	Pro	Ile	Arg	Thr	Gly
65					70				75					80	
Glu	Ile	Val	Val	Phe	Asn	Ile	Asp	Gly	Arg	Glu	Ile	Pro	Ile	Val	His
			85					90					95		
Arg	Val	Ile	Lys	Val	His	Glu	Arg	Gln	Asp	Thr	Ala	Glu	Val	Asp	Ile
			100					105					110		
Leu	Thr	Lys	Gly	Asp	Asn	Asn	Phe	Gly	Asp	Asp	Arg	Leu	Leu	Tyr	Ala
		115					120					125			
His	Gly	Gln	Leu	Trp	Leu	Gln	Gln	His	His	Ile	Met	Gly	Arg	Ala	Val
		130					135				140				
Gly	Tyr	Leu	Pro	Tyr	Val	Gly	Trp	Val	Thr	Ile	Ile	Met	Thr	Glu	Lys
		145			150				155					160	
Pro	Phe	Ile	Lys	Tyr	Leu	Leu	Ile	Gly	Ala	Leu	Gly	Leu	Leu	Val	Ile

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(2) INFORMATION FOR SEQ ID NO:3014:
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 167 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: peptide
  (ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..167
      (D) OTHER INFORMATION: / Ceres Seq. ID 1575166
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3014:
Met  Gln  Ile  Arg  Gln  Val  Leu  Met  Gln  Ile  Ile  Ser  Leu  Gly  Met  Ile
 1          5          10          15
Val  Thr  Ser  Ala  Leu  Ile  Ile  Trp  Lys  Gly  Leu  Ile  Val  Phe  Thr  Gly
          20          25          30
Ser  Glu  Ser  Pro  Val  Val  Val  Leu  Ser  Gly  Ser  Met  Glu  Pro  Gly
          35          40          45
Phe  Lys  Arg  Gly  Asp  Ile  Leu  Phe  Leu  His  Met  Ser  Lys  Asp  Pro  Ile
          50          55          60
Arg  Thr  Gly  Glu  Ile  Val  Val  Phe  Asn  Ile  Asp  Gly  Arg  Glu  Ile  Pro
 65          70          75          80
Ile  Val  His  Arg  Val  Ile  Lys  Val  His  Glu  Arg  Gln  Asp  Thr  Ala  Glu
          85          90          95

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Val Asp Ile Leu Thr Lys Gly Asp Asn Asn Phe Gly Asp Asp Arg Leu
100 105 110
Leu Tyr Ala His Gly Gln Leu Trp Leu Gln Gln His His Ile Met Gly
115 120 125
Arg Ala Val Gly Tyr Leu Pro Tyr Val Gly Trp Val Thr Ile Ile Met
130 135 140
Thr Glu Lys Pro Phe Ile Lys Tyr Leu Leu Ile Gly Ala Leu Gly Leu
145 150 155 160
Leu Val Ile Thr Ser Lys Asp
165

(2) INFORMATION FOR SEQ ID NO:3015:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 961 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..961

(D) OTHER INFORMATION: / Ceres Seq. ID 1575181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3015:

acgtacgtat agnmcggcgg gaacgcgtac carghgcgg crgggcggcg ggacgggtcc 60
gtgtcgccgc cgtcgccacac cagcaacctg ccgccgcga cgcccaacct cgcccaacca 120
cgcatctctt cggcaccacag ggcctgacgc agaaggagat ggtctatctg tcgggcgcgc 180
acaccatcgg ctctctgcac tgcagctnnt tcarcggcgc gctgtcgggg tcggccacga 240
cgccrgccgg gcaggaccgc accatggacc ccgcgtacgt rgcgcastgn gncrcggcag 300
tcgccgcagg gncngaccgc cgtcgtgccc atgGaCtaac tctcccccac gcctctcgac 360
gaggGctctt acaagggcgt catggccaac cggggcctgc tgtctctcga ccaggcgctg 420
ctcagcgaca agaacacgcgc cgtgcaggtc gtcacctacg ccaacgaccc ggccaccttc 480
caggcccgat tcgccccgcgc catggtcaag atgggctcgc tcggcgctgt caccggcacc 540
agcggoaagg tcagggcacaa ctgcagagtc gcctgattca tctcatcacc tcgtgtggag 600
ttgtagattc attatattga ttgatttga cgggacgacg tcgacgggat gctacatggc 660
ctstttcgca attgtatgta tgcctgtact tgcgcgtgta tgggtttcgc tgtgcaaat 720
ttcgtttgct cccccgattg attgaggcgt gtgtgcgtgt gtgtctcttc tgaatctgaa 780
tggaataatct gtaacctgag ctaaaactgc tcgtgtacta ccaaatagtt gcttcaaat 840
acgatggatt ttatttcaaa ctatcacttc caaacacgca caaatatgta tccaatcaac 900
tagggatcgg agaaactggt ttgtaaaagg aattttataa acacaagcta ttcagacatg 960
t

(2) INFORMATION FOR SEQ ID NO:3016:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..247

(D) OTHER INFORMATION: / Ceres Seq. ID 1575182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3016:

Arg Thr Xaa Xaa Ala Gly Thr Arg Thr Xaa Xaa Arg Xaa Gly Gly
1 5 10 15
Gly Thr Gly Pro Cys Arg Ala Arg Arg Thr Pro Ala Thr Cys Arg Arg
20 25 30
Arg Arg Pro Thr Ser Arg Xaa His Ala Asp Leu Arg His Gln Gly Pro
35 40 45
Asp Ala Glu Gly Asp Gly His Pro Val Gly Arg Ala His His Arg Leu
50 55 60
Leu Ala Leu Gln Xaa Xaa Xaa Arg Pro Ala Val Gly Val Gly His Asp
65 70 75 80

Gly	Xaa	Arg	Ala	Gly	Pro	Asp	His	Gly	Pro	Arg	Val	Arg	Xaa	Ala	Xaa	
				85					90					95		
Xaa	Xaa	Gly	Ser	Ala	Arg	Arg	Xaa	Xaa	Thr	Arg	Ser	Cys	Pro	Trp	Thr	
				100					105				110			
Thr	Ser	Pro	Pro	Thr	Pro	Ser	Thr	Arg	Ala	Ser	Thr	Arg	Ala	Ser	Trp	
				115					120				125			
Pro	Thr	Gly	Ala	Cys	Cys	Pro	Arg	Thr	Arg	Arg	Cys	Ser	Ala	Thr	Arg	
				130					135				140			
Thr	Pro	Pro	Cys	Arg	Ser	Ser	Pro	Thr	Pro	Thr	Thr	Arg	Pro	Pro	Ser	
				145					150				155		160	
Arg	Pro	Thr	Ser	Pro	Pro	Pro	Trp	Ser	Arg	Trp	Ala	Pro	Ser	Ala	Cys	
				165					170					175		
Ser	Pro	Ala	Pro	Ala	Ala	Arg	Ser	Gly	Pro	Thr	Ala	Glu	Ser	Pro	Asp	
				180					185				190			
Ser	Ser	Ser	Ser	Leu	Val	Trp	Ser	Cys	Arg	Phe	Ile	Ile	Leu	Ile	Asp	
				195				200				205				
Leu	Asp	Arg	Thr	Thr	Ser	Thr	Gly	Cys	Tyr	Met	Ala	Xaa	Cys	Ala	Ile	
				210				215				220				
Val	Cys	Met	Pro	Val	Leu	Ala	Arg	Val	Trp	Val	Ser	Leu	Cys	Lys	Phe	
				225				230				235			240	
Ser	Leu	Ser	Pro	Pro	Ile	Asp										
				245												

(2) INFORMATION FOR SEQ ID NO:3017:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..205

(D) OTHER INFORMATION: / Ceres Seq. ID 1575183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3017:

Val	Arg	Ile	Xaa	Xaa	Arg	Glu	Arg	Val	Pro	Xaa	Ala	Gly	Xaa	Ala	Ala	
1				5					10				15			
Gly	Arg	Val	Arg	Val	Ala	Arg	Val	Gly	His	Gln	Gln	Pro	Ala	Ala	Ala	
				20				25				30				
Asp	Gly	Gln	Arg	Arg	Ala	Xaa	Thr	Gln	Ile	Phe	Gly	Thr	Lys	Gly	Leu	
				35			40					45				
Thr	Gln	Lys	Glu	Met	Val	Ile	Leu	Ser	Gly	Ala	His	Thr	Ile	Gly	Ser	
				50			55			60						
Ser	His	Cys	Ser	Xaa	Phe	Xaa	Gly	Arg	Leu	Ser	Gly	Ser	Ala	Thr	Thr	
				65			70			75				80		
Xaa	Gly	Gly	Gln	Asp	Pro	Thr	Met	Asp	Pro	Ala	Tyr	Xaa	Ala	Xaa	Xaa	
				85				90					95			
Xaa	Xaa	Ala	Val	Pro	Ala	Gly	Xaa	Xaa	Pro	Ala	Arg	Ala	His	Gly	Leu	
				100				105					110			
Arg	Leu	Pro	Gln	Arg	Leu	Arg	Arg	Gly	Leu	Leu	Gln	Gly	Arg	His	Gly	
				115				120					125			
Gln	Pro	Gly	Pro	Ala	Val	Leu	Gly	Pro	Gly	Ala	Ala	Gln	Arg	Gln	Glu	
				130				135				140				
His	Arg	Arg	Ala	Gly	Arg	His	Leu	Arg	Gln	Arg	Pro	Gly	His	Leu	Pro	
				145				150				155			160	
Gly	Arg	Leu	Arg	Arg	Arg	His	Gly	Gln	Asp	Gly	Leu	Arg	Arg	Arg	Ala	
				165					170					175		
His	Arg	His	Gln	Arg	Gln	Gly	Gln	Gly	Gln	Leu	Gln	Ser	Arg	Leu	Ile	
				180				185					190			
His	Arg	His	His	Ser	Cys	Gly	Val	Val	Asp	Ser	Leu	Tyr				
				195				200				205				

(2) INFORMATION FOR SEQ ID NO:3018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3018:

Met Val Ile Leu Ser Gly Ala His Thr Ile Gly Ser Ser His Cys Ser
1 5 10 15
Xaa Phe Xaa Gly Arg Leu Ser Gly Ser Ala Thr Thr Xaa Gly Gly Gln
20 25 30
Asp Pro Thr Met Asp Pro Ala Tyr Xaa Ala Xaa Xaa Xaa Ala Val
35 40 45
Pro Ala Gly Xaa Xaa Pro Ala Arg Ala His Gly Leu Arg Leu Pro Gln
50 55 60
Arg Leu Arg Arg Gly Leu Leu Gln Gly Arg His Gly Gln Pro Gly Pro
65 70 75 80
Ala Val Leu Gly Pro Gly Ala Ala Gln Arg Gln Glu His Arg Arg Ala
85 90 95
Gly Arg His Leu Arg Gln Arg Pro Gly His Leu Pro Gly Arg Leu Arg
100 105 110
Arg Arg His Gly Gln Asp Gly Leu Arg Arg Arg Ala His Arg His Gln
115 120 125
Arg Gln Gly Gln Gly Gln Leu Gln Ser Arg Leu Ile His Arg His His
130 135 140
Ser Cys Gly Val Val Asp Ser Leu Tyr
145 150

(2) INFORMATION FOR SEQ ID NO:3019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..424
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3019:

atcacatttcg actctcaacy cccaaggtcc ctttttttt ctcgatctgg aagcncgcga 60
gtacgacgca tggacgtgag cggagcaggc ggtaaggcga agaaggcgcg ggcggggcgcg 120
aaggccggcg ggcgcagcaa gaagtgggtg tcgcggtcct ccagggcggc gccccgctcg 180
tctctggtcc agcccgagcg caccatctcc gccaaattaa gcccatgttg catggtatgt 240
cttgggtacac atgcatgaag tagtagagag caacggtcaa cttactcctt atattcccat 300
aataataaaa tacttaggag tacttacttc aaaaaaagaa ggatctcatg actgtaacgg 360
aagtacatt ttctcttgag ttggggtgta acataaaccc agcaccaaaag ctatttgcga 420
tctc

(2) INFORMATION FOR SEQ ID NO:3020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1575192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3020:

Ile	His	Phe	Asp	Ser	Gln	Xaa	Pro	Arg	Ser	Leu	Phe	Phe	Ser	Arg	Ser	
1			5				10						15			
Gly	Ser	Xaa	Ala	Val	Ala	Ala	Met	Asp	Val	Ser	Gly	Ala	Gly	Gly	Lys	
			20				25					30				
Ala	Lys	Lys	Gly	Ala	Ala	Gly	Arg	Lys	Ala	Gly	Gly	Pro	Thr	Lys	Lys	
			35				40					45				
Ser	Val	Ser	Arg	Ser	Ser	Arg	Ala	Gly	Pro	Ala	Cys	Ser	Trp	Ser	Gln	
			50				55				60					
Pro	Asp	Ala	Thr	Ile	Ser	Ala	Lys	Leu	Ser	Pro	Cys	Cys	Met	Asp	Ala	
					70					75				80		
Leu	Gly	Thr	His	Ala												

(2) INFORMATION FOR SEQ ID NO:3021:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1575193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3021:

Met	Asp	Val	Ser	Gly	Ala	Gly	Gly	Lys	Ala	Lys	Lys	Gly	Ala	Ala	Gly	
1			5				10						15			
Arg	Lys	Ala	Gly	Gly	Pro	Thr	Lys	Lys	Ser	Val	Ser	Arg	Ser	Ser	Arg	
			20				25					30				
Ala	Gly	Pro	Ala	Cys	Ser	Trp	Ser	Gln	Pro	Asp	Ala	Thr	Ile	Ser	Ala	
			35				40					45				
Lys	Leu	Ser	Pro	Cys	Cys	Met	Asp	Ala	Leu	Gly	Thr	His	Ala			
			50				55				60					

(2) INFORMATION FOR SEQ ID NO:3022:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1575194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3022:

Met	Leu	Leu	Val	His	Met	His	Glu	Val	Val	Glu	Ser	Asn	Gly	Gln	Leu	
1			5				10						15			
Thr	Pro	Tyr	Ile	Pro	Ile	Ile	Lys	Tyr	Leu	Gly	Val	Leu	Thr	Ser		
			20				25				30					
Lys	Lys	Glu	Gly	Ser	His	Asp	Cys	Asn	Arg	Ser	Asp	Ile	Phe	Ser		
			35				40				45					

(2) INFORMATION FOR SEQ ID NO:3023:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 631 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(D) OTHER INFORMATION: / Ceres Seq. ID 1575195

tggttaaggt	tcttgaacg	gagaaacgccc	aggccaatgt	tgtcgtatgt	ggatctcaact	120
tggttgagcg	ctctgaacatc	ctcttcagaca	acagccagaat	tatagggtat	gttagagaaa	160
ggggaaacat	gtctgggggtg	gaactctgtca	cggaacagaaa	ggagaaagacc	cctgcgaagt	180
gggaacacat	tgaactgttt	gagaaagtcca	gagatctcgg	ggactagctt	ggaaaggcgc	200
gtctcgtatg	gaactctcttc	agaataaaaac	caacgtagtg	cttctcgaag	gacgtagcag	300
actctcttgc	gaactccatg	gaactcagcaa	cttcaaggct	cttaaggdaa	atgcctctgag	360
ttgacaatgt	gtctcgtgtg	aaatacaact	tcttcgaacc	gcaagatgca	tggtctgtaa	420
tgaactgaa	aggcagatga	tataattggc	atgctccccg	gtgtgttatg	tcgctgttat	480
gtgaagtta	aatgtccccc	tccccccaat	aaattgatga	atagggaacg	aacgctctgc	540
cgaactgtta	ctactgtttg	aaqaagaactg	caqttaataa	ataagatacg	gaqcaaacga	600

(2) INFORMATION FOR SEO ID NO:3024

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: $1 \text{ in } 10^4$

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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(A) NAME/KEY: peptide
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(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1575196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3024:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1575197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3025:

Met	Leu	Gly	Val	Glu	Leu	Val	Thr	Asp	Arg	Lys	Glu	Lys	Thr	Pro	Ala	
1				5				10						15		
Lys	Ser	Glu	Thr	Ile	Glu	Leu	Phe	Glu	Lys	Leu	Arg	Asp	Leu	Gly	Val	
			20					25					30			
Leu	Val	Gly	Lys	Gly	Gly	Leu	His	Gly	Asn	Val	Phe	Arg	Ile	Lys	Pro	
			35				40					45				
Pro	Met	Cys	Phe	Ser	Lys	Asp	Asp	Ala	Asp	Phe	Leu	Val	Asp	Ser	Met	

50
Asp Tyr Ala Met Ser Arg Leu
65 70

60

(2) INFORMATION FOR SEQ ID NO:3026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..595

(D) OTHER INFORMATION: / Ceres Seq. ID 1575202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3026:

atatatttgc	ccatttgg	ggttttcgtg	aagttcgtct	tgtaacaag	gagtcacagac	60
atcctgggtg	agatccacat	gtgttggtgt	tcgtcgattt	tgacaaccct	gctcaggcta	120
caattgctct	ggaagcatta	caaggttata	agtttgacga	acacgagcgt	gattcagccc	180
atttgcgtct	gcaattctca	cgctttcccg	gtccaaggtc	agctgggtgg	cctgcgggta	240
ggcgtaaaga	cgtgcgggacc	tcgtggttgc	cgaacctatc	gtttatacga	gcgatccaac	300
tacgggGggc	taacgcttcg	atatgcgctg	aatttcgggg	cggtggtgtt	ttagggttcg	360
tcagctcatt	tcgtgaatgc	gtgaaaggga	caatgcaata	agtgatattc	tgccatatgt	420
tattagatgc	cgtataatgt	gttaggcgat	gaaagtattt	cgacatactg	tatctgctgc	480
cttagctatt	gtggtctact	gtaacttcat	taccttgctt	cacatccgag	acaatttgag	540
tttgttatca	tgtggattat	ctgttttgaa	aatgaaacct	agatgatgtt	agcct	

(2) INFORMATION FOR SEQ ID NO:3027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1575203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3027:

Ile	Tyr	Phe	Ala	His	Leu	Leu	Val	Phe	Val	Lys	Phe	Val	Leu	Ser	Thr	
1			5					10					15			
Arg	Ser	Pro	Asp	Ile	Leu	Val	Glu	Ile	His	Met	Cys	Cys	Val	Ser	Ser	
			20					25					30			
Ile	Leu	Thr	Thr	Leu	Leu	Arg	Leu	Gln	Leu	Leu	Trp	Lys	His	Tyr	Lys	
			35					40					45			
Val	Ile	Ser	Leu	Thr	Asn	Thr	Ser	Val	Ile	Gln	Pro	Ile	Cys	Val	Cys	
			50					55					60			
Asn	Ser	His	Ala	Phe	Pro	Val	Gln	Gly	Gln	Leu	Val	Gly	Leu	Ala	Val	
65								70					75		80	
Gly	Val	Lys	Thr	Cys	Gly	Pro	Arg	Gly	Cys	Arg	Thr	Tyr	Arg	Leu	Tyr	
								85					90		95	
Glu	Arg	Ser	Asn	Tyr	Gly	Gly	Leu	Thr	Leu	Arg	Tyr	Ala	Leu	Asn	Phe	
								100					105		110	
Gly	Ala	Val	Ala	Phe												
																115

(2) INFORMATION FOR SEQ ID NO:3028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..81
(D) OTHER INFORMATION: / Ceres Seq. ID 1575204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3028:

Ile	Phe	Arg	Pro	Phe	Val	Gly	Phe	Arg	Glu	Val	Arg	Leu	Val	Asn	Lys
1			5					10					15		
Glu	Ser	Arg	His	Pro	Gly	Gly	Asp	Pro	His	Val	Leu	Cys	Phe	Val	Asp
			20				25					30			
Phe	Asp	Asn	Pro	Ala	Gln	Ala	Thr	Ile	Ala	Leu	Glu	Ala	Leu	Gln	Gly
		35					40					45			
Tyr	Lys	Phe	Asp	Glu	His	Glu	Arg	Asp	Ser	Ala	His	Leu	Arg	Leu	Gln
	50					55				60					
Phe	Ser	Arg	Phe	Pro	Gly	Pro	Arg	Ser	Ala	Gly	Pro	Arg	Gly	Arg	
				70						75				80	
Arg															

(2) INFORMATION FOR SEQ ID NO:3029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1575205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3029:

Met	Cys	Cys	Val	Ser	Ser	Ile	Leu	Thr	Thr	Leu	Leu	Arg	Leu	Gln	Leu
1			5					10					15		
Leu	Trp	Lys	His	Tyr	Lys	Val	Ile	Ser	Leu	Thr	Asn	Thr	Ser	Val	Ile
			20					25					30		
Gln	Pro	Ile	Cys	Val	Cys	Asn	Ser	His	Ala	Phe	Pro	Val	Gln	Gly	Gln
		35					40					45			
Leu	Val	Gly	Leu	Ala	Val	Gly	Val	Lys	Thr	Cys	Gly	Pro	Arg	Gly	Cys
		50				55				60					
Arg	Thr	Tyr	Arg	Leu	Tyr	Glu	Arg	Ser	Asn	Tyr	Gly	Gly	Leu	Thr	Leu
				70						75				80	
Arg	Tyr	Ala	Leu	Asn	Phe	Gly	Ala	Val	Ala	Phe					
				85					90						

(2) INFORMATION FOR SEQ ID NO:3030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..688

(D) OTHER INFORMATION: / Ceres Seq. ID 1575210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3030:

gaaccgcatcc	ggtttaaaag	atccgctact	agtgtcacccg	gcaacgtgtc	gacgcggtcg	60
tgctcgtgtgt	gttctctgtg	aggaagcgaa	ccctgcctgc	ctgcttgctt	gccgggcaag	120
aagtgaagac	agcgtgghgg	tgccgaagcg	accggaccga	ggatggctac	aagaaggaac	180
gtrgcgcga	gcgttactgc	ccaccagcct	gcgtrggcgg	ccgtggcgag	gagatggag	240
ggcgtgtgcg	gctacttcag	cgacaaggcc	tccggcaggg	tgctcagcga	rgaggagcgc	300
gcgcgcgaga	agctctacat	acagaagatg	gawcaggaba	agctggagaa	actnawgang	360
aaggadgaca	agggccaaggc	cgadgcggcc	aagadggccc	cgccgcgcgc	agrvgsacac	420
gaagaatggt	gaggaggctc	atccgagctg	atcatgcgca	aaatcggaac	agtgctccgc	480
tgaatcggt	gatgctgtac	tactgatgac	acgtagatgc	aaatagacgc	cgctgctacta	540

(2) INFORMATION FOR SEQ ID NO:3031:

(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1575211

[illegible]

(2) INFORMATION FOR SEO ID NO:3032:

(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1575212

[illegible]

(2) INFORMATION FOR SEQ ID NO:3033:

(4) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 555 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..555
(D) OTHER INFORMATION: / Ceres Seq. ID 1575217
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3033:
aaccacctgc agaggaccgc cgctgcgcgc tatcattcgt ttctggagac ccttctagcc 60
ccgcgcgcac cacaccacca ccaccaatgg caggactcgg atcaaggcc ctcgcgcgtg 120
tcgcgcgtct ggccgcgcgc gtctctctcag tgkctccgc gcccgaggcg ccgcgcgcga 180
gcccgctctN ccgCgcgcgc cgcgcgcgcgc cgcckttcgc cgcggccctc gtgcgcctct 240
ccgcgcgcctt cctctctgcgc gccgtccgcgc actgagccga tggggccctt ccaccgcgcg 300
cgccgcgcgc tagactctatt tattggagtg gtattcagta gtactggtag tagggagatt 360
ttctcggttg tgctgtgtgc tcgtgcgcatt ttggtcggat ctggtgtcct tgggtgggtg 420
agggtttgta ccgcgcgcgc gtgtcgggtg tgtgactcga ttctgatccc ctgttagata 480
ctctgctatc tcgcgcgtgat cgtgagtgat gattcgcgtc gtttgctact gatacatat 540
tgttccttat tgggt

(2) INFORMATION FOR SEQ ID NO:3034:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..158
(D) OTHER INFORMATION: / Ceres Seq. ID 1575218
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3034:
Asn His Leu Gln Arg Thr Arg Ala Arg Arg Tyr His Ser Phe Leu Glu
1 5 10 15
Thr Leu Leu Ala Pro Pro Pro Pro His His His His Gln Trp Gln Asp
20 25 30
Ser Asp Gln Arg Pro Ser Pro Trp Ser Pro Ser Trp Arg Pro Ser Ser
35 40 45
Ser Gln Xaa Pro Pro Arg Pro Arg Arg Pro Arg Pro Ala Pro Ser Xaa
50 55 60
Ala Ala Ala Xaa Arg Arg Arg Xaa Ser Pro Arg Pro Ser Ser Pro Pro
65 70 75 80
Pro Pro Pro Ser Ser Ser Pro Pro Ser Ala Thr Glu Pro Met Gly Pro
85 90 95
Phe His Arg Arg Arg Arg Leu Asp Leu Phe Ile Gly Val Val Phe
100 105 110
Ser Ser Thr Gly Thr Arg Glu Ile Ser Ser Leu Val Ser Cys Arg Arg
115 120 125
Arg Ile Leu Val Gly Ser Gly Val Leu Gly Gly Trp Arg Val Cys Thr
130 135 140
Ala Ser Trp Cys Arg Leu Cys Asp Leu Ile Leu Ile Pro Leu
145 150 155

(2) INFORMATION FOR SEQ ID NO:3035:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide

(B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 1575219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3035:

```
Pro Pro Ala Glu Asp Pro Arg Ser Pro Leu Ser Phe Val Ser Gly Asp
1      5      10      15
Pro Ser Ser Pro Ala Ala Thr Thr Pro Pro Pro Met Ala Gly Leu
20      25      30
Gly Ser Lys Ala Leu Ala Val Val Ala Val Leu Ala Ala Val Val Leu
35      40      45
Ser Val Xaa Ser Ala Ala Glu Ala Pro Ala Pro Ser Pro Val Xaa Arg
50      55      60
Arg Arg Xaa Ala Ser Ala Xaa Phe Ala Ala Ala Leu Val Ala Ser Ser
65      70      75      80
Ala Ala Phe Leu Phe Ala Ala Val Arg His
85      90
```

(2) INFORMATION FOR SEQ ID NO:3036:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 614 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..614

(D) OTHER INFORMATION: / Ceres Seq. ID 1575232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3036:

```
accacacac atcacaccca gctgccattg ccactctactg acctgtgacc tccgcatttc      60
caaacagccc gagcgagcga gctagcagag cggNcggcag gcacctccct cctcaaggaa      120
catggcccgc accagcagct tggcagtagt ggcgcgcgcc gtgtggccct tgggtgcgcg      180
ggcgctcagc gccccaacgc cggtaacgcc gccagcatcc cctccaagtg cggcgctcagc      240
atcccctaca ccatcagcac ctcccacgcac tgctccaggg tgaactgaac cctaaacgcac      300
gacgacggcg ccggcgccgc cctgaagacg atccatctct atcccgcgtg cgtcggcgct      360
gcggtttcga cgtcatgac catatctacc taoccatgat cagcacttgc atgtctacta      420
ctactactga ataaaaaacc tctccgcgca cgtctgtctt gtgtctgtgt gtgtgagaga      480
gagaggagag ccggccatgt ccttttggct gtttggttta tttttgagtt catcggtct      540
ttattttatt ccatgtacc agtaaccacc ttgtaccatg catgttcctt atgatacact      600
cacccttttt ttgt
```

(2) INFORMATION FOR SEQ ID NO:3037:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1575233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3037:

```
Met Ala Arg Thr Gln Gln Leu Ala Val Val Ala Ala Val Val Ala
1      5      10      15
Leu Val Pro Pro Ala Ser Ala Ala Ser Thr Pro Val Thr Pro Pro Ala
20      25      30
Ser Pro Pro Ser Ala Ala Ser Ala Ser Pro Thr Pro Ser Ala Pro Pro
35      40      45
Pro Thr Ala Pro Gly
50
```

(2) INFORMATION FOR SEQ ID NO:3038:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..39
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575234
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3038:
Met Ser Phe Trp Leu Phe Gly Leu Phe Leu Ser Ser Cys Gly Leu Tyr
1 5 10 15
Leu Phe Pro Cys Thr Gln Tyr Pro Pro Cys Thr Met His Val Pro Tyr
 20 25 30
Asp Thr Leu Thr Ser Phe Cys
 35
(2) INFORMATION FOR SEQ ID NO:3039:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 615 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..615
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575235
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3039:
gcaaacccgcg tctcgcgcga agaatacgcga ttcccccctc ccgcacccca acccccgtcg 60
gagagagaga tggcatcggg ggGcggagat gcagcccctc gcgcgcggcg ggtaccggbG 120
cgcgccggag atgaaggaga aggtggaggc gtcggtggtg gacctggagg ccggcacccg 180
ggagcgcgtg taccgcggga tctcgcgcgg ggagagcgcc ctccgatggg gcttcgtccg 240
caaggtctac ggcattctcg tgcgcagctg ctctcacc caagcgcgtc cgcctcacc 300
gttctccacc ccacccctca cgccacgctc tccgactccc cgggcctcgc gctcgtgctc 360
gccgtcctgc ccttcattct gatgatccca ttgtatcatt atcagcacaa gaaccacac 420
aatttgcttt tctctgggtc gtccacgttg tcttgagct tcagcatcgg tgtggttgt 480
gctaacaccc aagggaataa cgttctggag gctttagtgc tcacggctgg cgtggtgggt 540
tctctgagcg gtatgccttc tgggcgtcaa agaagggcaa ggaattggg tacctggggc 600
ctatcctgtc ttccg
(2) INFORMATION FOR SEQ ID NO:3040:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..205
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575236
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3040:
Ala Asn Arg Val Ser Arg Glu Glu Ser Ala Phe Pro Leu Pro Arg Thr
1 5 10 15
Gln Pro Pro Ser Glu Arg Glu Met Ala Ser Val Gly Gly Asp Ala Ala
 20 25 30
Pro Arg Ala Gly Gly Val Pro Xaa Arg Ala Gly Asp Glu Gly Glu Gly
 35 40 45
Gly Gly Val Gly Gly Gly Pro Gly Gly Arg His Arg Gly Asp Ala Val
 50 55 60
Pro Gly Asp Leu Ala Arg Gly Glu Arg Pro Pro Met Gly Leu Arg Pro
65 70 75 80
Gln Gly Leu Arg His Pro Arg Ala Gln Leu Leu Thr Thr Ala Val

85 90 95
Ser Ala Leu Thr Val Leu His Pro Thr Leu Asn Ala Thr Leu Ser Asp
100 105 110
Ser Pro Gly Leu Ala Leu Val Leu Ala Val Leu Pro Phe Ile Leu Met
115 120 125
Ile Pro Leu Tyr His Tyr Gln His Lys His Pro His Asn Phe Val Phe
130 135 140
Leu Gly Leu Phe Thr Leu Cys Leu Ser Phe Ser Ile Gly Val Ala Cys
145 150 155 160
Ala Asn Thr Gln Gly Lys Ile Val Leu Glu Ala Leu Val Leu Thr Ala
165 170 175
Gly Val Val Val Ser Leu Xaa Arg Met Pro Ser Gly Arg Gln Arg Arg
180 185 190
Ala Arg Asn Ser Gly Thr Trp Gly Leu Ser Cys Leu Pro
195 200 205

(2) INFORMATION FOR SEQ ID NO:3041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3041:

Met Ala Ser Val Gly Gly Asp Ala Ala Pro Arg Ala Gly Gly Val Pro
1 5 10 15
Xaa Arg Ala Gly Asp Glu Gly Glu Gly Gly Val Gly Gly Pro
20 25 30
Gly Gly Arg His Arg Gly Asp Ala Val Pro Gly Asp Leu Ala Arg Gly
35 40 45
Glu Arg Pro Pro Met Gly Leu Arg Pro Gln Gly Leu Arg His Pro Arg
50 55 60
Ala Gln Leu Leu Leu Thr Thr Ala Val Ser Ala Leu Thr Val Leu His
65 70 75 80
Pro Thr Leu Asn Ala Thr Leu Ser Asp Ser Pro Gly Leu Ala Leu Val
85 90 95
Leu Ala Val Leu Pro Phe Ile Leu Met Ile Pro Leu Tyr His Tyr Gln
100 105 110
His Lys His Pro His Asn Phe Val Phe Leu Gly Leu Phe Thr Leu Cys
115 120 125
Leu Ser Phe Ser Ile Gly Val Ala Cys Ala Asn Thr Gln Gly Lys Ile
130 135 140
Val Leu Glu Ala Leu Val Leu Thr Ala Gly Val Val Val Ser Leu Xaa
145 150 155 160
Arg Met Pro Ser Gly Arg Gln Arg Arg Ala Arg Asn Ser Gly Thr Trp
165 170 175
Gly Leu Ser Cys Leu Pro
180

(2) INFORMATION FOR SEQ ID NO:3042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1575238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3042:

Met Gly Leu Arg Pro Gln Gly Leu Arg His Pro Arg Ala Gln Leu Leu
1 5 10 15
Leu Thr Thr Ala Val Ser Ala Leu Thr Val Leu His Pro Thr Leu Asn
20 25 30
Ala Thr Leu Ser Asp Ser Pro Gly Leu Ala Leu Val Leu Ala Val Leu
35 40 45
Pro Phe Ile Leu Met Ile Pro Leu Tyr His Tyr Gln His Lys His Pro
50 55 60
His Asn Phe Val Phe Leu Gly Leu Phe Thr Leu Cys Leu Ser Phe Ser
65 70 75 80
Ile Gly Val Ala Cys Ala Asn Thr Gln Gly Lys Ile Val Leu Glu Ala
85 90 95
Leu Val Leu Thr Ala Gly Val Val Val Ser Leu Xaa Arg Met Pro Ser
100 105 110
Gly Arg Gln Arg Arg Ala Arg Asn Ser Gly Thr Trp Gly Leu Ser Cys
115 120 125
Leu Pro
130

(2) INFORMATION FOR SEQ ID NO:3043:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 519 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..519

(D) OTHER INFORMATION: / Ceres Seq. ID 1575243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3043:

cagascagaa ascagccgca gccccagccc ccacaagacg aggcacaacat ggcgctagaa 60
gcagcccaacg ccccccgccg actctctgcc gcgtgcctcg tctctgtggt cctcgggcggc 120
ggcaccggccc cgtcgtcggt gCtgcgcggc gccggggggc agcccgccgag gggagccgga 180
tccaggatac gtcattgtat cggcatgggg ccccgccctc cactaatcgt cgtcgttcga 240
ggcgacgac gacgCtccgc cgccaacgac ggogagtgcc acatgcctat gctctcgtgt 300
gggcccogta cgttatttag cgctactagt actagggaaa gtgtacgtgt gatgtgtgtc 360
actcagtgct gattgatcaa tgatgctcat ttctgagcag acccaggaat gctgagtcca 420
gagagcagag cgtNtgttct acaagtgcac cgaggaataa agtgacaga aatgttgctg 480
ggttcacgtg cctctcgtgt aataaaatgg acatcttcg

(2) INFORMATION FOR SEQ ID NO:3044:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1575244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3044:

Gln Xaa Arg Xaa Gln Pro Gln Pro Gln Pro Gln Asp Glu Ala Thr
1 5 10 15
Met Ala Leu Glu Ala Ala Thr Ala Pro Arg Ala Leu Leu Ala Cys
20 25 30
Leu Val Leu Val Leu Gly Gly Thr Gly Pro Ser Ser Val Leu
35 40 45
Arg Gly Ala Gly Ala Gln Ala Gly Arg Gly Ala Gly Ser Arg Ile Arg
50 55 60

His Val Ser Gly Met Gly Pro Arg Arg Pro Leu Ile Val Val Val Arg
65 70 75 80
Gly Arg Arg Arg Arg Ser Ala Ala Asn Asp Gly Glu Cys His Met Pro
85 90 95
Met Leu Ser Cys Gly Pro Arg Thr Leu Leu Ser Ala Thr Ser Thr Arg
100 105 110
Glu Ser Val Arg Val Met Cys Val Thr Gln Cys Arg Leu Ile Asn Asp
115 120 125
Ala His Phe Arg Ala Asp Pro Gly Met Leu Ser Ala Glu Ser Arg Ala
130 135 140
Xaa Val Leu Gln Val His Arg Gly Ile Lys Trp Thr Glu Met Leu Ala
145 150 155 160
Gly Ser Arg Ala Phe
165

(2) INFORMATION FOR SEQ ID NO:3045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3045:

Xaa Gln Lys Xaa Ala Ala Ala Pro Ala Pro Thr Arg Arg Gly Asn Asn
1 5 10 15
Gly Ala Arg Ser Ser His Arg Pro Pro Arg Thr Pro Arg Arg Val Pro
20 25 30
Arg Pro Ala Gly Pro Arg Arg Arg His Arg Pro Val Val Gly Ala Ala
35 40 45
Arg Arg Arg Gly Ala Gly Arg Gln Gly Ser Arg Ile Gln Asp Thr Ser
50 55 60
Cys Ile Arg His Gly Ala Pro Pro Ser Thr Asn Arg Arg Arg Ser Arg
65 70 75 80
Ala Thr Thr Thr Leu Arg Arg Gln Arg Arg Arg Val Pro His Ala Tyr
85 90 95
Ala Leu Val Trp Ala Pro Tyr Val Ile Glu Arg Tyr
100 105

(2) INFORMATION FOR SEQ ID NO:3046:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3046:

Met Ala Leu Glu Ala Ala Thr Ala Pro Arg Ala Leu Leu Ala Ala Cys
1 5 10 15
Leu Val Leu Leu Val Leu Gly Gly Gly Thr Gly Pro Ser Ser Val Leu
20 25 30
Arg Gly Ala Gly Ala Gln Ala Gly Arg Gly Ala Gly Ser Arg Ile Arg
35 40 45
His Val Ser Gly Met Gly Pro Arg Arg Pro Leu Ile Val Val Val Arg
50 55 60
Gly Arg Arg Arg Arg Ser Ala Ala Asn Asp Gly Glu Cys His Met Pro

65	70	75	80
Met Leu Ser Cys Gly	Pro Arg Thr Leu Leu Ser Ala Thr Ser Thr Arg		
	85	90	95
Glu Ser Val Arg Val Met Cys Val Thr Gln Cys Arg Leu Ile Asn Asp			
	100	105	110
Ala His Phe Arg Ala Asp Pro Gly Met Leu Ser Ala Glu Ser Arg Ala			
	115	120	125
Xaa Val Leu Gln Val His Arg Gly Ile Lys Trp Thr Glu Met Leu Ala			
	130	135	140
Gly Ser Arg Ala Phe			
145			

(2) INFORMATION FOR SEQ ID NO:3047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..945
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3047:

ataaaccttt	tcactgtcc	agccgcgcgc	gccgccgttt	cttcgtcttc	ctcgcagcgc	60
cgccgcctca	tcttcgcgt	atccgcctgc	tcccgccctt	cgccacgcag	gcggcgccgc	120
tcaggcccg	gatttcagcg	acggcgctca	ggcttccctt	cccgctcttt	ccagtcgcc	180
tcggcgccct	gcctccgggt	ctccgcacac	cgcccggtga	ccctgcattc	accatgactg	240
gtgtcagcac	tggattgttt	acggcgcttg	ggagggtcat	ggaacagcaa	aggatttcaa	300
ccgctttctg	cagacaatca	cgagtttcga	gctctactgt	ttcttctct	gacctgatg	360
agaagggttg	catggaatat	gatgatAact	ctccaaatc	aaagaggagg	ttaacgcccc	420
aaggtgtaga	tcocaaataa	ggctgggaat	tccgtgggtg	gcaacaggcc	atcatctgtg	480
gcaaaagtgg	acaagtcctc	gtgcacaaaa	ttttaaggaa	tgggcataca	gtaaccgttt	540
ttactgttgg	aactggtggc	atgtttgacc	agagggtaat	tgggcctaa	gatttgcoc	600
agccagctca	gtggcacccg	atagtgtgcc	ataatgacta	cttaagtgtc	tatgtgttc	660
agaagctggt	gaagaattcg	cacgagacct	tcaacatcaa	gaatgacttc	accocctgag	720
aggaagagga	gatccgcagg	gagaaccagt	gggccttcga	gtaaggaggt	gctggatcta	780
ttgatgccta	agtttcgttg	tgctactac	tatgtctact	ttatgtgttc	ctaagtgttg	840
taagtatttt	ggagtcact	tgtcttcgca	atgtctcgcg	taagacttat	gtgtgcaatt	900
gtcgttatt	aacttattac	catgaaagcm	ytgctgtgct	gcccc		

(2) INFORMATION FOR SEQ ID NO:3048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..253
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3048:

Lys Pro Phe His Cys Ser Ser Arg Arg Arg Arg Arg Phe Phe Val Phe			
1	5	10	15
Leu Ala Ala Pro Pro Leu His Leu Pro Leu Ile Arg Ser Leu Pro Pro			
	20	25	30
Leu Ala Thr Gln Ala Ala Ala Leu Arg Pro Val Ile Ser Ala Thr Ala			
	35	40	45
Ser Xaa Leu Pro Leu Pro Ser Leu Pro Ser Arg Leu Ala Pro Ser Pro			
	50	55	60
Pro Val Leu Arg Thr Pro Ala Gly Asp Pro Ala Ser Thr Met Thr Gly			
65	70	75	80

Val	Ser	Thr	Gly	Leu	Leu	Thr	Gly	Leu	Arg	Arg	Val	Met	Glu	Gln	Gln	
				85					90					95		
Arg	Ile	Ser	Thr	Ala	Phe	Cys	Arg	Gln	Ser	Arg	Val	Ser	Ser	Ser	Thr	
				100					105					110		
Val	Ser	Phe	Ser	Asp	Leu	Asp	Glu	Lys	Gly	Asp	Met	Glu	Tyr	Asp	Asp	
				115					120					125		
Asn	Ser	Pro	Asn	Ser	Lys	Arg	Glu	Leu	Arg	Pro	Gln	Gly	Val	Asp	Pro	
				130					135					140		
Asn	Lys	Gly	Trp	Glu	Phe	Arg	Gly	Val	His	Arg	Ala	Ile	Ile	Cys	Gly	
				145					150					155		
Lys	Val	Gly	Gln	Val	Pro	Val	Gln	Lys	Ile	Leu	Arg	Asn	Gly	His	Thr	
				165					170					175		
Val	Thr	Val	Phe	Thr	Val	Gly	Thr	Gly	Gly	Met	Phe	Asp	Gln	Arg	Val	
				180					185					190		
Ile	Gly	Pro	Lys	Asp	Leu	Pro	Lys	Pro	Ala	Gln	Trp	His	Arg	Ile	Ala	
				195					200					205		
Val	His	Asn	Asp	Tyr	Leu	Ser	Ala	Tyr	Ala	Val	Gln	Lys	Leu	Val	Lys	
				210					215					220		
Asn	Ser	His	Glu	Thr	Phe	Asn	Ile	Lys	Asn	Asp	Phe	Thr	Pro	Glu	Glu	
				225					230					235		
Glu	Glu	Glu	Ile	Arg	Arg	Glu	Asn	Gln	Trp	Ala	Phe	Glu				
				245					250							

(2) INFORMATION FOR SEQ ID NO:3049:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1575338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3049:

Met	Thr	Gly	Val	Ser	Thr	Gly	Leu	Leu	Thr	Gly	Leu	Arg	Arg	Val	Met	
1				5					10					15		
Glu	Gln	Gln	Arg	Ile	Ser	Thr	Ala	Phe	Cys	Arg	Gln	Ser	Arg	Val	Ser	
				20					25					30		
Ser	Ser	Thr	Val	Ser	Phe	Ser	Asp	Leu	Asp	Glu	Lys	Gly	Asp	Met	Glu	
				35					40					45		
Tyr	Asp	Asp	Asn	Ser	Pro	Asn	Ser	Lys	Arg	Glu	Leu	Arg	Pro	Gln	Gly	
				50					55					60		
Val	Asp	Pro	Asn	Lys	Gly	Trp	Glu	Phe	Arg	Gly	Val	His	Arg	Ala	Ile	
				65					70					75		
Ile	Cys	Gly	Lys	Val	Gly	Gln	Val	Pro	Val	Gln	Lys	Ile	Leu	Arg	Asn	
				85					90					95		
Gly	His	Thr	Val	Thr	Val	Phe	Thr	Val	Gly	Thr	Gly	Gly	Met	Phe	Asp	
				100					105					110		
Gln	Arg	Val	Ile	Gly	Pro	Lys	Asp	Leu	Pro	Lys	Pro	Ala	Gln	Trp	His	
				115					120					125		
Arg	Ile	Ala	Val	His	Asn	Asp	Tyr	Leu	Ser	Ala	Tyr	Ala	Val	Gln	Lys	
				130					135					140		
Leu	Val	Lys	Asn	Ser	His	Glu	Thr	Phe	Asn	Ile	Lys	Asn	Asp	Phe	Thr	
				145					150					155		
Pro	Glu	Glu	Glu	Glu	Glu	Ile	Arg	Arg	Glu	Asn	Gln	Trp	Ala	Phe	Glu	
				165					170					175		

(2) INFORMATION FOR SEQ ID NO:3050:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..161
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575339
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3050:

Met	Glu	Gln	Gln	Arg	Ile	Ser	Thr	Ala	Phe	Cys	Arg	Gln	Ser	Arg	Val
1			5						10					15	
Ser	Ser	Ser	Thr	Val	Ser	Phe	Ser	Asp	Leu	Asp	Glu	Lys	Gly	Asp	Met
			20					25					30		
Glu	Tyr	Asp	Asp	Asn	Ser	Pro	Asn	Ser	Lys	Arg	Glu	Leu	Arg	Pro	Gln
		35					40				45				
Gly	Val	Asp	Pro	Asn	Lys	Gly	Trp	Glu	Phe	Arg	Gly	Val	His	Arg	Ala
	50					55					60				
Ile	Ile	Cys	Gly	Lys	Val	Gly	Gln	Val	Pro	Val	Gln	Lys	Ile	Leu	Arg
65				70				75					80		
Asn	Gly	His	Thr	Val	Thr	Val	Phe	Thr	Val	Gly	Thr	Gly	Gly	Met	Phe
			85					90					95		
Asp	Gln	Arg	Val	Ile	Gly	Pro	Lys	Asp	Leu	Pro	Lys	Pro	Ala	Gln	Trp
			100				105						110		
His	Arg	Ile	Ala	Val	His	Asn	Asp	Tyr	Leu	Ser	Ala	Tyr	Ala	Val	Gln
		115					120					125			
Lys	Leu	Val	Lys	Asn	Ser	His	Glu	Thr	Phe	Asn	Ile	Lys	Asn	Asp	Phe
		130					135					140			
Thr	Pro	Glu	Glu	Glu	Glu	Glu	Ile	Arg	Arg	Glu	Asn	Gln	Trp	Ala	Phe
					150					155					160
Glu															

(2) INFORMATION FOR SEQ ID NO:3051:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 762 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..762
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3051:

acaagtcctts	agcgaaacctc	gccactcgccc	caactccgctc	ccaaaagaaga	agaagacgacg	60
gacgacagca	argtgccgcgc	gtcacgagat	ycgtccgagg	tgaccatgtc	taccgcctaag	120
anaagacgtc	ccaggaaaac	caacggctcc	acgtcgctgt	cgctcgccgc	gatgcgtcgg	180
acgacgagcc	tgtmggagat	cgcgcggcmg	ccggatctct	ccgggaggcc	caagamcgcg	240
gcggcgaggg	ggcatcgcggt	ggcaggggcca	gggacccggt	ggggcgccga	gataacgatg	300
acgcactcgg	cggactctct	ccccgccatg	gagacggcag	ccttctctaa	ggCctgcggg	360
atctgcaaac	gcgcgctcgg	ccccggccgt	gacaccttca	tctacatggg	tgagggtggcc	420
ttctgcagcc	aggagttktag	gcagcagcag	atgaacctcg	acgagctcat	ggagaagaag	480
tgctccactc	cggctggcgg	cggcggtggt	ggcgtcgccg	cgcgcgccgg	tgggtgcctca	540
gatoagcccg	gcaagagcag	caccgtatcg	gccgcctagc	atcgccagag	gggttaataac	600
aacgaagaaa	aattttggag	ccctggtggc	gtaggcccca	aaaacgcagc	agtttccatc	660
agcctatgta	tatcctgtat	ttctggagtc	actgtgtgtg	tatatgtgtg	ggaagggggaa	720
ggatgtaggg	attccaactg	ggggcatggt	ttgcaatgca	tc		

(2) INFORMATION FOR SEQ ID NO:3052:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..192
(D) OTHER INFORMATION: / Ceres Seq. ID 1575344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3052:

Thr Ser Pro Xaa Arg Thr Ser Pro Leu Ala His Ser Ala Pro Lys Glu
1 5 10 15
Glu Glu Asp Asp Asp Ser Xaa Val Pro Pro Ser Arg Asp Xaa Ser
20 25 30
Glu Val Thr Met Ser Thr Pro Thr Xaa Lys Arg Pro Arg Lys Thr Asn
35 40 45
Gly Ser Thr Ser Ser Ser Ser Ser Ala Met Arg Arg Thr Thr Ser Leu
50 55 60
Xaa Xaa Leu Ala Pro Xaa Pro Asp Leu Ser Gly Arg Pro Lys Xaa Arg
65 70 75 80
Ala Ala Arg Gly His Ala Val Ala Gly Pro Gly Thr Ala Trp Gly Ala
85 90 95
Glu Ile Thr Met Thr His Ser Ala Asp Phe Leu Pro Ala Met Glu Thr
100 105 110
Ala Ala Phe Leu Lys Ala Cys Gly Ile Cys Asn Arg Arg Leu Gly Pro
115 120 125
Gly Arg Asp Thr Phe Ile Tyr Met Gly Glu Val Ala Phe Cys Ser Gln
130 135 140
Glu Xaa Arg Gln Gln Gln Met Asn Leu Asp Glu Leu Met Glu Lys Lys
145 150 155 160
Cys Ser Thr Pro Ala Gly Gly Gly Gly Gly Val Gly Gly Gly Gly
165 170 175
Gly Gly Gly Ser Asp Gln Pro Gly Lys Ser Ser Thr Val Ala Ala Ala
180 185 190

(2) INFORMATION FOR SEQ ID NO:3053:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..157
(D) OTHER INFORMATION: / Ceres Seq. ID 1575345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3053:

Met Ser Thr Pro Thr Xaa Lys Arg Pro Arg Lys Thr Asn Gly Ser Thr
1 5 10 15
Ser Ser Ser Ser Ser Ala Met Arg Arg Thr Thr Ser Leu Xaa Xaa Leu
20 25 30
Ala Pro Xaa Pro Asp Leu Ser Gly Arg Pro Lys Xaa Arg Ala Ala Arg
35 40 45
Gly His Ala Val Ala Gly Pro Gly Thr Ala Trp Gly Ala Glu Ile Thr
50 55 60
Met Thr His Ser Ala Asp Phe Leu Pro Ala Met Glu Thr Ala Ala Phe
65 70 75 80
Leu Lys Ala Cys Gly Ile Cys Asn Arg Arg Leu Gly Pro Gly Arg Asp
85 90 95
Thr Phe Ile Tyr Met Gly Glu Val Ala Phe Cys Ser Gln Glu Xaa Arg
100 105 110
Gln Gln Gln Met Asn Leu Asp Glu Leu Met Glu Lys Lys Cys Ser Thr
115 120 125

Pro Ala Gly Gly Gly Gly Gly Gly Val Gly Gly Gly Gly Gly Gly Gly
130 135 140
Ser Asp Gln Pro Gly Lys Ser Ser Thr Val Ala Ala Ala
145 150 155

(2) INFORMATION FOR SEQ ID NO:3054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3054:

Met Arg Arg Thr Thr Ser Leu Xaa Xaa Leu Ala Pro Xaa Pro Asp Leu
1 5 10 15
Ser Gly Arg Pro Lys Xaa Arg Ala Ala Arg Gly His Ala Val Ala Gly
20 25 30
Pro Gly Thr Ala Trp Gly Ala Glu Ile Thr Met Thr His Ser Ala Asp
35 40 45
Phe Leu Pro Ala Met Glu Thr Ala Ala Phe Leu Lys Ala Cys Gly Ile
50 55 60
Cys Asn Arg Arg Leu Gly Pro Gly Arg Asp Thr Phe Ile Tyr Met Gly
65 70 75 80
Glu Val Ala Phe Cys Ser Gln Glu Xaa Arg Gln Gln Gln Met Asn Leu
85 90 95
Asp Glu Leu Met Glu Lys Lys Cys Ser Thr Pro Ala Gly Gly Gly Gly
100 105 110
Gly Gly Val Gly Gly Gly Gly Gly Gly Gly Ser Asp Gln Pro Gly Lys
115 120 125
Ser Ser Thr Val Ala Ala Ala
130 135

(2) INFORMATION FOR SEQ ID NO:3055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..699
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3055:

accatacact gcagctcaaa cacagaagcg ccccaagaag cagcagcgca ggagcgcgcg 60
atcgctatgg ctcagggaag aggcagctgcg acgcgggggc ttgcctctcg cgcctactc 120
gccgcgcgctt tctctctctc cctcggcgctc gcgcagcgcg ccacccacag ggtcgactgg 180
tccttcaacg cggacagctg gtccaaaggc aagagcttcC gtgcgcgcga cgtcctcgag 240
ttcaactacg acccctccgt gcacaacgtg gtggccgctg acgcgcgcgcg ctacaacggc 300
tgccggccct cgggcacgtc gtacggctcc gggagcgacc gcatacagct cggccccgcg 360
accagctact tcactctcag cctcaacagg cactcgcgga tggggatgaa gatggtcgct 420
aatgccagct gagcaacgag cttatatgtt agtactgcaa aaatatatgg gctagtgtgtg 480
gtccgataga tcgtgcaaga actcaatcgt gtggcatact cgtaccgtgt gttcgatgga 540
cacggttcac gtgttgtgtg tgcatcgac tgctgttagg tcaggcatga tgcactgtgt 600
gctgtggcg tggttagtaa gcgtctcgca gctttgttgt tactttgttc gatcgaaaga 660
gcggtctctt ttgtttgttc atcaataaca tcttcatt

(2) INFORMATION FOR SEQ ID NO:3056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..143
(D) OTHER INFORMATION: / Ceres Seq. ID 1575352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3056:

Thr	His	His	Cys	Ser	Ser	Asn	Thr	Glu	Ala	Pro	Gln	Glu	Ala	Ala	Ala
1			5					10						15	
Gln	Glu	Arg	Ala	Ile	Ala	Met	Ala	Gln	Gly	Arg	Gly	Ser	Ala	Thr	Arg
			20					25					30		
Gly	Leu	Ala	Leu	Gly	Ala	Leu	Leu	Ala	Ala	Ala	Phe	Leu	Leu	Leu	Leu
			35				40					45			
Gly	Val	Ala	Asp	Ala	Ala	Thr	His	Arg	Val	Asp	Trp	Ser	Phe	Asn	Ala
			50				55				60				
Asp	Ser	Trp	Ser	Lys	Gly	Lys	Ser	Phe	Arg	Ala	Gly	Asp	Val	Leu	Glu
65				70				75						80	
Phe	Asn	Tyr	Asp	Pro	Ser	Val	His	Asn	Val	Val	Ala	Val	Asp	Ala	Gly
			85					90					95		
Gly	Tyr	Asn	Gly	Cys	Arg	Pro	Ser	Gly	Thr	Ser	Tyr	Gly	Ser	Gly	Ser
			100					105					110		
Asp	Arg	Ile	Thr	Leu	Gly	Pro	Gly	Thr	Ser	Tyr	Phe	Ile	Cys	Ser	Leu
			115				120					125			
Asn	Arg	His	Cys	Gly	Met	Gly	Met	Lys	Met	Val	Val	Asn	Ala	Ser	
			130				135					140			

(2) INFORMATION FOR SEQ ID NO:3057:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..135
(D) OTHER INFORMATION: / Ceres Seq. ID 1575353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3057:

Pro	Ile	Thr	Ala	Ala	Gln	Thr	Gln	Lys	Arg	Pro	Lys	Lys	Gln	Gln	Arg
1				5				10					15		
Arg	Ser	Glu	Arg	Ser	Leu	Trp	Leu	Arg	Glu	Glu	Ala	Val	Arg	Arg	Gly
			20					25				30			
Gly	Leu	Pro	Ser	Ala	Pro	Tyr	Ser	Pro	Pro	Leu	Ser	Ser	Ser	Ser	Ser
			35				40				45				
Ala	Ser	Pro	Thr	Arg	Pro	Pro	Thr	Gly	Ser	Thr	Gly	Pro	Ser	Thr	Arg
			50				55				60				
Thr	Ala	Gly	Pro	Arg	Ala	Arg	Ala	Ser	Val	Pro	Ala	Thr	Ser	Ser	Ser
65				70				75					80		
Ser	Thr	Thr	Thr	Pro	Pro	Cys	Thr	Thr	Trp	Pro	Trp	Thr	Pro	Ala	
				85				90					95		
Ala	Thr	Thr	Ala	Ala	Gly	Pro	Pro	Ala	Arg	Arg	Thr	Ala	Pro	Gly	Ala
			100					105				110			
Thr	Ala	Ser	Arg	Ser	Ala	Pro	Ala	Pro	Ala	Thr	Ser	Ser	Ala	Ala	Ser
			115				120					125			
Thr	Gly	Thr	Ala	Gly	Trp	Gly									
			130			135									

(2) INFORMATION FOR SEQ ID NO:3058:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..149
(D) OTHER INFORMATION: / Ceres Seq. ID 1575354
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3058:

Pro Ser Leu Gln Leu Lys His Arg Ser Ala Pro Arg Ser Ser Ser Ala
1 5 10 15
Gly Ala Ser Asp Arg Tyr Gly Ser Gly Lys Arg Gln Cys Asp Ala Gly
20 25 30
Ala Cys Pro Arg Arg Pro Thr Arg Arg Arg Phe Pro Pro Pro Pro Arg
35 40 45
Arg Arg Arg Arg Gly His Pro Gln Gly Arg Leu Val Leu Gln Arg Gly
50 55 60
Gln Leu Val Gln Gly Gln Glu Leu Pro Cys Arg Arg Arg Pro Arg Val
65 70 75 80
Gln Leu Arg Pro Leu Arg Ala Gln Arg Gly Gly Arg Gly Arg Arg Arg
85 90 95
Leu Gln Arg Leu Pro Ala Leu Arg His Val Val Arg Leu Arg Glu Arg
100 105 110
Pro His His Ala Arg Pro Arg His Gln Leu Leu His Leu Gln Pro Gln
115 120 125
Gln Ala Leu Arg Asp Gly Asp Glu Asp Gly Arg Gln Cys Gln Leu Ser
130 135 140
Thr Thr Leu Ile Cys
145

- (2) INFORMATION FOR SEQ ID NO:3059:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 685 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..685
(D) OTHER INFORMATION: / Ceres Seq. ID 1575361

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3059:

gacgatgtct cttgccgcgg cgtaaccctt cgctccatt cccgcgcgca tcgcgcgtca 60
ggctccttgc gcggcattcc tgctccatcc cttaggtrgc gcgacggcga cgcggttgcg 120
tggaactggc gtggcctcgc agccagcggga gckwcgcgcc gcggcgatgg tcacgatggc 180
gaagaggggg caggagctgg aggatgaccg ggccatgacg acggaacaga tgggaagarga 240
ccttgtagac ctcaaggggg agcttttctt gctccgcctt aaGcgctcgg cgcgccagga 300
gttcaagaac agcgagttca gcgcgatgcg caagaggatt gctcgtatgc taaccgtgaa 360
aagagagcgg gaaattgaac aaggaatcaa taaaagattg tctagggaagc ttgataggaa 420
atggaagcag agcatctggt tcagaccacc accatctcta agggggaaca aagaggagta 480
gaaagcgcga aaaagagggc aatgtgcaaa agtcgtttca tgcgagtgtt gcaggaaggt 540
cccttcatga tttaaccctt tattgcgttg ttatgtattc catgtttaca ttttgcataag 600
cattgctatc tgaatctgaa tttaagttgt tagtctcttc tgtaaatttc gacttattta 660
aatttacctc tctatctgtg ttatc

- (2) INFORMATION FOR SEQ ID NO:3060:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1575362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3060:

Thr Met Ser Leu Ala Ala Ala Ser Pro Leu Ala Ser Ile Pro Arg Gly
1 5 10 15
Ile Ala Ala Gln Ala Pro Cys Ala Ala Phe Leu Ser Ile Arg Leu Gly
20 25 30
Xaa Ala Thr Ala Thr Arg Phe Ala Gly Leu Ala Val Ala Ser Gln Pro
35 40 45
Ala Glu Xaa Arg Ala Ala Ala Met Val Thr Met Ala Lys Arg Glu Gln
50 55 60
Glu Leu Glu Glu Ile Arg Ala Met Thr Thr Glu Gln Met Glu Xaa Glu
65 70 75 80
Val Val Asp Leu Lys Gly Glu Leu Phe Leu Leu Arg Leu Lys Arg Ser
85 90 95
Ala Arg Gln Glu Phe Lys Asn Ser Glu Phe Ser Arg Met Arg Lys Arg
100 105 110
Ile Ala Arg Met Leu Thr Val Lys Arg Glu Arg Glu Ile Glu Gln Gly
115 120 125
Ile Asn Lys Arg Leu Ser Arg Lys Leu Asp Arg Lys Trp Lys Gln Ser
130 135 140
Ile Val Val Arg Pro Pro Ser Leu Arg Gly Asn Lys Glu Glu
145 150 155

(2) INFORMATION FOR SEQ ID NO:3061:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1575363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3061:

Met Ser Leu Ala Ala Ala Ser Pro Leu Ala Ser Ile Pro Arg Gly Ile
1 5 10 15
Ala Ala Gln Ala Pro Cys Ala Ala Phe Leu Ser Ile Arg Leu Gly Xaa
20 25 30
Ala Thr Ala Thr Arg Phe Ala Gly Leu Ala Val Ala Ser Gln Pro Ala
35 40 45
Glu Xaa Arg Ala Ala Ala Met Val Thr Met Ala Lys Arg Glu Gln Glu
50 55 60
Leu Glu Glu Ile Arg Ala Met Thr Thr Glu Gln Met Glu Xaa Glu Val
65 70 75 80
Val Asp Leu Lys Gly Glu Leu Phe Leu Leu Arg Leu Lys Arg Ser Ala
85 90 95
Arg Gln Glu Phe Lys Asn Ser Glu Phe Ser Arg Met Arg Lys Arg Ile
100 105 110
Ala Arg Met Leu Thr Val Lys Arg Glu Arg Glu Ile Glu Gln Gly Ile
115 120 125
Asn Lys Arg Leu Ser Arg Lys Leu Asp Arg Lys Trp Lys Gln Ser Ile
130 135 140
Val Val Arg Pro Pro Pro Ser Leu Arg Gly Asn Lys Glu Glu
145 150 155

(2) INFORMATION FOR SEQ ID NO:3062:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1575364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3062:

```
Met Val Thr Met Ala Lys Arg Glu Gln Glu Leu Glu Glu Ile Arg Ala
1          5          10          15
Met Thr Thr Glu Gln Met Glu Xaa Glu Val Val Asp Leu Lys Gly Glu
20          25          30
Leu Phe Leu Leu Arg Leu Lys Arg Ser Ala Arg Gln Glu Phe Lys Asn
35          40          45
Ser Glu Phe Ser Arg Met Arg Lys Arg Ile Ala Arg Met Leu Thr Val
50          55          60
Lys Arg Glu Arg Glu Ile Glu Gln Gly Ile Asn Lys Arg Leu Ser Arg
65          70          75          80
Lys Leu Asp Arg Lys Trp Lys Gln Ser Ile Val Val Arg Pro Pro Pro
85          90          95
Ser Leu Arg Gly Asn Lys Glu Glu
100
```

(2) INFORMATION FOR SEQ ID NO:3063:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 794 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..794

(D) OTHER INFORMATION: / Ceres Seq. ID 1575386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3063:

```
cagaaggggg caaagctcgc ggcctcgcgt cgcgcgcgtc gttccggtcc aacgcggcga 60
cscaaaggct gccgtccccc ggcctcctcc tcccccctac cccctccccc cgmcacaacca 120
caggaaagaag cgagcagggc atcgagtttt ctgcgatgat gccatcgcgcg cctgcgcgatt 180
cctacggggtg cgcggcgctgc ggcgcgcgcc tgaacctgtc gccggcgcac ctgtaccogg 240
cggacttcta cttcgaggcc ggggaacaagg gcacgctgtc ctctctgtgg gtggacgagt 300
cgcgCctgcg gttcgcgcgc gaggacgcga tcgcgccctt ctctcgagacc ctcaactact 360
ggggcatcca ggggaagcgc acgcgcatca gctcgcgnacc tgcggccacc tgccttgcca 420
skctacgaag acggtctcgcc gcccatgcag gccaccgcgcc agttcgggat gggggccagc 480
caggctcctcc cgcgcgcgcc caggtaccgc ttcaagatca aggccatcgc gccagctccc 540
tcggcacctg cgcgcgcgcc ctatgaaaag tgatgtccca tagatttctt catctgggtg 600
cgtgtcctgt gtgctgtcgt tgcgtgggtt cgtgacttcc tgtaaattac gtatgcttcc 660
gcaattcgcg tectgcgttg tttcttttag aaacagtggt tttgaaatgg catgcgactg 720
aaactatgat tgaataggca tgcgacttct aatatacaca caagacagaa gatataaata 780
aaaaactatg attg
```

(2) INFORMATION FOR SEQ ID NO:3064:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1575387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3064:

```
Arg Arg Gly Gln Ser Ser Arg Pro Arg Val Ala Pro Val Val Pro Val
1          5          10          15
Gln Arg Gly Asp Xaa Lys Ala Ala Val Pro Gly Leu Pro Pro Pro Pro
```

	20		25		30
His Pro Phe Pro Ser Xaa Asn His Arg Lys Lys Arg Ala Gly His Arg	35	40	45		
Val Phe Ser Ile Asp Gly Ile Gly Ala Cys Arg Phe Leu Arg Val Arg	50	55	60		
Gly Val Arg Arg Ala Pro Glu Pro Val Gly Gly Ala Pro Val Pro Gly	65	70	75	80	
Gly Leu Leu Leu Arg Gly Arg Glu Gln Gly His Ala Val Leu Leu Val	85	90	95		
Gly Gly Arg Val Ala Pro Ala Val Arg Ala Arg Gly Pro His Pro Pro	100	105	110		
Leu Leu Arg Asp Pro Gln Leu Leu Gly His Pro Ala Glu Ala His Ala	115	120	125		
His Gln Leu Xaa Thr Cys Gly His Leu Leu Gly Xaa Xaa Thr Thr Thr	130	135	140		
Val Arg Arg Pro Cys Arg Ala Pro Ala Ser Ser Gly Trp Gly Pro Ala	145	150	155	160	
Arg Ser Ser Arg Ala Ala Pro Gly Thr Ala Ser Arg Ser Arg Pro Ser	165	170	175		
Pro Pro Ala Pro Arg His Leu Pro Pro Pro Met Lys Ser Asp Ala	180	185	190		

Pro

(2) INFORMATION FOR SEQ ID NO:3065:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1575388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3065:

Glu Gly Gly Lys Ala Arg Gly Leu Ala Ser Arg Arg Ser Phe Arg Ser	1	5	10	15
Asn Ala Ala Xaa Gln Arg Leu Pro Ser Pro Gly Phe Leu Leu Pro Leu	20	25	30	
Thr Pro Ser Pro Xaa Gln Thr Thr Gly Arg Ser Glu Gln Gly Ile Glu	35	40	45	
Phe Ser Arg Ser Met Ala Ser Ala Pro Ala Asp Ser Tyr Gly Cys Ala	50	55	60	
Ala Cys Gly Ala Pro Leu Asn Leu Ser Ala Ala His Leu Tyr Pro Ala	65	70	75	80
Asp Phe Tyr Phe Glu Ala Gly Asn Lys Gly Thr Leu Ser Phe Ser Trp	85	90	95	
Val Asp Glu Ser Arg Leu Arg Phe Ala Pro Glu Asp Arg Ile Arg Pro	100	105	110	
Phe Phe Glu Thr Leu Asn Tyr Trp Gly Ile Gln Arg Lys Arg Thr Arg	115	120	125	
Ile Ser Cys Xaa Pro Ala Ala Thr Cys Leu Ala Xaa Leu Arg Arg Arg	130	135	140	
Ser Ala Gly His Ala Gly His Arg Pro Val Arg Asp Gly Ala Gln Pro	145	150	155	160
Gly His Pro Ala Pro Pro Gln Val Pro Leu Gln Asp Gln Gly His Arg	165	170	175	
Arg Gln Leu Leu Gly Thr Cys Arg Arg Arg Leu	180	185		

(2) INFORMATION FOR SEQ ID NO:3066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..135
(D) OTHER INFORMATION: / Ceres Seq. ID 1575389
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3066:

Met Ala Ser Ala Pro Ala Asp Ser Tyr Gly Cys Ala Ala Cys Gly Ala
1 5 10 15
Pro Leu Asn Leu Ser Ala Ala His Leu Tyr Pro Ala Asp Phe Tyr Phe
20 25 30
Glu Ala Gly Asn Lys Gly Thr Leu Ser Phe Ser Trp Val Asp Glu Ser
35 40 45
Arg Leu Arg Phe Ala Pro Glu Asp Arg Ile Arg Pro Phe Phe Glu Thr
50 55 60
Leu Asn Tyr Trp Gly Ile Gln Arg Lys Arg Thr Arg Ile Ser Cys Xaa
65 70 75 80
Pro Ala Ala Thr Cys Leu Ala Xaa Leu Arg Arg Arg Ser Ala Gly His
85 90 95
Ala Gly His Arg Pro Val Arg Asp Gly Ala Gln Pro Gly His Pro Ala
100 105 110
Pro Pro Gln Val Pro Leu Gln Asp Gln Gly His Arg Arg Gln Leu Leu
115 120 125
Gly Thr Cys Arg Arg Arg Leu
130 135

- (2) INFORMATION FOR SEQ ID NO:3067:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 836 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..836
(D) OTHER INFORMATION: / Ceres Seq. ID 1575402

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3067:

atccgatccg agccatattta aacagacgca tgcacgcngc gccggccgga gcgcacggcg 60
gcggcgccct cctgcggacc cagcttcgcg ctattagcta gcttgctgca cgacgctacg 120
tgcttttctg tegtccctgcc ggtcgccatg accttcccgc tggtttgcta ctgctacggc 180
gtgcgcggcc ccgctggccgc gctgctcaag ctctcccaag ccgcgctgct cgtgttcgtg 240
ctgctcctct ccttctctcg cctctacgag ttctcctacg accccgagga tcacgcgcca 300
ccagccatca acggcgccgc cccagggcca gagcgcggtga agcggcgccct cccgctcgtc 360
gagttctctg agctggtgta ttctgctctg tcacgctcgt cgggggtggg ggcggaGCcg 420
acgtgcggcg tgtgctctga gtggcttgag gccaaaggac aggtgcggcg gctgggcaac 480
tgcacccacc cgttccacac gcgtgtgcat gacgcgtgga tcgacctggg cgaggtgacg 540
tgcccgcttt gccgttccca cctgctgcgc gcgcggcgcg ccggcctact cagcatggca 600
cggtctggct agtcgcgcgt cctgtgttcc ctctcatcct taattgccag tacgatacgt 660
gcccgctcac agccgtgcct ggcttcaggc cagcgcgcgcg cggtctggtac gcgcacagat 720
gccactgggc actgtgtccg gatgggggca gaccatgaga ccaaccgtga actaggacga 780
ctgtctatgt aaagaatttt ttccgctcaa tggatggcg cgaagccaaat tactwg

- (2) INFORMATION FOR SEQ ID NO:3068:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1575403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3068:

Met	Thr	Phe	Pro	Leu	Val	Cys	Tyr	Cys	Tyr	Ala	Val	Pro	Arg	Pro	Val
1				5					10					15	
Ala	Ala	Leu	Leu	Lys	Leu	Leu	His	Ala	Ala	Val	Leu	Val	Phe	Val	Leu
			20				25					30			
Leu	Leu	Ser	Phe	Leu	Gly	Leu	Tyr	Glu	Phe	Ser	Tyr	Asp	Pro	Glu	Asp
		35			40						45				
His	Ala	Pro	Pro	Ala	Ile	Asn	Gly	Gly	Arg	Pro	Arg	Pro	Glu	Ala	Val
		50			55					60					
Lys	Arg	Arg	Leu	Pro	Leu	Val	Glu	Phe	Leu	Glu	Leu	Val	Asp	Ser	Ser
		65			70				75					80	
Ser	Ser	Pro	Ser	Ser	Gly	Val	Gly	Ala	Glu	Pro	Thr	Cys	Arg	Val	Cys
			85						90					95	
Leu	Glu	Trp	Leu	Glu	Ala	Lys	Asp	Glu	Val	Arg	Arg	Leu	Gly	Asn	Cys
		100					105					110			
Thr	His	Ala	Phe	His	Thr	Arg	Cys	Ile	Asp	Arg	Trp	Ile	Asp	Leu	Gly
		115					120					125			
Glu	Val	Thr	Cys	Pro	Leu	Cys	Arg	Ser	His	Leu	Leu	Pro	Arg	Arg	Arg
		130				135						140			
Ala	Gly	Leu	Leu	Ser	Met	Ala	Arg	Leu	Gly						
145					150										

(2) INFORMATION FOR SEQ ID NO:3069:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 674 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..674

(D) OTHER INFORMATION: / Ceres Seq. ID 1575404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3069:

catcaacaat	gatgcctcta	aggtgaactc	tcattggtcca	catcagagtt	ctggttccac	60
ttgtctatgg	gagaaaaaatg	agcctccagt	caatctacc	cgctacaact	tgtccgcatt	120
tgcataaaca	ctaaatgagt	taacaccaga	gctcgaggag	aagctgccac	cgacggattc	180
aaggctgaga	ccagatcaac	ggcacctgga	gaatggggag	tacgagaag	ccaatgctga	240
aaaactgcgc	ctcgagacac	agcaacggat	ggcaaggag	atgcaggaga	gtggctggaa	300
accaagatgg	ttccaaagg	acagcgagga	tggaaactac	cgctacgtcg	gaggttactg	360
ggaggcaagg	gagcagagaa	catgggtcgg	ctgcaatgac	atatttggt	actgtctatg	420
cagccagaag	ctcccaccat	ccgctctcta	cacgagctga	agtatatagg	ggtgggtaag	480
gccggaagg	catgttcagt	agttgtgtac	atcgcattaa	ccagaggggt	tttctctcgt	540
ttctgWttdg	tgttaagctg	tgagctaaaca	tgtttttctt	gtcaattgtc	acattgaagc	600
caaggacatc	caagcataac	ccaacctttt	gtcgatacta	ggatacttat	gagagatctt	660
gtggacatta	ttgc					

(2) INFORMATION FOR SEQ ID NO:3070:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1575405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3070:

Ile Asn Asn Asp Ala Ser Lys Val Asn Ser His Gly Pro His Gln Ser
1 5 10 15
Ser Gly Ser Thr Leu Leu Trp Glu Lys Asn Glu Pro Pro Val Asn Pro
20 25 30
Thr Arg Tyr Asn Leu Ser Ala Phe Ala Ile Thr Leu Asn Glu Leu Thr
35 40 45
Pro Glu Leu Glu Glu Lys Leu Pro Pro Thr Asp Ser Arg Leu Arg Pro
50 55 60
Asp Gln Arg His Leu Glu Asn Gly Glu Tyr Glu Lys Ala Asn Ala Glu
65 70 75 80
Lys Leu Arg Leu Glu Thr Gln Gln Arg Met Ala Arg Lys Met Gln Glu
85 90 95
Ser Gly Trp Lys Pro Arg Trp Phe Gln Arg Asp Ser Glu Asp Gly Thr
100 105 110
Tyr Arg Tyr Val Gly Gly Tyr Trp Glu Ala Arg Glu Gln Arg Thr Trp
115 120 125
Val Gly Cys Asn Asp Ile Phe Gly Asn Leu Ser Ser Ser Gln Lys Leu
130 135 140
Pro Pro Ser Ala Leu Tyr Thr Ser
145 150

(2) INFORMATION FOR SEQ ID NO:3071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3071:

Met Gly Ser Thr Arg Arg Pro Met Leu Lys Asn Cys Ala Ser Arg His
1 5 10 15
Ser Asn Gly Trp Gln Gly Arg Cys Arg Arg Val Ala Gly Asn Gln Asp
20 25 30
Gly Ser Lys Gly Thr Ala Arg Met Glu Arg Thr Ala Thr Ser Glu Val
35 40 45
Thr Gly Arg Gln Gly Ser Arg Glu His Gly Ser Ala Ala Met Thr Tyr
50 55 60
Leu Val Thr Cys Leu Ala Ala Arg Ser Ser His His Pro Leu Ser Thr
65 70 75 80
Arg Ala Glu Val Tyr Arg Gly Gly
85

(2) INFORMATION FOR SEQ ID NO:3072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..81
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3072:

Met Leu Lys Asn Cys Ala Ser Arg His Ser Asn Gly Trp Gln Gly Arg
1 5 10 15
Cys Arg Arg Val Ala Gly Asn Gln Asp Gly Ser Lys Gly Thr Ala Arg
20 25 30
Met Glu Arg Thr Ala Thr Ser Glu Val Thr Gly Arg Gln Gly Ser Arg

	35		40		45	
Glu	His	Gly	Ser	Ala	Ala	Met
50					55	
Arg	Ser	Ser	His	His	Pro	Leu
65				70		
Gly						

(2) INFORMATION FOR SEQ ID NO:3073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..521
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3073:

cggttatctc	ttcttccact	gctctccaac	caCttcgtcc	tcgcccggctc	gcaactcctt	60
gatggcgccc	acggcgagtc	tcactaccac	tgctccctcc	cctccagctc	tcctcaaaagc	120
atcagctcct	ttgttatctc	cttttcgccc	cgtctccgcg	cactgcaaga	acctgtgcac	180
caagaccaag	gccacagaaa	atgatcagtc	tgctaaaaag	catcagaagg	tgaagagcat	240
tctttgcacg	gactgcgaag	gaaatggggc	aatcacatgc	accaaaatgtg	aagggaaatgg	300
ggtaaatctc	gttgactatt	tgaaggccg	atttaaagct	ggatctttat	gctgtgtgtc	360
agaattgtgt	cggcaggtgt	ctaataaagg	cttctgtgtg	ggaaagaatt	ggatccacgg	420
gcagctttta	gtcatttgtt	tggaggcatt	ggattcattg	gagggtcgat	ttgtgattgt	480
aatcacgatt	aatgtaatgg	attggaaatt	cggaaggggc	c		

(2) INFORMATION FOR SEQ ID NO:3074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..173
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3074:

Val	Tyr	Leu	Phe	Phe	His	Cys	Leu	Pro	Thr	Thr	Ser	Ser	Pro	Ala
1			5						10				15	
Arg	Asn	Ser	Leu	Met	Ala	Ala	Thr	Ala	Ser	Leu	Thr	Thr	Thr	Ala
			20					25					30	
Ser	Pro	Pro	Ala	Leu	Leu	Lys	Ala	Ser	Ala	Pro	Leu	Leu	Ile	Ser
			35				40						45	
Arg	Pro	Val	Ser	Arg	His	Cys	Lys	Asn	Leu	Cys	Ile	Lys	Thr	Lys
			50			55				60				
Thr	Glu	Asn	Asp	Gln	Ser	Ala	Lys	Lys	His	Gln	Lys	Val	Lys	Ser
			65			70			75				80	
Leu	Cys	Gln	Asp	Cys	Glu	Gly	Asn	Gly	Ala	Ile	Thr	Cys	Thr	Lys
			85				90						95	
Glu	Gly	Asn	Gly	Val	Asn	Ser	Val	Asp	Tyr	Phe	Glu	Gly	Arg	Phe
			100					105					110	
Ala	Gly	Ser	Leu	Cys	Trp	Leu	Ser	Glu	Leu	Val	Arg	Gln	Val	Ser
			115				120						125	
Lys	Gly	Phe	Leu	Leu	Gly	Lys	Asn	Trp	Ile	His	Gly	Gln	Leu	Leu
			130				135						140	
Ile	Cys	Leu	Glu	Ala	Leu	Asp	Ser	Leu	Glu	Gly	Arg	Phe	Val	Ile
			145				150			155			160	
Ile	Thr	Ile	Asn	Val	Met	Asp	Trp	Lys	Phe	Gly	Arg	Gly		

165

170

(2) INFORMATION FOR SEQ ID NO:3075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1575430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3075:

Met	Ala	Ala	Thr	Ala	Ser	Leu	Thr	Thr	Thr	Ala	Pro	Ser	Pro	Pro	Ala
1				5						10				15	
Leu	Leu	Lys	Ala	Ser	Ala	Pro	Leu	Leu	Ile	Ser	Phe	Arg	Pro	Val	Ser
				20					25				30		
Arg	His	Cys	Lys	Asn	Leu	Cys	Ile	Lys	Thr	Lys	Ala	Thr	Glu	Asn	Asp
				35				40				45			
Gln	Ser	Ala	Lys	Lys	His	Gln	Lys	Val	Lys	Ser	Ile	Leu	Cys	Gln	Asp
				50				55				60			
Cys	Glu	Gly	Asn	Gly	Ala	Ile	Thr	Cys	Thr	Lys	Cys	Glu	Gly	Asn	Gly
				65				70				75			80
Val	Asn	Ser	Val	Asp	Tyr	Phe	Glu	Gly	Arg	Phe	Lys	Ala	Gly	Ser	Leu
				85					90				95		
Cys	Trp	Leu	Ser	Glu	Leu	Val	Arg	Gln	Val	Ser	Asn	Lys	Gly	Phe	Leu
				100					105				110		
Leu	Gly	Lys	Asn	Trp	Ile	His	Gly	Gln	Leu	Leu	Val	Ile	Cys	Leu	Glu
				115				120				125			
Ala	Leu	Asp	Ser	Leu	Glu	Gly	Arg	Phe	Val	Ile	Val	Ile	Thr	Ile	Asn
				130				135				140			
Val	Met	Asp	Trp	Lys	Phe	Gly	Arg	Gly							
				145				150							

(2) INFORMATION FOR SEQ ID NO:3076:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 854 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..854

(D) OTHER INFORMATION: / Ceres Seq. ID 1575435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3076:

gtagaggtct	tttactaaca	gggaaaggga	agggatggcc	acagcgcgcc	tgctccggtg	60
cgctctctcc	accttccttt	tcagcacctg	caccaccaat	ccgttgccgt	cgtrctcccc	120
tctcgtccgc	mgccagcacc	cccgcgcgcg	catggccacg	gactcctccg	ccgcctcgtt	180
ccagaaagtc	cagatccacc	gcgaggcacac	cacttttgat	gcttatgttg	ttggcaaaaga	240
aaatgctcct	ggaaattgtg	ttttgcaaga	atagtgrrcg	cggtggtgac	caagggccac	300
gacgagggga	tgaaggcrgc	ggcgcgcctg	ctggaggagt	tcgggctccc	gccggggctg	360
ctgcgcgtgg	aggaagtkac	ggaggtgggg	ttcgtgcggg	ccaccggcta	cttctggctc	420
gcgcaGCgca	agaaggtgga	gcaccggttc	cgcaagatcg	gcaagcaggt	gagctacgac	480
gtcagatcgc	ccggctacgt	ccggcccaagg	ggcatcagga	ggctcaaggg	ggtcaaggcc	540
aaggagctcg	tgctctggcc	gcccgctcac	gagatggccg	tcgacgacga	cccgcaccac	600
ggcaagatcc	acttcaagag	ctcgcgcggc	gtcaccaaga	ccttccccgt	tgannbcttc	660
gccgcgcggc	agtagccacc	cacgcgtacc	atcttatatt	atcactataa	taatacacata	720
tacaccatta	tatatggcgc	atatatatag	tattaattaa	tctcttgtgt	tactaacctta	780
tatatatggt	atgtgtgtac	ttgcttttgc	aatcctgatg	atgatgaaga	acgtaaacctc	840
tagttttttt	cctg					

(2) INFORMATION FOR SEQ ID NO:3077:

(A) LENGTH: 216 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..216

(D) OTHER INFORMATION: / Ceres Seq. ID 1575436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3077:

1	Gly	Leu	Leu	Leu	Thr	Gly	Lys	Gly	Lys	Gly	Trp	Pro	Gln	Arg	Ala
5								10						15	
Cys	Ser	Val	Ala	Pro	Pro	Gln	Pro	Ser	Phe	Ser	Ala	Pro	Ala	Pro	Pro
20								25					30		
Ile	Arg	Cys	Ala	Arg	Xaa	Pro	Leu	Ser	Ser	Xaa	Ala	Ser	Thr	Pro	Ala
35							40					45			
Pro	Pro	Trp	Pro	Arg	Thr	Pro	Pro	Pro	Arg	Ser	Arg	Arg	Ser	Arg	
50						55				60					
Ser	Ser	Ala	Arg	Thr	Pro	Leu	Leu	Met	Leu	Met	Leu	Leu	Ala	Lys	Lys
65					70				75					80	
Met	Leu	Leu	Glu	Leu	Trp	Phe	Cys	Lys	Asn	Ser	Xaa	Arg	Gly	Gly	Asp
85								90					95		
Gln	Gly	Pro	Arg	Arg	Gly	Asp	Glu	Gly	Xaa	Gly	Gly	Ala	Ala	Gly	Gly
100							105						110		
Val	Arg	Ala	Pro	Ala	Gly	Ala	Ala	Ala	Ala	Gly	Gly	Arg	Xaa	Gly	Gly
115							120					125			
Gly	Val	Arg	Ala	Gly	His	Arg	Leu	Leu	Leu	Ala	Arg	Ala	Ala	Gln	Glu
130						135						140			
Gly	Gly	Ala	Pro	Val	Pro	Gln	Asp	Arg	Gln	Ala	Gly	Glu	Leu	Arg	Arg
145					150					155					
Arg	Asp	Arg	Arg	Leu	Arg	Pro	Ala	Gln	Gly	His	Gln	Glu	Ala	Gln	Gly
165									170				175		
Gly	Gln	Gly	Gln	Gly	Ala	Arg	Ala	Leu	Ala	Ala	Arg	Pro	Arg	Asp	Gly
180							185					190			
Arg	Arg	Arg	Arg	Pro	Ala	His	Arg	Gln	Asp	Pro	Leu	Gln	Glu	Pro	Arg
195							200					205			
Arg	Arg	His	Gln	Asp	Leu	Pro	Arg								
210						215									

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1575437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3078:

Met	Leu	Met	Leu	Leu	Ala	Lys	Lys	Met	Leu	Leu	Glu	Leu	Trp	Phe	Cys
1				5					10					15	
Lys	Asn	Ser	Xaa	Arg	Gly	Gly	Asp	Gln	Gly	Pro	Arg	Arg	Gly	Asp	Glu
			20					25					30		
Gly	Xaa	Gly	Gly	Ala	Ala	Gly	Gly	Val	Arg	Ala	Pro	Ala	Gly	Ala	Ala
		35				40						45			
Ala	Ala	Gly	Gly	Arg	Xaa	Gly	Gly	Gly	Val	Arg	Ala	Gly	His	Arg	Leu
50						55					60				
Leu	Leu	Ala	Arg	Ala	Ala	Gln	Glu	Gly	Gly	Ala	Pro	Val	Pro	Gln	Asp
65				70						75				80	

Arg Gln Ala Gly Glu Leu Arg Arg Arg Asp Arg Arg Leu Arg Pro Ala
85 90 95
Gln Gly His Gln Glu Ala Gln Gly Gly Gln Gly Ala Arg Ala
100 105 110
Leu Ala Ala Arg Pro Arg Asp Gly Arg Arg Arg Pro Ala His Arg
115 120 125
Gln Asp Pro Leu Gln Glu Pro Arg Arg Arg His Gln Asp Leu Pro Arg
130 135 140

(2) INFORMATION FOR SEQ ID NO:3079:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1575438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3079:

Met Leu Leu Ala Lys Lys Met Leu Leu Glu Leu Trp Phe Cys Lys Asn
1 5 10 15
Ser Xaa Arg Gly Gly Asp Gln Gly Pro Arg Arg Gly Asp Glu Gly Xaa
20 25 30
Gly Gly Ala Ala Gly Gly Val Arg Ala Pro Ala Gly Ala Ala Ala Ala
35 40 45
Gly Gly Arg Xaa Gly Gly Val Arg Ala Gly His Arg Leu Leu Leu
50 55 60
Ala Arg Ala Ala Gln Glu Gly Gly Ala Pro Val Pro Gln Asp Arg Gln
65 70 75 80
Ala Gly Glu Leu Arg Arg Arg Asp Arg Arg Leu Arg Pro Ala Gln Gly
85 90 95
His Gln Glu Ala Gln Gly Gly Gln Gly Gln Gly Ala Arg Ala Leu Ala
100 105 110
Ala Arg Pro Arg Asp Gly Arg Arg Arg Arg Pro Ala His Arg Gln Asp
115 120 125
Pro Leu Gln Glu Pro Arg Arg Arg His Gln Asp Leu Pro Arg
130 135 140

(2) INFORMATION FOR SEQ ID NO:3080:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..826

(D) OTHER INFORMATION: / Ceres Seq. ID 1575439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3080:

gcagataaca accagcaatg gtcacgactg ccgtcgccgc ggtcgccgcg gccgtgccgc 60
cagctcggaa agcccaagcg gtaactgtgg ccacaaccac agcactacct cccaccctca 120
ctagaaggca gctcctcgcc cgggtcgcca ccggctccac cctcccccac gccgcgcct 180
cagctcgccg ccccaggttc cccgagatgc cgggtccggc cggcgtgaag gccctggacc 240
ttcgggaagg ttcgggagag atcccgccgc ttggcgacca ggttcgggtt cactattatg 300
ggagattagc agcgaaGcaa ggaatggcgt tggattcgac gtatgatcac aaggacgaga 360
ccggcgatcc catgccgttt gtcttcaccc ttgggtccgg caaggttata cctggcattg 420
aagcagcagt gaagtccatg agagtggcgg gtcttcgcgg agtgatcatt ccaccatcgc 480
agggatacca aaacacgtca caagaaccgg ttcttcctaa tttctttgat cggcagaggc 540

tggtcaccac tatattcaac ccgacgcgcc tcgcaaatgg cgagggttcc actctcggca 600
cacttatctt cgacatcgag ctaatacaaca ttaggcaacg ttcataactg ttctgctcca 660
tactcttggt tctaaaaagt tgttcctggt aagaatctgg ttatgcttta agtaactgtc 720
agcgctcttc ggtaaatccc caattacata ttgtaatgca tactgatcgc tgacagacga 780
tatatgaaga aaaatcaatt gaatgcggat ttgattccgt tggttct

(2) INFORMATION FOR SEQ ID NO:3081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..209

(D) OTHER INFORMATION: / Ceres Seq. ID 1575440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3081:

Met	Val	Thr	Thr	Ala	Val	Ala	Ala	Val	Ala	Gly	Ala	Val	Pro	Pro	Ala
1			5					10					15		
Arg	Lys	Ala	Gln	Ala	Val	Thr	Val	Ala	Thr	Thr	Thr	Ala	Leu	Pro	Pro
			20				25						30		
Thr	Leu	Thr	Arg	Arg	Gln	Leu	Leu	Ala	Ala	Val	Ala	Thr	Gly	Ser	Thr
			35				40					45			
Leu	Pro	Thr	Ala	Ala	Ala	Ser	Ala	Ala	Ala	Pro	Arg	Phe	Ala	Glu	Ile
			50				55					60			
Pro	Gly	Ser	Gly	Gly	Val	Lys	Ala	Leu	Asp	Leu	Arg	Glu	Gly	Ser	Gly
			65				70					75			80
Glu	Ile	Pro	Ala	Val	Gly	Asp	Gln	Val	Ala	Val	His	Tyr	Tyr	Gly	Arg
			85						90				95		
Leu	Ala	Ala	Lys	Gln	Gly	Trp	Arg	Phe	Asp	Ser	Thr	Tyr	Asp	His	Lys
			100					105					110		
Asp	Glu	Thr	Gly	Asp	Pro	Met	Pro	Phe	Val	Phe	Thr	Leu	Gly	Ser	Gly
			115				120					125			
Lys	Val	Ile	Pro	Gly	Met	Glu	Ala	Ala	Val	Lys	Ser	Met	Arg	Val	Gly
			130				135					140			
Gly	Leu	Arg	Arg	Val	Ile	Pro	Pro	Ser	Gln	Gly	Tyr	Gln	Asn	Thr	
			145				150					155		160	
Ser	Gln	Glu	Pro	Val	Pro	Pro	Asn	Phe	Phe	Asp	Arg	Gln	Arg	Leu	Phe
			165					170					175		
Thr	Thr	Ile	Phe	Asn	Pro	Thr	Arg	Leu	Ala	Asn	Gly	Glu	Gly	Ser	Thr
			180				185						190		
Leu	Gly	Thr	Leu	Ile	Phe	Asp	Ile	Glu	Leu	Ile	Asn	Ile	Arg	Gln	Arg
			195				200					205			
Ser															

(2) INFORMATION FOR SEQ ID NO:3082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..529

(D) OTHER INFORMATION: / Ceres Seq. ID 1575441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3082:

ctcgtctcca	ctgctctgct	gctcctcgca	ccgcgcgcgc	cgccgcgcgc	gcgcagtaat	60
gGcttcgcgc	cggtgtctcc	ggaacgcggg	ctcccggcgc	ctctctctct	acctactct	120
ccgcgcgcgt	gcgatatatg	tactctctgc	gctaccgcgt	gcgcgcgcgc	cgccgcgcgc	180
gccggNccca	gccgcaccgc	acggccggga	ccctctgggc	gaggtctatg	gccaccttca	240

cgcgacagaa gcccatgtg aatgtcggca ccattgggca cgtcgatcac ggcaaaacca 300
ctctcactgc tgcattacc aaggtcctgg ccgaggcagg gaaggccaaa gccgttggtt 360
tcgacgagat cgacaaggct ccggaggaga aagccagagg aatcaccatt gcgacagCtc 420
acgtcgagta tgagacggct aaaaggcatt atgtccacgt tgattgtcca ggtcacgcag 480
attatgtcaa gaacatgac actggagctg ctcagcggtt cctgtgttc

(2) INFORMATION FOR SEQ ID NO:3083:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3083:

Ser Ser Pro Leu Leu Cys Cys Ser Ser His Arg Arg Arg Arg Arg Arg
1 5 10 15
Ser Asp Val Met Ala Ser Ala Ala Val Leu Arg Asn Ala Gly Ser Arg
20 25 30
Arg Leu Phe Ser Tyr Pro Thr Leu Arg Ala Ala Ala Ile Tyr Val Pro
35 40 45
Ser Ala Leu Pro Asp Ala Pro Ala Ala Ala Ala Pro Xaa Pro Ala
50 55 60
Ala Thr Asp Gly Arg Asp Pro Leu Gly Glu Val Tyr Gly His Leu His
65 70 75 80
Ala His Glu Ala Pro Cys Glu Cys Arg His His Trp Ala Arg Arg Ser
85 90 95
Arg Gln Asn His Ser His Cys Cys His Tyr Gln Gly Pro Gly Arg Gly
100 105 110
Arg Glu Gly Gln Ser Arg Cys Phe Arg Arg Asp Arg Gln Gly Ser Gly
115 120 125
Gly Glu Ser Gln Arg Asn His His Cys Asp Ser Ser Arg Arg Val
130 135 140

(2) INFORMATION FOR SEQ ID NO:3084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3084:

Met Ala Ser Ala Ala Val Leu Arg Asn Ala Gly Ser Arg Arg Leu Phe
1 5 10 15
Ser Tyr Pro Thr Leu Arg Ala Ala Ala Ile Tyr Val Pro Ser Ala Leu
20 25 30
Pro Asp Ala Pro Ala Ala Ala Ala Pro Xaa Pro Ala Ala Thr Asp
35 40 45
Gly Arg Asp Pro Leu Gly Glu Val Tyr Gly His Leu His Ala His Glu
50 55 60
Ala Pro Cys Glu Cys Arg His His Trp Ala Arg Ser Arg Gln Asn
65 70 75 80
His Ser His Cys Cys His Tyr Gln Gly Pro Gly Arg Gly Arg Glu Gly
85 90 95
Gln Ser Arg Cys Phe Arg Arg Asp Arg Gln Gly Ser Gly Gly Glu Ser
100 105 110

Gln Arg Asn His His Cys Asp Ser Ser Arg Arg Val
115 120

(2) INFORMATION FOR SEQ ID NO:3085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3085:

Met	Tyr	Leu	Leu	Arg	Tyr	Pro	Met	Arg	Pro	Arg	Arg	Arg	Gln	Arg	Arg
1									10				15		
Xaa	Gln	Pro	Pro	Pro	Thr	Ala	Gly	Thr	Leu	Trp	Ala	Arg	Ser	Met	Ala
									25				30		
Thr	Phe	Thr	Arg	Thr	Lys	Pro	His	Val	Asn	Val	Gly	Thr	Ile	Gly	His
									40				45		
Val	Asp	His	Gly	Lys	Thr	Thr	Leu	Thr	Ala	Ala	Ile	Thr	Lys	Val	Leu
									55				60		
Ala	Glu	Ala	Gly	Lys	Ala	Lys	Ala	Val	Ala	Phe	Asp	Glu	Ile	Asp	Lys
									70				75		
Ala	Pro	Glu	Glu	Lys	Ala	Arg	Gly	Ile	Thr	Ile	Ala	Thr	Ala	His	Val
									90				95		
Glu	Tyr	Glu	Thr	Ala	Lys	Arg	His	Tyr	Ala	His	Val	Asp	Cys	Pro	Gly
									105				110		
His	Ala	Asp	Tyr	Val	Lys	Asn	Met	Ile	Thr	Gly	Ala	Ala	Gln	Arg	Phe
									120				125		

Leu Cys
130

(2) INFORMATION FOR SEQ ID NO:3086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 632 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..632
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3086:

atttctctc	ccactcccaa	ccaaaccgtc	gctaactatc	actagtgcgc	gtgtgggtggt	60
cgctgctcata	tcctctcgct	ctgcctcgac	cgcccgatcg	cccatagcct	gctggcctgc	120
tctgctagcg	atggaccggt	ccaagtcgta	cgcgggcggg	cgcatgcaga	tcgagccgta	180
ctacggcgccg	ggcggcgggc	gaggaggagg	cgcgggggcg	gacttcgggt	cctactccta	240
cagcgccggc	gggacggggc	cgctgctcta	ctgctacaac	cagtcacagt	acggaggccc	300
ggggggcggt	gaggaggagg	tgaagcagag	caagtcgaag	cgcggtggc	tggcggaacc	360
ggacatggac	cgcaagcgcc	cgctggcgcg	cgtacaaggc	gtacggcggt	gagggcaggg	420
tgaagggtc	cctccgaag	agcttcagg	gggtcaagga	ccgtacac	gacctgtct	480
acggttggtc	ctgatccta	gagcacgcac	accacgcgc	tcctggttg	tgtttgtgt	540
ctcgtagatg	ttgttcatac	ttcctggtga	tgtgaaacca	accagtacag	tgtatgtatt	600
catgagatgt	gtgactcaag	aggtgtgttc	ag			

(2) INFORMATION FOR SEQ ID NO:3087:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..181

(D) OTHER INFORMATION: / Ceres Seq. ID 1575461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3087:

Phe Leu Leu Pro Leu Pro Thr Lys Pro Ser Leu Thr Ile Thr Ser Arg
1 5 10 15
Arg Val Val Val Val Val Ile Ser Leu Ala Ser Ala Ser Thr Ala Arg
20 25 30
Ser Pro Ile Ala Cys Trp Pro Ala Leu Leu Ala Met Asp Arg Ser Lys
35 40 45
Ser Tyr Ala Gly Gly Arg Met Gln Ile Glu Pro Tyr Tyr Gly Gly Gly
50 55 60
Gly Gly Gly Gly Gly Gly Ala Arg Ala Asp Phe Arg Ser Tyr Ser Tyr
65 70 75 80
Ser Ala Gly Gly Thr Gly Pro Ser Ser Tyr Ser Tyr Asn Gln Tyr Glu
85 90 95
Tyr Gly Gly Pro Gly Ala Gly Glu Glu Glu Val Lys Gln Ser Lys Ser
100 105 110
Lys Arg Arg Trp Leu Ala Asp Pro Asp Met Asp Arg Lys Arg Pro Arg
115 120 125
Gly Gly Val Gln Gly Val Arg Arg Gly Gly Gln Gly Glu Gly Leu Pro
130 135 140
Pro Gln Glu Leu Gln Val Gly Gln Gly Pro Leu Pro Arg Pro Arg Leu
145 150 155 160
Arg Leu Val Leu Ile Leu Arg Ala Arg Thr Pro Pro Leu Ser Met Val
165 170 175
Val Val Trp Leu Ser
180

(2) INFORMATION FOR SEQ ID NO:3088:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1575462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3088:

Met Asp Arg Ser Lys Ser Tyr Ala Gly Gly Arg Met Gln Ile Glu Pro
1 5 10 15
Tyr Tyr Gly Gly Gly Gly Gly Gly Gly Ala Arg Ala Asp Phe
20 25 30
Arg Ser Tyr Ser Tyr Ser Ala Gly Gly Thr Gly Pro Ser Ser Tyr Ser
35 40 45
Tyr Asn Gln Tyr Glu Tyr Gly Gly Pro Gly Ala Gly Glu Glu Glu Val
50 55 60
Lys Gln Ser Lys Ser Lys Arg Arg Trp Leu Ala Asp Pro Asp Met Asp
65 70 75 80
Arg Lys Arg Pro Arg Gly Gly Val Gln Gly Val Arg Arg Gly Gly Gln
85 90 95
Gly Glu Gly Leu Pro Pro Gln Glu Leu Gln Val Gly Gln Gly Pro Leu
100 105 110
Pro Arg Pro Arg Leu Arg Leu Val Leu Ile Leu Arg Ala Arg Thr Pro
115 120 125
Pro Leu Ser Met Val Val Val Trp Leu Ser
130 135

(2) INFORMATION FOR SEQ ID NO:3089:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..127
(D) OTHER INFORMATION: / Ceres Seq. ID 1575463
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3089:
Met Gln Ile Glu Pro Tyr Tyr Gly Gly Gly Gly Gly Gly Gly Gly
1 5 10 15
Ala Arg Ala Asp Phe Arg Ser Tyr Ser Tyr Ser Ala Gly Gly Thr Gly
20 25 30
Pro Ser Ser Tyr Ser Tyr Asn Gln Tyr Glu Tyr Gly Gly Pro Gly Ala
35 40 45
Gly Glu Glu Glu Val Lys Gln Ser Lys Ser Lys Arg Arg Trp Leu Ala
50 55 60
Asp Pro Asp Met Asp Arg Lys Arg Pro Arg Gly Gly Val Gln Gly Val
65 70 75 80
Arg Arg Gly Gly Gln Gly Glu Gly Leu Pro Gln Glu Leu Gln Val
85 90 95
Gly Gln Gly Pro Leu Pro Arg Pro Arg Leu Arg Leu Val Leu Ile Leu
100 105 110
Arg Ala Arg Thr Pro Pro Leu Ser Met Val Val Val Trp Leu Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:3090:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 745 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..745
(D) OTHER INFORMATION: / Ceres Seq. ID 1575488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3090:

aaaaattcca agagatgaac atcttgttga gtcaactgttg ttgctgcatt cttattctag 60
gcattctacgc tccgacatcc gccacatcag acaatcctcc tctgcaggat gtagtccccca 120
tggtctcccca gggcgagcgg cgagagttgt ccatgaacgg gtctcctctgc aagcatccga 180
gcaccatcct ggcgtccgac ttcaagactc tgatgctaaa ccacgccgga gacctggaca 240
gcatagcctc ggctgtcggt gacgatgggt accgctgcgg agttcccagg cctgaacacc 300
ctgggcctgt cgatggcgcg caccgacatc gCccctacg ggtgtgtgct ccgcactcc 360
caccgcgggg cgtcgagagt gatgttcgta cacgggtgcca gcgtggtggc cggttctctg 420
gacacccagg gcaggctgtt ccagaagcgt ctcggtgagg gagaggtggt cgtcttcccc 480
cgcggcttgc ttactactgt catgaactac ggtttcgccc tcgcgacggc gttctcctgt 540
ctgaacacgc agaaaccccg cgtggctcgt gtgcgccacg ccatgttttt tgcgagtgag 600
tcggacgtag tcgaaggtct aatggccagg atgctcaagt ttggagagat ggaggtgact 660
agtgaacaaca acatcactgc tggtttccca tgggcattct gatctgagta ggtgcaattc 720
aagatcgttg gtggtttaag ttccc

(2) INFORMATION FOR SEQ ID NO:3091:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1575489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3091:

Lys Phe Gln Glu Met Asn Ile Leu Leu Ser His Leu Cys Cys Cys Ile
1 5 10 15
Leu Ile Leu Gly Ile Tyr Ala Pro Thr Ser Ala Thr Ser Asp Asn Pro
20 25 30
Pro Leu Gln Asp Val Cys Pro Met Ala Pro Gln Gly Glu Arg Arg Glu
35 40 45
Leu Ser Met Asn Gly Phe Leu Cys Lys His Pro Ser Thr Ile Leu Ala
50 55 60
Ser Asp Phe Lys Thr Leu Met Leu Asn His Ala Gly Asp Leu Asp Ser
65 70 75 80
Ile Ala Ser Val Val Gly Glu His Gly Asp Arg Cys Arg Val Pro Arg
85 90 95
Pro Glu His Pro Gly Pro Val Asp Gly Ala His Arg His Arg Pro Leu
100 105 110
Arg Gly Gly Ala Pro Ala Leu Pro Pro Ala Gly Val Gly Asp Asp Val
115 120 125
Arg Thr Arg Trp Gln Arg Gly Gly Arg Leu Pro Gly His Arg Gly Gln
130 135 140
Ala Val Pro Glu Ala Ser Arg
145 150

(2) INFORMATION FOR SEQ ID NO:3092:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1575490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3092:

Met Asn Ile Leu Leu Ser His Leu Cys Cys Cys Ile Leu Ile Leu Gly
1 5 10 15
Ile Tyr Ala Pro Thr Ser Ala Thr Ser Asp Asn Pro Pro Leu Gln Asp
20 25 30
Val Cys Pro Met Ala Pro Gln Gly Glu Arg Arg Glu Leu Ser Met Asn
35 40 45
Gly Phe Leu Cys Lys His Pro Ser Thr Ile Leu Ala Ser Asp Phe Lys
50 55 60
Thr Leu Met Leu Asn His Ala Gly Asp Leu Asp Ser Ile Ala Ser Val
65 70 75 80
Val Gly Glu His Gly Asp Arg Cys Arg Val Pro Arg Pro Glu His Pro
85 90 95
Gly Pro Val Asp Gly Ala His Arg His Arg Pro Leu Arg Gly Gly Ala
100 105 110
Pro Ala Leu Pro Pro Ala Gly Val Gly Asp Asp Val Arg Thr Arg Trp
115 120 125
Gln Arg Gly Gly Arg Leu Pro Gly His Arg Gly Gln Ala Val Pro Glu
130 135 140
Ala Ser Arg
145

(2) INFORMATION FOR SEQ ID NO:3093:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..145
(D) OTHER INFORMATION: / Ceres Seq. ID 1575491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3093:

Met	Val	Thr	Ala	Ala	Glu	Phe	Pro	Gly	Leu	Asn	Thr	Leu	Gly	Leu	Ser
1				5					10					15	
Met	Ala	Arg	Thr	Asp	Ile	Ala	Pro	Thr	Gly	Val	Val	Leu	Pro	His	Ser
				20				25					30		
His	Pro	Arg	Ala	Ser	Glu	Met	Met	Phe	Val	His	Gly	Gly	Ser	Val	Val
				35				40					45		
Ala	Gly	Phe	Leu	Asp	Thr	Glu	Gly	Arg	Leu	Phe	Gln	Lys	Arg	Leu	Gly
				50				55					60		
Glu	Gly	Glu	Val	Phe	Val	Phe	Pro	Arg	Gly	Leu	Leu	His	Tyr	Val	Met
				65				70					75		80
Asn	Tyr	Gly	Phe	Gly	Leu	Ala	Thr	Ala	Phe	Ser	Val	Leu	Asn	Ser	Gln
				85				90					95		
Asn	Pro	Gly	Val	Val	Gly	Val	Ala	His	Ala	Met	Phe	Phe	Ala	Ser	Glu
				100				105					110		
Ser	Asp	Val	Val	Glu	Gly	Leu	Met	Ala	Arg	Met	Leu	Lys	Phe	Gly	Glu
				115				120					125		
Met	Glu	Val	Thr	Ser	Asp	Asn	Asn	Ile	Thr	Ala	Gly	Phe	Pro	Trp	Ala
				130				135					140		

Phe
145

(2) INFORMATION FOR SEQ ID NO:3094:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1105
(D) OTHER INFORMATION: / Ceres Seq. ID 1575492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3094:

agaaggaaga	ggctgaccgc	ctgcaagagg	agaggcacca	tttgaagag	agtactcgga	60
aaaagcttct	ggagatggag	cttgcaattt	ctagggcaaa	tgctcagctg	gagaagacag	120
aagcttctgc	tcgcagacgt	gaggttgaga	atgcacaa	cacgtttacg	atggaagctg	180
caaagcganc	atgcagcaga	gtcagcaaca	aattattcag	agcttttaaa	gaaagacgag	240
aacagccgta	aaaggtctca	gcgttgggaa	cttgatagag	ccctattaca	agaggaactt	300
gcagcaccaa	agagcagggt	atttcgggtt	caagaacaac	tcacgcatgc	taagaaacta	360
aaggtaccaag	tgccaggcaag	gtggaaacaa	gaggaggctg	caaagactga	ggcaattgcc	420
cttgtaacct	cagtgaggaa	agagagaggg	caaattgaga	ctccatgag	gtcagaagag	480
aatttctctg	atctcaaac	agcgaatgac	gcacaaagat	acaagagtga	gatccgtgtc	540
cttgagcagc	gtattgcgca	Gctgaagggt	tcattggact	cttcaagggt	tgctgcccc	600
aagtggggag	gcagacaata	atccatgca	ttgcattctt	ctgaaggagg	aaagaacaa	660
aatgcccgaag	ttttgtccaa	cacagcagta	ccccaaagtc	tcgattttga	cgatatacag	720
cgcgaccggg	agtgctcgtat	gtgcttgagc	gaggagatgt	ccgtgggtgt	ctccctctgc	780
gcccaccagg	tcgtctgtgc	caaatgcagc	gacctccatg	agaagcaagg	gatgaaggaa	840
tgccctctgt	gcggggcccc	catccagcgc	agggtgcgag	ccgcctctgc	cggttgctag	900
atttcacata	tactatttgg	attttacttt	tcttcttttt	ttcactttga	ttgctcagct	960
taagttgatg	gaagatttga	gagaataato	aggtggtgtg	agtggttgaa	actgtgcaca	1020
taatacatcg	ttaaacacca	aaacaagccc	agcagacagt	gggtactggt	ttggtttggt	1080
atatggctat	accggtgtgt	ctctgt				

(2) INFORMATION FOR SEQ ID NO:3095:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 299 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..299
(D) OTHER INFORMATION: / Ceres Seq. ID 1575493
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3095:

Arg Arg Lys Arg Leu Thr Ala Cys Lys Arg Arg Gly Thr Ile Trp Lys
1 5 10 15
Arg Val Leu Gly Lys Ser Phe Trp Arg Trp Ser Leu Gln Phe Leu Gly
20 25 30
Gln Met Leu Ser Trp Arg Lys Gln Lys Leu Leu Leu Ala Asp Val Arg
35 40 45
Leu Arg Met His Asn Ser Arg Tyr Arg Trp Lys Leu Gln Ser Xaa His
50 55 60
Ala Ala Glu Ser Ala Thr Asn Ile Ser Glu Leu Leu Lys Lys Asp Glu
65 70 75 80
Asn Ser Arg Lys Arg Ser Gln Arg Trp Glu Ser Asp Arg Ala Leu Leu
85 90 95
Gln Glu Glu Leu Ala Ala Gln Lys Ser Arg Leu Phe Arg Val Gln Glu
100 105 110
Gln Leu Gln His Ala Lys Glu Leu Lys Asp Gln Val Gln Ala Arg Trp
115 120 125
Lys Gln Glu Glu Ala Ala Lys Thr Glu Ala Ile Ala Leu Val Thr Ser
130 135 140
Val Arg Lys Glu Arg Gly Gln Ile Glu Thr Ser Met Arg Ser Glu Glu
145 150 155 160
Asn Leu Leu His Leu Lys Ala Ala Asn Asp Ala Gln Arg Tyr Lys Ser
165 170 175
Glu Ile Arg Val Leu Glu Gln Arg Ile Ala Gln Leu Lys Val Ser Leu
180 185 190
Asp Ser Ser Arg Val Ala Ala Pro Lys Trp Gly Ala Asp Asn Lys Ser
195 200 205
Tyr Ala Leu His Leu Ser Glu Gly Arg Lys Asn Asn Asn Ala Gln Val
210 215 220
Leu Ser Asn Thr Ala Val Pro Gln Gly Leu Asp Phe Asp Asp Ile Gln
225 230 235 240
Arg Asp Arg Glu Cys Val Met Cys Leu Ser Glu Glu Met Ser Val Val
245 250 255
Phe Leu Pro Cys Ala His Gln Val Val Cys Ala Lys Cys Ser Asp Leu
260 265 270
His Glu Lys Gln Gly Met Lys Glu Cys Pro Ser Cys Arg Ala Pro Ile
275 280 285
Gln Arg Arg Val Arg Ala Arg Pro Ala Gly Cys
290 295

- (2) INFORMATION FOR SEQ ID NO:3096:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..266
(D) OTHER INFORMATION: / Ceres Seq. ID 1575494
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3096:

Met Leu Ser Trp Arg Lys Gln Lys Leu Leu Leu Ala Asp Val Arg Leu
1 5 10 15
Arg Met His Asn Ser Arg Tyr Arg Trp Lys Leu Gln Ser Xaa His Ala

20 25 30
Ala Glu Ser Ala Thr Asn Ile Ser Glu Leu Leu Lys Lys Asp Glu Asn
35 40 45
Ser Arg Lys Arg Ser Gln Arg Trp Glu Ser Asp Arg Ala Leu Leu Gln
50 55 60
Glu Glu Leu Ala Ala Gln Lys Ser Arg Leu Phe Arg Val Gln Glu Gln
65 70 75 80
Leu Gln His Ala Lys Glu Leu Lys Asp Gln Val Gln Ala Arg Trp Lys
85 90 95
Gln Glu Glu Ala Ala Lys Thr Glu Ala Ile Ala Leu Val Thr Ser Val
100 105 110
Arg Lys Glu Arg Gly Gln Ile Glu Thr Ser Met Arg Ser Glu Glu Asn
115 120 125
Leu Leu His Leu Lys Ala Ala Asn Asp Ala Gln Arg Tyr Lys Ser Glu
130 135 140
Ile Arg Val Leu Glu Gln Arg Ile Ala Gln Leu Lys Val Ser Leu Asp
145 150 155 160
Ser Ser Arg Val Ala Ala Pro Lys Trp Gly Ala Asp Asn Lys Ser Tyr
165 170 175
Ala Leu His Leu Ser Glu Gly Arg Lys Asn Asn Asn Ala Gln Val Leu
180 185 190
Ser Asn Thr Ala Val Pro Gln Gly Leu Asp Phe Asp Asp Ile Gln Arg
195 200 205
Asp Arg Glu Cys Val Met Cys Leu Ser Glu Glu Met Ser Val Val Phe
210 215 220
Leu Pro Cys Ala His Gln Val Val Cys Ala Lys Cys Ser Asp Leu His
225 230 235 240
Glu Lys Gln Gly Met Lys Glu Cys Pro Ser Cys Arg Ala Pro Ile Gln
245 250 255
Arg Arg Val Arg Ala Arg Pro Ala Gly Cys
260 265

(2) INFORMATION FOR SEQ ID NO:3097:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..249
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3097:

Met His Asn Ser Arg Tyr Arg Trp Lys Leu Gln Ser Xaa His Ala Ala
1 5 10 15
Glu Ser Ala Thr Asn Ile Ser Glu Leu Leu Lys Lys Asp Glu Asn Ser
20 25 30
Arg Lys Arg Ser Gln Arg Trp Glu Ser Asp Arg Ala Leu Leu Gln Glu
35 40 45
Glu Leu Ala Ala Gln Lys Ser Arg Leu Phe Arg Val Gln Glu Gln Leu
50 55 60
Gln His Ala Lys Glu Leu Lys Asp Gln Val Gln Ala Arg Trp Lys Gln
65 70 75 80
Glu Glu Ala Ala Lys Thr Glu Ala Ile Ala Leu Val Thr Ser Val Arg
85 90 95
Lys Glu Arg Gly Gln Ile Glu Thr Ser Met Arg Ser Glu Glu Asn Leu
100 105 110
Leu His Leu Lys Ala Ala Asn Asp Ala Gln Arg Tyr Lys Ser Glu Ile
115 120 125
Arg Val Leu Glu Gln Arg Ile Ala Gln Leu Lys Val Ser Leu Asp Ser
130 135 140

Ser Arg Val Ala Ala Pro Lys Trp Gly Ala Asp Asn Lys Ser Tyr Ala
145 150 155 160
Leu His Leu Ser Glu Gly Arg Lys Asn Asn Ala Gln Val Leu Ser
165 170 175
Asn Thr Ala Val Pro Gln Gly Leu Asp Phe Asp Asp Ile Gln Arg Asp
180 185 190
Arg Glu Cys Val Met Cys Leu Ser Glu Glu Met Ser Val Val Phe Leu
195 200 205
Pro Cys Ala His Gln Val Val Cys Ala Lys Cys Ser Asp Leu His Glu
210 215 220 235
Lys Gln Gly Met Lys Glu Cys Pro Ser Cys Arg Ala Pro Ile Gln Arg
225 230 240
Arg Val Arg Ala Arg Pro Ala Gly Cys
245

(2) INFORMATION FOR SEQ ID NO:3098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..780
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3098:

agcgagagta	gcggctgctg	atgattctgc	ctttwcttct	ccctccctca	cctgctctct	60
ctctctctcc	ctttcttttc	cgcgcgagcg	gtgacgacga	ccgcgcgass	ccgcgcgactc	120
ctactctgat	cagggtgcctc	ggccttcgtc	gtgctctcgc	ccgcgcaacga	gtatagacgg	180
gcgcgcgatg	ccaccttcga	gctgtaccgg	aggtccacca	tcggcatgtg	cctcaccgag	240
acgtcgcagc	agatggcttc	caacggcacc	ytcagccggc	agctcgttat	ccagggtctc	300
gtccagttcg	acaagtcctat	gacggatgct	ctggagaacc	aagtgaagag	caaggttact	360
gtcaagggtc	acctgcacac	ctacaggttc	tgtgacaacg	tgtggacctt	catcttgaca	420
gacgcaagct	tcaagaatga	ggaggccacg	gagcagggtg	gcaagggtga	gattgtggca	480
tgtgattcca	aattgctcgg	acaataggcc	tgtgtacctc	cgagggtcaag	gaagggaagct	540
ttnaagtcgc	gcgaggcggg	gtctgtctgc	gcgtcacgtg	tacacgccta	ggctaccogc	600
aggcggggtc	tgctcgcgtc	agctgtacac	gcctagggtac	cgcccgaaacg	gcatttcatt	660
tgctctcttc	gtactgtatg	tgatctcttc	tttttccctc	tgatatacaat	ctgctgcagc	720
tataccggcc	aagagtatgg	catggtatgg	cgccagggcag	ccgcaaaact	gtttttacct	780

(2) INFORMATION FOR SEQ ID NO:3099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3099:

Met	Ala	Thr	Phe	Glu	Leu	Tyr	Arg	Arg	Ser	Thr	Ile	Gly	Met	Cys	Leu
1		5						10					15		
Thr	Glu	Thr	Leu	Asp	Glu	Met	Val	Ser	Asn	Gly	Thr	Xaa	Ser	Pro	Glu
			20					25					30		
Leu	Ala	Ile	Gln	Val	Leu	Val	Gln	Phe	Asp	Lys	Ser	Met	Thr	Asp	Ala
		35					40					45			
Leu	Glu	Asn	Gln	Val	Lys	Ser	Lys	Val	Thr	Val	Lys	Gly	His	Leu	His
		50				55						60			
Thr	Thr	Arg	Phe	Cys	Asp	Asn	Val	Trp	Thr	Phe	Ile	Leu	Thr	Asp	Ala

(2) INFORMATION FOR SEQ ID NO:3100:

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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(B) LOCATION: 1..93

SEQUENCE DESCRIPTION:

SEQUENCE DESCRIPTION: SEQ ID NO:51600:
 ... Thr Glu Thr Leu Asp Glu Met Val Ser Asp Gly

Cys Leu Thr Glu Thr Leu Asp Glu Met Val Ser
5 10

(2) INFORMATION FOR SEO ID NO:3101:

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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(B) LOCATION: 1..84

SEQUENCE DESCRIPTION:

Val Ser Asp Gly Thr Xaa Ser Pro Glu Leu Ala

(2) INFORMATION FOR SEQ ID NO:3102:

(1) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..728
(D) OTHER INFORMATION: / Ceres Seq. ID 1575556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3102:

aaagtgactg	aaaagtcccg	catgtttctc	tgccctccgt	ccgccgcgcg	aacaaccatt	60
tcctttctta	gcgcgcgcct	cgatccccct	cccgaaggcta	cagaaccagt	tcattccaggc	120
gcgaatggcg	gcggcgagga	gcctgtctct	gaggcacctc	cgcttgccgg	cgcccccgtc	180
agcggcgctc	gtgaggccga	cggcgctcgt	gcattgaggcc	ctgtgggggg	agcgggtggat	240
gtcttcggag	gatgccaagg	gccttttctc	ggacaagagc	gaggtcactg	aacgcattcat	300
caaggtcgtc	aagagcttcc	cgaagatcga	tgacccctcc	aaggtgacac	cagatgcccac	360
tttcaagaat	gatcttggcc	tagacagttt	ggatgcagtg	gaggttgtca	tccgctcgga	420
agaggaaattc	agattcgaga	tacctgacaa	tgaaGgctga	caagattgac	tcggctcaag	480
ttgcagttga	cttcattgcc	tcacaccgcc	aagcgaaatg	ataaagatgc	gttgctctggt	540
atagcaaaag	tatatcgta	ttaatctctg	tttatgaaga	aagttcagtt	tgaagatgta	600
cactaccgtg	cccatttggg	tacttctgct	gatgctactg	tcctttttgg	aacgaatttt	660
gctactgtgg	attgtctgca	ctaaataaaa	tgtttgaaac	tgagaaggaa	cttgatggcc	720
gtttggtt						

(2) INFORMATION FOR SEQ ID NO:3103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..71
(D) OTHER INFORMATION: / Ceres Seq. ID 1575557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3103:

Lys	Val	Thr	Glu	Lys	Ser	Arg	Met	Phe	Ser	Cys	Leu	Arg	Ser	Ala	Ala
1				5						10				15	
Ala	Thr	Thr	Ile	Ser	Phe	Ser	Ser	Arg	Arg	Leu	Arg	Ser	Pro	Pro	Glu
				20				25					30		
Ala	Thr	Glu	Pro	Val	His	Pro	Gly	Ala	Asn	Gly	Gly	Gly	Glu	Glu	Pro
		35					40						45		
Ala	Ser	Glu	Ala	Pro	Pro	Leu	Gly	Gly	Gly	Pro	Val	Ser	Gly	Val	Arg
		50				55					60				
Glu	Ala	Asp	Gly	Val	Val	Ala									
65				70											

(2) INFORMATION FOR SEQ ID NO:3104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..111
(D) OTHER INFORMATION: / Ceres Seq. ID 1575558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3104:

Met	Ala	Ala	Ala	Arg	Ser	Leu	Leu	Leu	Arg	His	Leu	Arg	Leu	Ala	Ala
1				5					10					15	
Ala	Pro	Ser	Ala	Ala	Ser	Val	Arg	Pro	Thr	Ala	Ser	Leu	His	Glu	Ala
				20					25				30		
Leu	Trp	Gly	Gln	Arg	Trp	Met	Ser	Ser	Glu	Asp	Ala	Lys	Gly	Ser	Phe
		35				40						45			
Leu	Asp	Lys	Ser	Glu	Val	Thr	Glu	Arg	Ile	Ile	Lys	Val	Val	Lys	Ser
		50				55					60				
Phe	Pro	Lys	Ile	Asp	Asp	Pro	Ser	Lys	Val	Thr	Pro	Asp	Ala	His	Phe
65				70					75					80	

Lys Asn Asp Leu Gly Leu Asp Ser Leu Asp Ala Val Glu Val Val Met
85 90 95
Ala Leu Glu Glu Glu Phe Arg Phe Glu Ile Pro Asp Asn Glu Gly
100 105 110

- (2) INFORMATION FOR SEQ ID NO:3105:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..73

(D) OTHER INFORMATION: / Ceres Seq. ID 1575559

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3105:

Met Ser Ser Glu Asp Ala Lys Gly Ser Phe Leu Asp Lys Ser Glu Val
1 5 10 15
Thr Glu Arg Ile Ile Lys Val Val Lys Ser Phe Pro Lys Ile Asp Asp
20 25 30
Pro Ser Lys Val Thr Pro Asp Ala His Phe Lys Asn Asp Leu Gly Leu
35 40 45
Asp Ser Leu Asp Ala Val Glu Val Val Met Ala Leu Glu Glu Phe
50 55 60
Arg Phe Glu Ile Pro Asp Asn Glu Gly
65 70

- (2) INFORMATION FOR SEQ ID NO:3106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 546 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..546

(D) OTHER INFORMATION: / Ceres Seq. ID 1575573

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3106:

tacatcgagc acgacggcga cgtgttcac gtggaccgca tcaaggagct catcaagtac 60
aagggtcttc aggtcgcccc tgccagagctg gaggccatcc tgcgtgtcca cccgtccgctc 120
gaggaCgcgc cgcgtctcgg gctgcgggac gaggagggcg gcgaggtccc ggcgtgtgtgc 180
gtggtgcggc gacgtggcgc gccggagagc gaggcggaca tgatggcgta cgtggcgggg 240
cgcggttcgct gctacaagaa gctccggctG ctgcgcttcg tggacggcat ccccaagtcg 300
gtgtccggca agatccctgc gaggcagctc agggacgagt tcRgtcaaga agacggcagc 360
agcgtaataa tgcacatcat cctgtggggtg gctgcttgat tataccagtg caagctcctg 420
cattgcggcc ttgatgaaga caataataca attagggtag agtcagatgt tccaggctac 480
tgatacaatt gttgtttctg caaaaggtag tcccaactag tgcataataca ttggcattgt 540
ggacct

- (2) INFORMATION FOR SEQ ID NO:3107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1575574

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3107:

Tyr Ile Asp Asp Asp Gly Asp Val Phe Ile Val Asp Arg Ile Lys Glu

1 5 10 15
Leu Ile Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala Glu Leu Glu Ala
20 25 30
Ile Leu Leu Ser His Pro Ser Val Glu Asp Ala Ala Val Phe Gly Leu
35 40 45
Pro Asp Glu Glu Ala Gly Glu Val Pro Ala Ser Cys Val Val Arg Arg
50 55 60
Arg Gly Ala Pro Glu Ser Glu Ala Asp Met Met Ala Tyr Val Ala Gly
65 70 75 80
Arg Val Ala Ser Tyr Lys Lys Leu Arg Leu Leu Arg Phe Val Asp Ala
85 90 95
Ile Pro Lys Ser Val Ser Gly Lys Ile Leu Arg Arg Gln Leu Arg Asp
100 105 110
Glu Phe Xaa Gln Glu Asp Gly Ser Ser Val Ile Met His Ile Ile Leu
115 120 125
Trp Val Ala Ala
130

(2) INFORMATION FOR SEQ ID NO:3108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3108:

Thr Ser Thr Thr Thr Ala Thr Cys Ser Ser Trp Thr Ala Ser Arg Ser
1 5 10 15
Ser Ser Ser Thr Arg Ala Ser Arg Ser Pro Leu Pro Ser Trp Arg Pro
20 25 30
Ser Cys Cys Leu Thr Arg Pro Ser Arg Thr Pro Pro Ser Ser Gly Cys
35 40 45
Arg Thr Arg Arg Pro Ala Arg Ser Arg Arg Arg Ala Trp Cys Gly Asp
50 55 60
Val Ala Arg Arg Arg Ala Arg Arg Thr
65 70

(2) INFORMATION FOR SEQ ID NO:3109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3109:

His Arg Arg Arg Arg Arg Val His Arg Gly Pro His Gln Gly Ala
1 5 10 15
His Gln Val Gln Gly Leu Pro Gly Arg Pro Cys Arg Ala Gly Gly His
20 25 30
Pro Ala Val Ser Pro Val Arg Arg Gly Arg Arg Leu Arg Ala Ala
35 40 45
Gly Arg Gly Gly Arg Arg Gly Pro Gly Val Val Arg Gly Ala Ala Thr
50 55 60
Trp Arg Ala Gly Glu Arg Gly Gly His Asp Gly Val Arg Gly Gly Ala
65 70 75 80

(2) INFORMATION FOR SEO ID NO:3110:

(A) LENGTH: 883 base pairs

- (A) LENGTH: 883 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ix) FEATURE:
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- (A) NAME/KEY: -

- (B) LOCATION: 1..883

- (D) OTHER INFORMATION: / Ceres Seq. ID 1575588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3110:

(2) INFORMATION FOR SEQ ID NO:3111:

(A) LENGTH: 223 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..22

- (D) OTHER INFORMATION: / Ceres Seq. ID 1575589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3111:

Ser	Thr	Phe	Arg	Gly	His	Arg	Leu	Leu	Leu	Ser	Cys	Tyr	Ala	Thr	Ala
1			5					10						15	
Pro	Leu	Val	Tyr	Leu	Trp	Ser	Pro	Pro	Ile	His	Glu	Ala	Gly	Ala	Gly
			20					25					30		
Arg	Glu	Leu	Ser	Arg	Thr	Thr	Ser	Ala	Gly	Ser	Ala	Pro	Ala	Pro	Pro
		35					40					45			
Pro	Pro	Ser	Trp	Pro	Pro	Arg	Glu	Leu	Gly	Leu	Val	Ser	Val	Ser	Ser
		50				55					60				
Ser	Arg	Arg	Pro	Val	Arg	Gly	Ala	Ile	Ile	Met	Ala	Ala	Val	Glu	Thr
65					70					75				80	
Val	Val	Leu	Lys	Val	Ala	Met	Ser	Cys	Glu	Gly	Cys	Ala	Gly	Ala	Val
			85						90					95	
Arg	Arg	Val	Leu	Ser	Lys	Met	Glu	Gly	Val	Glu	Thr	Phe	Asp	Ile	Asp
			100					105					110		

Leu Lys Glu Gln Lys Val Thr Val Lys Gly Asn Val Lys Pro Glu Asp
115 120 125
Val Phe Gln Thr Val Ser Lys Ser Gly Lys Arg Thr Ser Tyr Trp Glu
130 135 140
Gly Glu Ala Thr Ala Pro Asp Ala Ala Ala Pro Glu Ala Glu Ala
145 150 155 160
Ala Pro Ser Thr Ala Ala Glu Ala Pro Pro Ala Ala Pro Ala Ala
165 170 175
Pro Glu Ile Thr Pro Ala Lys Xaa Thr Pro Asp Arg His Ala Ile Ile
180 185 190
His Ser His Val Met Leu Arg Leu Arg Leu Leu Asn Leu Lys Ser Arg
195 200 205
Asn Ser Trp Gly Leu Ser Leu His Cys Ile Val Phe Leu Pro Val
210 215 220

(2) INFORMATION FOR SEQ ID NO:3112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1575590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3112:

Met Ala Ala Val Glu Thr Val Val Leu Lys Val Ala Met Ser Cys Glu
1 5 10 15
Gly Cys Ala Gly Ala Val Arg Arg Val Leu Ser Lys Met Glu Gly Val
20 25 30
Glu Thr Phe Asp Ile Asp Leu Lys Glu Gln Lys Val Thr Val Lys Gly
35 40 45
Asn Val Lys Pro Glu Asp Val Phe Gln Thr Val Ser Lys Ser Gly Lys
50 55 60
Arg Thr Ser Tyr Trp Glu Gly Glu Ala Thr Ala Pro Asp Ala Ala Ala
65 70 75 80
Ala Pro Glu Ala Glu Ala Ala Pro Ser Thr Ala Ala Glu Ala Pro Pro
85 90 95
Ala Ala Ala Pro Ala Ala Pro Glu Ile Thr Pro Ala Lys Xaa Thr Pro
100 105 110
Asp Arg His Ala Ile Ile His Ser His Val Met Leu Arg Leu Arg Leu
115 120 125
Leu Asn Leu Lys Ser Arg Asn Ser Trp Gly Leu Ser Leu His Cys Ile
130 135 140
Val Phe Leu Pro Val
145

(2) INFORMATION FOR SEQ ID NO:3113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1575591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3113:

Met Ser Cys Glu Gly Cys Ala Gly Ala Val Arg Arg Val Leu Ser Lys
1 5 10 15
Met Glu Gly Val Glu Thr Phe Asp Ile Asp Leu Lys Glu Gln Lys Val

Thr	Val	Lys	Gly	Asn	Val	Lys	Pro	Glu	Asp	Val	Phe	Gln	Thr	Val	Ser
		35					40					45			
Lys	Ser	Gly	Lys	Arg	Thr	Ser	Tyr	Trp	Glu	Gly	Glu	Ala	Thr	Ala	Pro
		50				55					60				
Asp	Ala	Ala	Ala	Ala	Pro	Glu	Ala	Glu	Ala	Ala	Pro	Ser	Thr	Ala	Ala
		65			70					75				80	
Glu	Ala	Pro	Pro	Ala	Ala	Ala	Pro	Ala	Ala	Pro	Glu	Ile	Thr	Pro	Ala
			85				90						95		
Lys	Xaa	Thr	Pro	Asp	Arg	His	Ala	Ile	Ile	His	Ser	His	Val	Met	Leu
			100				105						110		
Arg	Leu	Arg	Leu	Leu	Asn	Leu	Lys	Ser	Arg	Asn	Ser	Trp	Gly	Leu	Ser
		115				120						125			
Leu	His	Cys	Ile	Val	Phe	Leu	Pro	Val							
		130				135									

(2) INFORMATION FOR SEQ ID NO:3114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 698 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..698

- (D) OTHER INFORMATION: / Ceres Seq. ID 1575592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3114:

acacatatc	cctacgcctc	gctatcgctc	tccgcgaact	gaggactccc	gagaggccga	60
gaccaccccg	atgtccgcga	tggagaccga	catcaacgcg	ccgccgccg	ccccagcccg	120
cgagggatcc	tcgtcggtc	cgtctcctc	atctcccg	aagcccaaca	agcgcttoga	180
gatcaagaag	tggaaacgcg	tcgcgtctg	ggcatgggat	atcgtcgtcg	acaactgcgc	240
catctgccgc	aaccacatca	tggatctatg	catcgagtgc	caggcggaacc	aaGctagcgc	300
gaccagcgag	gagtgactg	tcgcttgggg	tgtctgtaat	catgcttttc	acttccactg	360
catcagcagg	tggcttaaga	ctcgccaaat	gtgccatta	gataacagtg	agtgaggagt	420
ccagaaatat	ggccactagt	tctctggcac	cgtcatgtga	tgttggggct	tgtctggcac	480
tcaagtgttt	tgtcttgcca	aacagctcca	tctcttactg	ctttcgatgc	tgcacatcat	540
caccctgcaa	ttataactag	ctagcagtag	gtacacctgg	gactgtattt	ggacgaccca	600
ttgagaggat	agtagggcca	ttttatcaat	ggtagtgga	tcttcataag	tgagcttgta	660
ttgtgctgtg	gtaccatttt	ctgaagtcac	gttttttt			

(2) INFORMATION FOR SEQ ID NO:3115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..145

- (D) OTHER INFORMATION: / Ceres Seq. ID 1575593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3115:

His	Ile	Phe	Pro	Thr	Pro	Arg	Tyr	Arg	Leu	Pro	Arg	Thr	Glu	Asp	Ser
			5					10					15		
Arg	Glu	Ala	Glu	Thr	Thr	Pro	Met	Ser	Ala	Met	Glu	Thr	Asp	Ile	Asn
			20				25					30			
Ala	Pro	Pro	Pro	Ala	Pro	Ala	Gly	Glu	Gly	Ser	Ser	Val	Gly	Pro	Ser
		35				40					45				
Ser	Ser	Ser	Ser	Arg	Lys	Pro	Asn	Lys	Arg	Phe	Glu	Ile	Lys	Lys	Trp
		50			55					60					
Asn	Ala	Val	Ala	Leu	Trp	Ala	Trp	Asp	Ile	Val	Val	Asp	Asn	Cys	Ala
		65			70			75						80	

Ile Cys Arg Asn His Ile Met Asp Leu Cys Ile Glu Cys Gln Ala Asn
85 90 95
Gln Ala Ser Ala Thr Ser Glu Glu Cys Thr Val Ala Trp Gly Val Cys
100 105 110
Asn His Ala Phe His Phe His Cys Ile Ser Arg Trp Leu Lys Thr Arg
115 120 125
Gln Val Cys Pro Leu Asp Asn Ser Glu Trp Glu Phe Gln Lys Tyr Gly
130 135 140
His
145

(2) INFORMATION FOR SEQ ID NO:3116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1575594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3116:

Thr Tyr Ser Leu Arg Leu Ala Ile Ala Phe Arg Glu Leu Arg Thr Pro
1 5 10 15
Glu Arg Pro Arg Pro Pro Arg Cys Pro Pro Trp Arg Pro Thr Ser Thr
20 25 30
Arg Arg Arg Pro Pro Gln Pro Ala Arg Asp Pro Pro Ser Val Arg Pro
35 40 45
Pro His Pro Pro Ala Ser Pro Thr Ser Ala Ser Arg Ser Arg Ser Gly
50 55 60
Thr Pro Ser Arg Ser Gly His Gly Ile Ser Ser Ser Thr Thr Ala Pro
65 70 75 80
Ser Ala Ala Thr Thr Ser Trp Ile Tyr Ala Ser Ser Ala Arg Arg Thr
85 90 95
Lys Leu Ala Arg Pro Ala Arg Ser Ala Leu Ser Leu Gly Val Ser Val
100 105 110
Ile Met Leu Phe Thr Ser Thr Ala Ser Ala Gly Gly Leu Arg Leu Ala
115 120 125
Lys Cys Ala His
130

(2) INFORMATION FOR SEQ ID NO:3117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1575595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3117:

Met Ser Ala Met Glu Thr Asp Ile Asn Ala Pro Pro Pro Ala Pro Ala
1 5 10 15
Gly Glu Gly Ser Ser Val Gly Pro Ser Ser Ser Ser Arg Lys Pro
20 25 30
Asn Lys Arg Phe Glu Ile Lys Lys Trp Asn Ala Val Ala Leu Trp Ala
35 40 45
Trp Asp Ile Val Val Asp Asn Cys Ala Ile Cys Arg Asn His Ile Met
50 55 60
Asp Leu Cys Ile Glu Cys Gln Ala Asn Gln Ala Ser Ala Thr Ser Glu

1	ser	Lys	Lys	Asp	Ile	Arg	Asn	Gln	Val	Pro	Ala	Pro	Leu	Thr	Thr	Lys
				5												
1	Pro	Pro	Ile	Met	Ala	Ala	Thr	Leu	His	Leu	His	Leu	Leu	Val	Thr	Leu
				20					25						30	
Leu	Phe	Val	Ala	Thr	Leu	Thr	Val	Ala	Ser	Val	Ala	Asp	Asp	Ser	Ser	Pro
				35				40					45			
Pro	Ala	Pro	Thr	Pro	Pro	Ala	Pro	Pro	Gln	Pro	Thr	Ala	Tyr	Gln	Met	
				50			55				60					
Leu	Glu	Arg	Tyr	Asn	Phe	Thr	Gln	Gly	Ile	Leu	Pro	Gln	Gly	Val	Thr	
65						70				75					80	
Gly	Tyr	Val	Leu	Xaa	Arg	Arg	Arg	Leu	Leu	Arg	Gly	Val	Pro	Pro	Gly	
				85					90						95	
Gly	Leu	Gln	Leu	Pro	Arg	Arg	Gln	His	Ala	Gly	Pro	Val	Gln	Gln	Pro	
				100				105					110			
Arg	Arg	Arg	Pro	His	Ser	Ala	Ala	Val	His	His	Ile	Pro	Gly	Gly	Ser	
				115			120					125				
Glu	Gly	Glu	Gly	Ala	Val	Leu	Val	Gly	Arg	Arg	Gln	Ala	Gly	Arg	Pro	
				130			135					140				

Arg Arg Arg Pro Ala Pro Phe Leu Arg Arg Pro Tyr Val Glu Ile Val
145 150 155 160
Pro His Arg His Ile Cys Gln Gln Pro Pro Met Gln Leu Arg Pro Phe
165 170 175
Gly Arg Leu Arg Lys Lys Ser Leu Leu Val Ser Phe Phe Leu Cys Xaa
180 185 190
Phe Ser Leu
195

(2) INFORMATION FOR SEQ ID NO:3120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1575598

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3120:

Met Ala Ala Thr Leu His Leu His Leu Val Thr Leu Leu Phe Val
1 5 10 15
Ala Thr Leu Thr Val Ala Ser Val Ala Asp Asp Ser Pro Pro Ala Pro
20 25 30
Thr Pro Pro Ala Pro Pro Gln Pro Thr Ala Tyr Gln Met Leu Glu Arg
35 40 45
Tyr Asn Phe Thr Gln Gly Ile Leu Pro Gln Gly Val Thr Gly Tyr Val
50 55 60
Leu Xaa Arg Arg Arg Leu Leu Arg Gly Val Pro Pro Gly Gly Leu Glu
65 70 75 80
Leu Pro Arg Arg Gln His Ala Gly Pro Val Gln Gln Pro Arg Arg Arg
85 90 95
Pro His Ser Ala Ala Val His His Ile Pro Gly Gly Ser Glu Gly Glu
100 105 110
Gly Ala Val Leu Val Gly Arg Arg Gln Ala Gly Arg Pro Arg Arg Arg
115 120 125
Pro Ala Pro Phe Leu Arg Arg Pro Tyr Val Glu Ile Val Pro His Arg
130 135 140
His Ile Cys Gln Gln Pro Pro Met Gln Leu Arg Pro Phe Gly Arg Leu
145 150 155 160
Arg Lys Lys Ser Leu Leu Val Ser Phe Phe Leu Cys Xaa Phe Ser Leu
165 170 175

(2) INFORMATION FOR SEQ ID NO:3121:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1575599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3121:

Met Leu Glu Arg Tyr Asn Phe Thr Gln Gly Ile Leu Pro Gln Gly Val
1 5 10 15
Thr Gly Tyr Val Leu Xaa Arg Arg Arg Leu Leu Arg Gly Val Pro Pro
20 25 30
Gly Gly Leu Gln Leu Pro Arg Arg Gln His Ala Gly Pro Val Gln Gln

35	40	45
Pro Arg Arg Arg Pro His Ser Ala Ala Val His His Ile Pro Gly Gly		
50	55	60
Ser Glu Gly Glu Gly Ala Val Leu Val Gly Arg Arg Gln Ala Gly Arg		
65	70	75
Pro Arg Arg Arg Pro Ala Pro Phe Leu Arg Arg Pro Tyr Val Glu Ile		
85	90	95
Val Pro His Arg His Ile Cys Gln Gln Pro Pro Met Gln Leu Arg Pro		
100	105	110
Phe Gly Arg Leu Arg Lys Lys Ser Leu Leu Val Ser Phe Phe Leu Cys		
115	120	125
Xaa Phe Ser Leu		
130		

(2) INFORMATION FOR SEQ ID NO:3122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..588
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3122:

gtccgcgcgc	tcogtgttca	ttgccccact	ccctcacgcc	tctcgcgcgc	gccgctccac	60
cacccccac	caogctcagg	gaaagggggt	ctgggttgca	tacaggcgaa	agggcacgac	120
cgccgCtgc	gcgcgagcct	ctccgtcccc	atcgccgcgc	agatggatcc	gtcgtcgag	180
ccccgtgacg	cgaggttoga	gcccgtacac	tccgggttcc	tcaaggtctc	cgatgtccac	240
accatctact	acgagcagtc	cgggaaaccg	caggscatg	cgccggtgtt	tctccacgc	300
ggtcccgagg	ccggcacgct	gcccggcaac	aggaggttct	ttgacccgca	gttctacagg	360
atcgttctgt	ttgaccagag	gggtgcaggc	agaagcactc	cccatgcttg	tttagagcag	420
aacactactt	gggacttggt	agctgacatt	gagaagctca	gggagcatct	tggcatccct	480
gaatggcagg	tgtttgggtg	ttcatgggga	agcaccttgg	cacttgccata	cagccaggag	540
caccctgata	aggtcactgg	cttgtgtctg	agagggaattt	tcttgcctt		

(2) INFORMATION FOR SEQ ID NO:3123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3123:

Val Arg Pro Leu Arg Val His Cys Pro Thr Pro Ser Arg Leu Ser Arg		
1	5	10
Pro Pro Leu His His Pro His Pro Arg Ser Gly Lys Gly Gly Leu Gly		
20	25	30
Cys Ile Gln Ala Lys Gly Thr Arg Arg Cys Arg Ala Ser Leu Ser		
35	40	45
Val Pro Ile Ala Ala Gln Met Asp Pro Ser Ser Glu Pro Leu Tyr Ala		
50	55	60
Gln Val Glu Pro Tyr Asp Ser Gly Phe Leu Lys Val Ser Asp Val His		
65	70	75
Thr Ile Tyr Tyr Glu Gln Ser Gly Asn Pro Gln Xaa His Ala Val		
85	90	95
Phe Leu His Gly Gly Pro Gly Ala Gly Thr Ser Pro Gly Asn Arg		
100	105	110

Phe Phe Asp Pro Gln Phe Tyr Arg Ile Val Leu Phe Asp Gln Arg Gly
115 120 125
Ala Gly Arg Ser Thr Pro His Ala Cys Leu Glu Gln Asn Thr Thr Trp
130 135 140
Asp Leu Val Ala Asp Ile Glu Lys Leu Arg Glu His Leu Gly Ile Pro
145 150 155 160
Glu Trp Gln Val Phe Gly Gly Ser Trp Gly Ser Thr Leu Ala Leu Ala
165 170 175
Tyr Ser Gln Glu His Pro Asp Lys Val Thr Gly Leu Val Leu Arg Gly
180 185 190
Ile Phe Leu Leu
195

(2) INFORMATION FOR SEQ ID NO:3124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..137
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3124:

Ser Ala Arg Ser Val Phe Ile Ala Pro Leu Pro His Ala Ser Arg Ala
1 5 10 15
Arg Arg Ser Thr Thr Pro Ile His Ala Gln Gly Lys Gly Val Trp Val
20 25 30
Ala Tyr Arg Arg Lys Ala Arg Ala Ala Ala Ala Arg Ala Ser Pro
35 40 45
Ser Pro Ser Pro Arg Arg Trp Ile Arg Arg Arg Ser Pro Cys Thr Arg
50 55 60
Arg Ser Ser Arg Thr Thr Pro Gly Ser Ser Arg Ser Pro Met Ser Thr
65 70 75 80
Pro Ser Thr Thr Ser Ser Pro Gly Thr Arg Arg Xaa Met Arg Arg Cys
85 90 95
Phe Ser Thr Ala Val Pro Glu Pro Ala Arg Arg Pro Ala Thr Gly Gly
100 105 110
Ser Leu Thr Arg Ser Ser Thr Gly Ser Phe Cys Leu Thr Arg Gly Val
115 120 125
Gln Ala Glu Ala Leu Pro Met Leu Val
130 135

(2) INFORMATION FOR SEQ ID NO:3125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3125:

Met Asp Pro Ser Ser Glu Pro Leu Tyr Ala Gln Val Glu Pro Tyr Asp
1 5 10 15
Ser Gly Phe Leu Lys Val Ser Asp Val His Thr Ile Tyr Trp Glu Gln
20 25 30
Ser Gly Asn Pro Gln Xaa His Ala Ala Val Phe Leu His Gly Gly Pro
35 40 45
Gly Ala Gly Thr Ser Pro Gly Asn Arg Arg Phe Phe Asp Pro Gln Phe

50	55	60
Tyr Arg Ile Val Leu Phe Asp Gln Arg Gly Ala Gly Arg Ser Thr Pro		
65	70	75
His Ala Cys Leu Glu Gln Asn Thr Thr Trp Asp Leu Val Ala Asp Ile		
	85	90
Glu Lys Leu Arg Glu His Leu Gly Ile Pro Glu Trp Gln Val Phe Gly		
	100	105
Gly Ser Trp Gly Ser Thr Leu Ala Leu Ala Tyr Ser Gln Glu His Pro		
	115	120
Asp Lys Val Thr Gly Leu Val Leu Arg Gly Ile Phe Leu Leu		
	130	135
		140

(2) INFORMATION FOR SEQ ID NO:3126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..406
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3126:

gacacacctc ccaaacccta cactcccgcc gccggcgccg gccggcgagC agcgccagca	60
gcataccgaag atggtggaagt tcttcaagcc cgrcaaggcc gttatctctcc tccaggcgccg	120
Cttcgccggc aggaaggcag ttatctctgcg cgtgttcgag gagggcacc ccgaccgccc	180
ctatggccac tcgctcgtcg caggccctgc caagtaccca aagaagtgta tccgcaagga	240
ctctctttac ctgtaaatag ataataggt cttggccaga ttttctgtgt tttgcagctg	300
caggatttgt cctaagacga gtcatgatgt taatgtgaag caacttctcc agggatagat	360
ctcaaccaag ttgtgtgsc atacgaaGtt attgaactgga atttag	

(2) INFORMATION FOR SEQ ID NO:3127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3127:

Asp Thr Pro Pro Lys Pro Tyr Thr Pro Gly Gly Gly Gly Ala	
1	5
	10
Ala Ala Ala Ala Ala Ser Glu Asp Gly Glu Val Pro Gln Ala Xaa Gln	
	20
	25
Gly Arg Tyr Pro Pro Pro Gly Pro Leu Arg Arg Gln Glu Gly Ser Tyr	
	35
	40
Pro Ala Arg Val Arg Gly Gly His Pro Arg Pro Pro Leu Trp Pro Leu	
	50
	55
Pro Arg Arg Arg Pro Arg Gln Val Pro Lys Glu Gly Asp Pro Gln Gly	
65	70
	75
Leu Leu Leu Pro Val Asn Arg	
	85

(2) INFORMATION FOR SEQ ID NO:3128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..84
(D) OTHER INFORMATION: / Ceres Seq. ID 1575637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3128:

Thr His Leu Pro Asn Pro Thr Leu Pro Ala Ala Ala Ala Gln
1 5 10 15
Gln Arg Gln Gln His Pro Lys Met Val Lys Phe Leu Lys Pro Xaa Lys
20 25 30
Ala Val Ile Leu Leu Gln Gly Arg Phe Ala Gly Arg Lys Ala Val Ile
35 40 45
Leu Arg Val Phe Glu Glu Gly Thr Arg Asp Arg Pro Tyr Gly His Cys
50 55 60
Leu Val Ala Gly Leu Ala Lys Tyr Pro Lys Lys Val Ile Arg Lys Asp
65 70 75 80
Ser Ser Tyr Leu

(2) INFORMATION FOR SEQ ID NO:3129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..61
(D) OTHER INFORMATION: / Ceres Seq. ID 1575638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3129:

Met Val Lys Phe Leu Lys Pro Xaa Lys Ala Val Ile Leu Leu Gln Gly
1 5 10 15
Arg Phe Ala Gly Arg Lys Ala Val Ile Leu Arg Val Phe Glu Glu Gly
20 25 30
Thr Arg Asp Arg Pro Tyr Gly His Cys Leu Val Ala Gly Leu Ala Lys
35 40 45
Tyr Pro Lys Lys Val Ile Arg Lys Asp Ser Ser Tyr Leu
50 55 60

(2) INFORMATION FOR SEQ ID NO:3130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 880 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..880
(D) OTHER INFORMATION: / Ceres Seq. ID 1575645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3130:

caatgtaagt	tcgaacaaca	agaagggggt	gtacagcttg	atcggtgggt	caaatgcgga	60
cgtaaatgtt	tcctacggcc	atacatgctt	caattcgggt	ttgactctgg	gaaaagctct	120
cctctacaca	gagcaatcag	cctctccatc	taacgggaagt	ctagatgttt	ttgaccgcga	180
tccactcgag	aagggttgta	ccggggattc	tgtttctcct	gccagccaaa	gcgcccgat	240
agacggtccg	gacgatttat	ttgaagggtt	atctttgctc	catctagcat	gccgcgtgc	300
gacctggcca	tggttgagct	gctcttcgag	tacggcgcca	atgtaaaccc	cacagattca	360
agagggcgga	cgccgcttca	tcacagcatc	atgaaagggc	gacatgtgta	cgccaagcta	420
ctgctttcca	ggggcgctga	ttctcaagcc	gcggatagag	atggtagaac	agcgttacag	480
tatgcaatcg	acagcggaac	catagaggac	gaagagatcc	ttgttttgc	agagaccctA	540
agtagataaa	tcacgtaGgt	gtagtagtcc	aagtctcgag	ttctcggtg	gtgcattgtg	600
gctgcctttt	gcagtcacct	ggcacacaca	ggggccgagg	atgccttgct	agtattcagt	660
ctctgccttt	gtggcaagag	gaagttatag	ttttctag	ctctctcg	gttttggtcg	720

(2) INFORMATION FOR SEQ ID NO:3131:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1575646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3131:

[illegible]

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

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{D} TOPOLOGY: linear
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(11) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1575647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3132:

[illegible]

(2) INFORMATION FOR SEQ ID NO:3133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..79
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3133:

Met	Val	Glu	Leu	Leu	Gln	Tyr	Gly	Ala	Asn	Val	Asn	Pro	Thr	Asp
1			5				10					15		
Ser	Arg	Gly	Arg	Thr	Pro	Leu	His	His	Ser	Ile	Met	Lys	Gly	Arg
			20				25					30		
Val	Tyr	Ala	Lys	Leu	Leu	Leu	Ser	Arg	Gly	Ala	Asp	Ser	Gln	Ala
			35				40					45		
Asp	Arg	Asp	Gly	Arg	Thr	Ala	Leu	Gln	Tyr	Ala	Ile	Asp	Ser	Gly
			50				55					60		
Ile	Glu	Asp	Glu	Glu	Ile	Leu	Val	Leu	Leu	Glu	Asp	Pro	Ser	Arg
			65				70					75		

(2) INFORMATION FOR SEQ ID NO:3134:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 762 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..762
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3134:

accgtgcgcg	cgcgcgcctc	tccaccgttc	attctccat	ggcatctact	cacgcaagca	60
gtcctattcc	tgattccttg	ctcggcttgc	gtggcccatg	gattcgatgt	catatcatgt	120
gtgtgtttgt	caccgcctgt	gtcgcagttc	gtgtcggatg	gcgtgttctt	cgcggaatga	180
atgagatgct	cgcggaggac	ggctactccg	gcgtcgaggt	ccgcgtcacc	cccatgtgca	240
tcgagatcat	catccgtgcc	accgcgcgcc	agaacatact	cgcgagaagg	gccggaggat	300
cagagagctg	gcttctgtga	ttcagaagcg	ctttaactta	tcagaggggtg	gcgttgagct	360
ctacgcagag	aagctgaaca	accgcgggct	ctgcgcacat	gcccaggccg	agwgcTcccg	420
ctacaagctt	ctcgtggaac	tcgcgcgtgag	aaGggggcatg	ttatgggtgt	ctcttatttg	480
tcacgcagag	tggctactaa	ggctgcgaga	tcagtttcaa	tcggaacatg	ccaagctgaa	540
gcgatactca	ctctgcaagga	gcgtcttctc	tgtgtactgc	gtcgaagctt	tacottttta	600
tgtaaattac	gctgtaaatg	tacagttctc	ctggacactg	aatttctaag	ggcttttttt	660
atctttctga	cgcaccattc	actgatagct	ttatcgttgc	atagattttt	cttgaaatta	720
tatgccattc	taacgaacaa	taatatgtga	gtatcattct	tt		

(2) INFORMATION FOR SEQ ID NO:3135:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..105
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3135:

Arg	Ala	Ala	Gly	Leu	Ser	Thr	Val	His	Ser	Pro	Met	Ala	Ser	Thr
1			5				10					15		
His	Ala	Ser	Ser	Pro	Ile	Pro	Asp	Ser	Leu	Leu	Gly	Leu	Arg	Gly
			20				25					30		
Trp	Ile	Arg	Cys	His	Ile	Met	Cys	Cys	Leu	Leu	Thr	Arg	Leu	Val
			35				40					45		
Val	Arg	Val	Gly	Trp	Arg	Val	Leu	Arg	Gly	Xaa	Asn	Glu	Met	Leu
			50				55					60		

Glu Asp Gly Tyr Ser Gly Val Glu Val Arg Val Thr Pro Met Cys Ile
65 70 75 80
Glu Ile Ile Ile Arg Ala Thr Arg Ala Gln Asn Ile Leu Ala Arg Arg
85 90 95

Ala Gly Gly Ser Glu Ser Trp Leu Leu
100 105

(2) INFORMATION FOR SEQ ID NO:3136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1575684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3136:

Met Ala Ser Thr His Ala Ser Ser Pro Ile Pro Asp Ser Leu Leu Gly
1 5 10 15
Leu Arg Gly Trp Ile Arg Cys His Ile Met Cys Cys Leu Thr
20 25 30
Arg Leu Val Ala Val Arg Val Gly Trp Arg Val Leu Arg Gly Xaa Asn
35 40 45
Glu Met Leu Ala Glu Asp Gly Tyr Ser Gly Val Glu Val Arg Val Thr
50 55 60
Pro Met Cys Ile Glu Ile Ile Arg Ala Thr Arg Ala Gln Asn Ile
65 70 75 80
Leu Ala Arg Arg Ala Gly Gly Ser Glu Ser Trp Leu Leu
85 90

(2) INFORMATION FOR SEQ ID NO:3137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1575685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3137:

Met Val Phe Ser Tyr Leu Ser Ser Arg Val Val Leu Arg Ala Ala Arg
1 5 10 15
Ser Val Ser Ile Gly Thr Cys Gln Ala Glu Ala Ile Leu Thr Cys Lys
20 25 30
Glu Arg Leu Leu Cys Val Leu Arg Arg Ser Phe Thr Phe Leu Cys Lys
35 40 45
Leu Arg Cys Lys Cys Thr Val Pro Leu Asp Thr Glu Phe Leu Arg Ala
50 55 60
Phe Phe Ile Phe Leu Thr His His Ser Leu Ile Ala Leu Ser Leu His
65 70 75 80
Ser Ile Phe Leu Lys Leu Tyr Ala Ile Leu Thr Asn Asn Asn Ile Val
85 90 95

Val Ser Phe Phe
100

(2) INFORMATION FOR SEQ ID NO:3138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 689 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..689
(D) OTHER INFORMATION: / Ceres Seq. ID 1575704
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3138:
tattgaagtc cattctgtttg gcatcgtccc atctcccttg aaccctttcg cccacaccac 60
agcacccgtg ccgaagtggg aaagaaggcg gcggcgaggg caccggcacc ggcaccgcct 120
aggaaaggaa accgaggaaa ctacagccat ggtggtaagg atccgtctgg cgcggttcgg 180
gtgcgggaat cgccctctct accgggtgat ggcgcgcgat agccgctccc ctccgagacgg 240
caagcacctc gaggctcctg gctactataa cccgctccca gggaaggatg gaggcaagag 300
gatgggctcg aaattcgacc gggtaagta ttggctgtca gttGGGgggg acagccatca 360
gatccgtgac agagtattct ctctcgtgcc ggactctgc caccacctcc attgctagct 420
atggcacgga aggggtgggccc acgtgatagg cgcccccatt atccaatgac tgggcgccct 480
ctggatctcg aggggtgtcgc aattattgat aattccaatg ctccgtgaag cgatactgaa 540
gtgcctacag atgaggtggc tcaataagcc ttttgtatta gcatagcata tgtagcggtg 600
ctgcaaaaaga aaactgttt gatgtgcttg tggcaagact ttgggtactc gtacaaatgtg 660
gcaaaccttt aaacaggtaa ctttcatcc
(2) INFORMATION FOR SEQ ID NO:3139:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..138
(D) OTHER INFORMATION: / Ceres Seq. ID 1575705
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3139:
Ile Glu Val His Ser Val Gly Ile Val Pro Ser Pro Leu Asn Pro Phe
1 5 10 15
Ala His Thr Thr Ala Pro Leu Pro Lys Trp Glu Arg Arg Arg Arg
20 25 30
Arg His Arg His Arg His Arg Leu Gly Lys Glu Thr Glu Thr Thr
35 40 45
Ala Met Val Val Arg Ile Arg Leu Ala Arg Phe Gly Cys Arg Asn Arg
50 55 60
Pro Phe Tyr Arg Val Met Ala Ala Asp Ser Arg Ser Pro Arg Asp Gly
65 70 75 80
Lys His Leu Glu Val Leu Gly Tyr Tyr Asn Pro Leu Pro Gly Lys Asp
85 90 95
Gly Gly Lys Arg Met Gly Leu Lys Phe Asp Arg Val Lys Tyr Trp Leu
100 105 110
Ser Val Gly Gly His Ser His Gln Ile Leu Cys Arg Val Phe Ser Phe
115 120 125
Val Pro Asp Phe Cys His His Leu His Cys
130 135
(2) INFORMATION FOR SEQ ID NO:3140:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..89
(D) OTHER INFORMATION: / Ceres Seq. ID 1575706
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3140:

Met Val Val Arg Ile Arg Leu Ala Arg Phe Gly Cys Arg Asn Arg Pro
1 5 10 15
Phe Tyr Arg Val Met Ala Ala Asp Ser Arg Ser Pro Arg Asp Gly Lys
20 25 30
His Leu Glu Val Leu Gly Tyr Tyr Asn Pro Leu Pro Gly Lys Asp Gly
35 40 45
Gly Lys Arg Met Gly Leu Lys Phe Asp Arg Val Lys Tyr Trp Leu Ser
50 55 60
Val Gly Gly His Ser His Gln Ile Leu Cys Arg Val Phe Ser Phe Val
65 70 75 80
Pro Asp Phe Cys His His Leu His Cys
85

(2) INFORMATION FOR SEQ ID NO:3141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..69
(D) OTHER INFORMATION: / Ceres Seq. ID 1575707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3141:

Met Ala Ala Asp Ser Arg Ser Pro Arg Asp Gly Lys His Leu Glu Val
1 5 10 15
Leu Gly Tyr Tyr Asn Pro Leu Pro Gly Lys Asp Gly Gly Lys Arg Met
20 25 30
Gly Leu Lys Phe Asp Arg Val Lys Tyr Trp Leu Ser Val Gly Gly His
35 40 45
Ser His Gln Ile Leu Cys Arg Val Phe Ser Phe Val Pro Asp Phe Cys
50 55 60
His His Leu His Cys
65

(2) INFORMATION FOR SEQ ID NO:3142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..767
(D) OTHER INFORMATION: / Ceres Seq. ID 1575720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3142:

gtgtgtgctag aagcaactga aaacagccga gcgatctct ctcctctctc ctctccgcatc 60
cattctccag cgcasanang taaacatgtc tgaccgggga aagatgtcgt ggcaggcgta 120
cgtggacgag caccatgatgt gcgagatcga rggccaccac ctccggcgcg cgcccatcgt 180
cggccacgas gntgcgcctt gggcgcaagag caccggcgctt ccagagtcca agaccaggga 240
catggccaac atcatgaagg acttcgacga gccaggggcac ctccgcgccga caggCctggt 300
cctcggacat accaagtaca tggctcatcca aggcgagcct ggtgcctcca tccgtggcaa 360
gaagggatca ggaggcatca cctgaagaa gacaggggcag gcaactcgtcg ttggcatcta 420
cgacgagcgc atgacgcctg gccagtgcac catggtgtgt gaaaggctgg gcgactacct 480
gcttgaaacg ggcattgaac tactacgtac cagctggaat gcatgtcgac gacgatgggt 540
tcgagtcttcg acttccaata atagtaacaa caaagcaaa gccctctctc cgccgtattt 600
gctttgtctc ttctctctca cgcataaaga tatctagcaa ttggtgactc gctttaatta 660
gttcgctttt cttttgaggt tgactcgacc attttgctgt agcgtgaatt gcatgcattg 720
acatgcaacg ctccaatgkc ytttgmmtg tggaattttt ttttttc

(2) INFORMATION FOR SEQ ID NO:3143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..137
(D) OTHER INFORMATION: / Ceres Seq. ID 1575721
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3143:

Met Ser Asp Arg Ala Lys Met Ser Trp Gln Ala Tyr Val Asp Glu His
1 5 10 15
Leu Met Cys Glu Ile Xaa Gly His His Leu Ala Ala Ala Ile Val
20 25 30
Gly His Xaa Xaa Ala Ala Trp Ala Gln Ser Thr Ala Phe Pro Glu Phe
35 40 45
Lys Thr Glu Asp Met Ala Asn Ile Met Lys Asp Phe Asp Glu Pro Gly
50 55 60
His Leu Ala Pro Thr Gly Leu Phe Leu Gly Pro Thr Lys Tyr Met Val
65 70 75 80
Ile Gln Gly Glu Pro Gly Ala Val Ile Arg Gly Lys Lys Gly Ser Gly
85 90 95
Gly Ile Thr Val Lys Lys Thr Gly Gln Ala Leu Val Val Gly Ile Tyr
100 105 110
Asp Glu Pro Met Thr Pro Gly Gln Cys Asn Met Val Val Glu Arg Leu
115 120 125
Gly Asp Tyr Leu Leu Glu Gln Gly Met
130 135

(2) INFORMATION FOR SEQ ID NO:3144:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..131
(D) OTHER INFORMATION: / Ceres Seq. ID 1575722
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3144:

Met Ser Trp Gln Ala Tyr Val Asp Glu His Leu Met Cys Glu Ile Xaa
1 5 10 15
Gly His His Leu Ala Ala Ala Ala Ile Val Gly His Xaa Xaa Ala Ala
20 25 30
Trp Ala Gln Ser Thr Ala Phe Pro Glu Phe Lys Thr Glu Asp Met Ala
35 40 45
Asn Ile Met Lys Asp Phe Asp Glu Pro Gly His Leu Ala Pro Thr Gly
50 55 60
Leu Phe Leu Gly Pro Thr Lys Tyr Met Val Ile Gln Gly Glu Pro Gly
65 70 75 80
Ala Val Ile Arg Gly Lys Lys Gly Ser Gly Gly Ile Thr Val Lys Lys
85 90 95
Thr Gly Gln Ala Leu Val Val Gly Ile Tyr Asp Glu Pro Met Thr Pro
100 105 110
Gly Gln Cys Asn Met Val Val Glu Arg Leu Gly Asp Tyr Leu Leu Glu
115 120 125
Gln Gly Met
130

(2) INFORMATION FOR SEQ ID NO:3145:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..120
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575723
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3145:
Met Cys Glu Ile Xaa Gly His His Leu Ala Ala Ala Val Gly
1 5 10 15
His Xaa Xaa Ala Ala Trp Ala Gln Ser Thr Ala Phe Pro Glu Phe Lys
 20 25 30
Thr Glu Asp Met Ala Asn Ile Met Lys Asp Phe Asp Glu Pro Gly His
 35 40 45
Leu Ala Pro Thr Gly Leu Phe Leu Gly Pro Thr Lys Tyr Met Val Ile
 50 55 60
Gln Gly Glu Pro Gly Ala Val Ile Arg Gly Lys Lys Gly Ser Gly Gly
65 70 75 80
Ile Thr Val Lys Lys Thr Gly Gln Ala Leu Val Val Gly Ile Tyr Asp
 85 90 95
Glu Pro Met Thr Pro Gly Gln Cys Asn Met Val Val Glu Arg Leu Gly
 100 105 110
Asp Tyr Leu Leu Glu Gln Gly Met
 115 120

(2) INFORMATION FOR SEQ ID NO:3146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..645
(D) OTHER INFORMATION: / Ceres Seq. ID 1575729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3146:

gaggaagaat caggcaggga gctctacccat tcgcatccca ggccaacctc aacccaatc 60
caatcogttg caggtcgca gatggcttcg cgtgagcacc accagcccca ggaggaggag 120
gacacgcgaG cgctcgctcaa gctcatcagc gccgagggct tcgaattcgt cgtcgacaag 180
aaggccgcga tggtctccaa caccctacgc aacatgctca catcgccagg cggcttctcc 240
gagacgcgcc agggcgaggt tcgcttcgcc gagatcccca ccaatctcct cgagaagatc 300
tgccagtaet tctattggtc gctccattat tccagctctt gggtcaacac tttggatggc 360
ctgcctattg aagagttatc tgggtccaga ttttgatgtg atggagtctg acaagcccaa 420
taagactgtc acatgtaatg ttatttgatt accaaaacat gaagagcagt caagataggt 480
tgagactgat cgtatatatt gttggttctt aggactcttg gtggaagata tgaggttgct 540
cccaacactg aatttatgta tggctgaagt aaattcactg ttctgatttt ggtgtccaca 600
ttcttatttg ttccaccatc agcaaaccta agttcagttt gtgtt

(2) INFORMATION FOR SEQ ID NO:3147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..131
(D) OTHER INFORMATION: / Ceres Seq. ID 1575730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3147:

Glu Glu Glu Ser Gly Arg Glu Leu Tyr His Ser His Pro Arg Pro Thr

1	5	10	15
Ser Thr Pro Ile Gln Ser Val Ala Gly Arg Arg Met Ala Ser Arg Glu	20	25	30
His His Gln Pro Gln Glu Glu Glu Asp Thr Ala Gly Val Val Lys Leu	35	40	45
Ile Ser Ala Glu Gly Phe Glu Phe Val Val Asp Lys Lys Ala Ala Met	50	55	60
Val Ser Asn Thr Leu Arg Asn Met Leu Thr Ser Pro Gly Gly Phe Ser	65	70	75
Glu Thr Arg Gln Gly Glu Val Arg Phe Pro Glu Ile Pro Thr Asn Ile	85	90	95
Leu Glu Lys Ile Cys Gln Tyr Phe Tyr Trp Ser Leu His Tyr Ser Ser	100	105	110
Ser Trp Phe Asn Thr Leu Asp Gly Leu Pro Ile Glu Glu Leu Ser Gly	115	120	125
Pro Glu Phe			
130			

(2) INFORMATION FOR SEQ ID NO:3148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1575731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3148:

Arg Lys Asn Gln Ala Gly Ser Ser Thr Ile Arg Ile Pro Gly Gln Pro	1	5	10	15
Gln Pro Gln Ser Asn Pro Leu Gln Val Ala Gly Trp Leu Arg Val Ser	20	25	30	
Thr Thr Ser Pro Arg Arg Arg Thr Pro Gln Ala Ser Ser Ser Ser	35	40	45	
Ser Ala Pro Arg Ala Ser Asn Ser Ser Ser Thr Arg Arg Pro Pro Trp	50	55	60	
Ser Pro Thr Pro Tyr Ala Thr Cys Ser His Arg Gln Ala Ala Ser Pro	65	70	75	80
Arg Arg Ala Arg Ala Arg Phe Ala Ser Arg Arg Ser Pro Pro Ile Ser	85	90	95	
Ser Arg Arg Ser Ala Ser Thr Ser Ile Gly Arg Ser Ile Ile Pro Ala	100	105	110	
Leu Gly Ser Thr Leu Trp Met Ala Cys Leu Leu Lys Ser Tyr Leu Val	115	120	125	
Gln Asn Phe Asp Val Met Glu Ser Asp Lys Ala Asn Lys Thr Val Thr	130	135	140	
Cys Asn Val Ile				
145				

(2) INFORMATION FOR SEQ ID NO:3149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1575732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3149:

Met Ala Ser Arg Glu His His Gln Pro Gln Glu Glu Glu Asp Thr Ala
1 5 10 15
Gly Val Val Lys Leu Ile Ser Ala Glu Gly Phe Glu Phe Val Val Asp
20 25 30
Lys Lys Ala Ala Met Val Ser Asn Thr Leu Arg Asn Met Leu Thr Ser
35 40 45
Pro Gly Gly Phe Ser Glu Thr Arg Gln Gly Glu Val Arg Phe Pro Glu
50 55 60
Ile Pro Thr Asn Ile Leu Glu Lys Ile Cys Gln Tyr Phe Tyr Trp Ser
65 70 75 80
Leu His Tyr Ser Ser Ser Trp Phe Asn Thr Leu Asp Gly Leu Pro Ile
85 90 95
Glu Glu Leu Ser Gly Pro Glu Phe
100

(2) INFORMATION FOR SEQ ID NO:3150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..330
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3150:

atatccgcac ccgcgcgcgc cgcctctcga gtctcgtcca ccgctgctcc tcctagctcc	60
tctactcgcc agtcgccatg ggcaagatta agatcggaat caacggcttc ggaaggatcg	120
gcaggctcgt agaggagctg gtgtctgagg aggacgcaga ggaccacgac gattctccgc	180
caaggaaaga gccggctgtt tcgcatcgta gaaaggctgt cgtgtttgat gacagcgagc	240
aggactaaaa ttgtaaaaac cgtatgacga cctgacatgC tacgcttgct ttttctcccc	300
attgttttaa gagaatgatt agttattttt	

(2) INFORMATION FOR SEQ ID NO:3151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3151:

Ile Ser Ala Ser Ala Ala Ser Ala Ser Arg Val Ser Ser Thr Arg Arg
1 5 10 15
Pro Pro Ser Ser Ser Thr Arg Gln Ser Pro Trp Ala Arg Leu Arg Ser
20 25 30
Glu Ser Thr Ala Ser Glu Gly Ser Ala Gly Ser
35 40

(2) INFORMATION FOR SEQ ID NO:3152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3152:

Met Gly Lys Ile Lys Ile Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg
1 5 10 15
Leu Val Glu Glu Leu Val Ser Glu Glu Asp Asp Glu Asp His Asp Asp
20 25 30
Ser Pro Pro Arg Lys Gln Pro Ala Val Ser His Arg Arg Lys Ala Val
35 40 45
Val Phe Asp Asp Ser Asp Glu Asp
50 55

(2) INFORMATION FOR SEQ ID NO:3153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 710 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..710
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3153:

atccacaatat taaactcacg cacacacaca attaggtcac atacacacct cccggctgcc 60
tccttagtta gcagcttcta caatggaggc atccaacaag ctgcagctct tgctcctgtg 120
gctggctcatg gcagctgccca ctgcogtgca cccttctac tctgagaatt cgcctcaaga 180
ctacctcaact ccccaaaaaca gcgcocgtgc gcgcogtggg gttggcccg gtagctggag 240
cacgaagctg cagcagttcg cacagaagta gcgcgcacag agggccggcg actgcccgtt 300
ccagcactcg ggcgggccct acggggagaa catcttctgg ggtccgcgc gcttcgattg 360
gaaggcggtg gcgcagctgc gatcggtggg agacagagaa cagtgggtaca actacgccac 420
caacagctgc gcgcgcggca aggtgtgtgg cactacacgc agtgtgtgtg gcgcgccact 480
acaagctcgc gCtgcgcgcgc cgtcgtgtgc cgcgacaacc gtggcgtctt tatcatctgc 540
aactacgagc cccgcggcga cattgccggg atgaagccct actgatatat tgtgcotgcg 600
aacgatggca actgatatta tatctagaca cgggcttgtt gcacgcgatg actttccacg 660
tgtatatga ataattttt ataataaat caaagaggtt tgttatttc

(2) INFORMATION FOR SEQ ID NO:3154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3154:

Met Glu Ala Ser Asn Lys Leu Ala Val Leu Leu Trp Leu Val Met
1 5 10 15
Ala Ala Ala Thr Ala Val His Pro Ser Tyr Ser Glu Asn Ser Pro Gln
20 25 30
Asp Tyr Leu Thr Pro Gln Asn Ser Ala Arg Ala Ala Val Gly Val Gly
35 40 45
Pro Val Thr Trp Ser Thr Lys Leu Gln Gln Phe Ala Glu Lys Tyr Ala
50 55 60
Ala Gln Arg Ala Gly Asp Cys Arg Leu Gln His Ser Gly Gly Pro Tyr
65 70 75 80
Gly Glu Asn Ile Phe Trp Gly Ser Ala Gly Phe Asp Trp Lys Ala Val
85 90 95
Asp Ala Val Arg Ser Trp Val Asp Glu Lys Gln Trp Tyr Asn Tyr Ala
100 105 110
Thr Asn Ser Cys Ala Ala Gly Lys Val Cys Gly Thr Thr Arg Trp
115 120 125

Cys Gly Ala Pro Leu Gln Ala Ser Ala Ala Arg Ala Ser Cys Ala Ala
130 135 140
Thr Thr Val Ala Ser Leu Ser Ser Ala Thr Thr Ser Pro Ala Ala Thr
145 150 155 160
Leu Pro Gly

(2) INFORMATION FOR SEQ ID NO:3155:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1575752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3155:

Met Ala Ala Ala Thr Ala Val His Pro Ser Tyr Ser Glu Asn Ser Pro
1 5 10 15
Gln Asp Tyr Leu Thr Pro Gln Asn Ser Ala Arg Ala Ala Val Gly Val
20 25 30
Gly Pro Val Thr Trp Ser Thr Lys Leu Gln Gln Phe Ala Glu Lys Tyr
35 40 45
Ala Ala Gln Arg Ala Gly Asp Cys Arg Leu Gln His Ser Gly Gly Pro
50 55 60
Tyr Gly Glu Asn Ile Phe Trp Gly Ser Ala Gly Phe Asp Trp Lys Ala
65 70 75 80
Val Asp Ala Val Arg Ser Trp Val Asp Glu Lys Gln Trp Tyr Asn Tyr
85 90 95
Ala Thr Asn Ser Cys Ala Ala Gly Lys Val Cys Gly Thr Thr Arg Arg
100 105 110
Trp Cys Gly Ala Pro Leu Gln Ala Ser Ala Ala Arg Ala Ser Cys Ala
115 120 125
Ala Thr Thr Val Ala Ser Leu Ser Ser Ala Thr Thr Ser Pro Ala Ala
130 135 140
Thr Leu Pro Gly
145

(2) INFORMATION FOR SEQ ID NO:3156:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 699 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..699

(D) OTHER INFORMATION: / Ceres Seq. ID 1575794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3156:

actttttctct cctcgtttccc aatttcaagg ctgcccaccc ctgtgcgcgg taggtggtgg 60
cggtgaggat agagggttac ctgaggaggc agtgaatggc gccacgattc agtacaaccg 120
gagcaaccgc gcggtgaagc ggatcctgca ggaggtcaag gagatgcagt ccaaccacctc 180
accgacttc atgtccctcc cctcgagga ggacatcttc gactggcaat ttgctatcct 240
tggtccgaga gacagcgagt ttgaggggtg aatttatcat gccaggtatcc agctaCcttc 300
ggattatcca ttcaagccac cgtccttcat gctacttacg ccaagtggac gctttgagat 360
tcagaagaag atttgcttga gcatatccaa ttaccaccct gagcactggc agccttcatg 420
gagtgctcgc acagcttttg tagccttgat tgccttcatg ccgacgaacc caRggtgggg 480
cattgggctc actggattac aaaccagaag acagacgagc acttgctata aaatcacgtg 540
aggtgccscg gaaatttggc tcccacaaac gtcagaaact aattgatgag atccatgagc 600
aaatgctcgt ccgtgtgtag tgttcgtct tctgatccat tgtcgtgctc ctgtactcta 660

gtgatcagcg tcaaaataaa gaaatgcctg yccttggtt

(2) INFORMATION FOR SEQ ID NO:3157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1575795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3157:

Leu	Phe	Ser	Pro	Arg	Ser	Gln	Phe	Gln	Gly	Cys	Pro	Thr	Leu	Ala	Pro	
1			5						10				15			
Val	Gly	Gly	Gly	Glu	Asp	Arg	Gly	Leu	Pro	Glu	Glu	Ala	Val	Met		
			20				25					30				
Ala	Ala	Thr	Ile	Gln	Tyr	Asn	Arg	Ser	Asn	Pro	Ala	Val	Lys	Arg	Ile	
			35				40				45					
Leu	Gln	Glu	Val	Lys	Glu	Met	Gln	Ser	Asn	Pro	Ser	Pro	Asp	Phe	Met	
			50			55					60					
Ser	Leu	Pro	Leu	Glu	Glu	Asp	Ile	Phe	Glu	Trp	Gln	Phe	Ala	Ile	Leu	
65					70					75				80		
Gly	Pro	Arg	Asp	Ser	Glu	Phe	Glu	Gly	Gly	Ile	Tyr	His	Gly	Arg	Ile	
					85				90				95			
Gln	Leu	Pro	Ser	Asp	Tyr	Pro	Phe	Lys	Pro	Pro	Ser	Phe	Met	Leu	Leu	
			100				105						110			
Thr	Pro	Ser	Gly	Arg	Phe	Glu	Ile	Gln	Lys	Lys	Ile	Cys	Leu	Ser	Ile	
			115				120					125				
Ser	Asn	Tyr	His	Pro	Glu	His	Trp	Gln	Pro	Ser	Trp	Ser	Val	Arg	Thr	
			130			135					140					
Ala	Leu	Val	Ala	Leu	Ile	Ala	Phe	Met	Pro	Thr	Asn	Pro	Xaa	Trp	Gly	
					150					155				160		
Ile	Gly	Leu	Thr	Gly	Leu	Gln	Thr	Arg	Arg	Gln	Thr	Ser	Thr	Cys	Tyr	
				165				170						175		
Lys	Ile	Thr														

(2) INFORMATION FOR SEQ ID NO:3158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1575796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3158:

Met	Ala	Ala	Thr	Ile	Gln	Tyr	Asn	Arg	Ser	Asn	Pro	Ala	Val	Lys	Arg	
1					5					10				15		
Ile	Leu	Gln	Glu	Val	Lys	Glu	Met	Gln	Ser	Asn	Pro	Ser	Pro	Asp	Phe	
			20				25					30				
Met	Ser	Leu	Pro	Leu	Glu	Glu	Asp	Ile	Phe	Glu	Trp	Gln	Phe	Ala	Ile	
			35				40					45				
Leu	Gly	Pro	Arg	Asp	Ser	Glu	Phe	Glu	Gly	Gly	Ile	Tyr	His	Gly	Arg	
					55					60						
Ile	Gln	Leu	Pro	Ser	Asp	Tyr	Pro	Phe	Lys	Pro	Pro	Ser	Phe	Met	Leu	
65					70					75				80		
Leu	Thr	Pro	Ser	Gly	Arg	Phe	Glu	Ile	Gln	Lys	Lys	Ile	Cys	Leu	Ser	
				85					90					95		

Ile Ser Asn Tyr His Pro Glu His Trp Gln Pro Ser Trp Ser Val Arg
100 105 110
Thr Ala Leu Val Ala Leu Ile Ala Phe Met Pro Thr Asn Pro Xaa Trp
115 120 125
Gly Ile Gly Leu Thr Gly Leu Gln Thr Arg Arg Gln Thr Ser Thr Cys
130 135 140
Tyr Lys Ile Thr
145

(2) INFORMATION FOR SEQ ID NO:3159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3159:

Met Gln Ser Asn Pro Ser Pro Asp Phe Met Ser Leu Pro Leu Glu Glu
1 5 10 15
Asp Ile Phe Glu Trp Gln Phe Ala Ile Leu Gly Pro Arg Asp Ser Glu
20 25 30
Phe Glu Gly Gly Ile Tyr His Gly Arg Ile Gln Leu Pro Ser Asp Tyr
35 40 45
Pro Phe Lys Pro Pro Ser Phe Met Leu Leu Thr Pro Ser Gly Arg Phe
50 55 60
Glu Ile Gln Lys Lys Ile Cys Leu Ser Ile Ser Asn Tyr His Pro Glu
65 70 75 80
His Trp Gln Pro Ser Trp Ser Val Arg Thr Ala Leu Val Ala Leu Ile
85 90 95
Ala Phe Met Pro Thr Asn Pro Xaa Trp Gly Ile Gly Leu Thr Gly Leu
100 105 110
Gln Thr Arg Arg Gln Thr Ser Thr Cys Tyr Lys Ile Thr
115 120 125

(2) INFORMATION FOR SEQ ID NO:3160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 707 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..707
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3160:

aaaagaatac ggtttaacaa acaccctacc caaaggggcg gaacccaagc cgccgtgacc 60
gccagaccga agccaacaag caagagcatt actactttct ctccgaccgc aaacottttc 120
tggaacgcga gaagaatccc aaccgccgacc gacctaccct aatcgcgcat ggcgacgggtg 180
gcgatggaca tctcgaagcc cactccagtg gcgtccggcg acgaggcgcg ccgcggccaa 240
ggggaggagc ggcggaggcg gcgaggggct gcggcagtag tacctgcagc acatccacga 300
cctgcagctc cagatccggc agaagaccga caacctcaac cgtctcgagg ccagcgcaa 360
tgacctcaac tcccagagta gaatgctcag ggaagagttg cagttgcttc aagagcctgg 420
ctcatatgtt ggtgaggttg tgaaggtcat ggggaaatca aaggttctgg tgaaggtaca 480
ccccgaagcc aaatatgttg ttgatataga taagagcatt gatatacaca agatcacacc 540
ttcaacaaga gtgcctcttc gtaatgacag ctatatgctc catctgaccc taccagaaca 600
agttgatcca ttggtcaatc tcatgaaagt tgagaaggtt cctgatttcta catatgatat 660
gattggaggc ctgaccagc aaattaaaga gatcaaaagc gtcattg

(2) INFORMATION FOR SEQ ID NO:3161:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..64
(D) OTHER INFORMATION: / Ceres Seq. ID 1575799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3161:

Met Ala Thr Val Ala Met Asp Ile Ser Lys Pro Thr Pro Val Ala Ser
1 5 10 15
Gly Asp Glu Ala Ala Gly Gly Gln Gly Glu Glu Arg Arg Arg Gly Arg
20 25 30
Gly Ala Ala Ala Val Leu Pro Ala Ala His Pro Arg Pro Ala Ala Pro
35 40 45
Asp Pro Ala Glu Asp Pro Gln Pro Gln Pro Ser Arg Gly Pro Ala Gln
50 55 60

(2) INFORMATION FOR SEQ ID NO:3162:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..108
(D) OTHER INFORMATION: / Ceres Seq. ID 1575800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3162:

Met Leu Arg Glu Glu Leu Gln Leu Leu Gln Glu Pro Gly Ser Tyr Val
1 5 10 15
Gly Glu Val Val Lys Val Met Gly Lys Ser Lys Val Leu Val Lys Val
20 25 30
His Pro Glu Gly Lys Tyr Val Val Asp Ile Asp Lys Ser Ile Asp Ile
35 40 45
Thr Lys Ile Thr Pro Ser Thr Arg Val Ala Leu Arg Asn Asp Ser Tyr
50 55 60
Met Leu His Leu Ile Leu Pro Ser Lys Val Asp Pro Leu Val Asn Leu
65 70 75 80
Met Lys Val Glu Lys Val Pro Asp Ser Thr Tyr Asp Met Ile Gly Gly
85 90 95
Leu Asp Gln Gln Ile Lys Glu Ile Lys Glu Val Ile
100 105

(2) INFORMATION FOR SEQ ID NO:3163:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..86
(D) OTHER INFORMATION: / Ceres Seq. ID 1575801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3163:

Met Gly Lys Ser Lys Val Leu Val Lys Val His Pro Glu Gly Lys Tyr
1 5 10 15

(2) INFORMATION FOR SEO ID NO:3164:

(A) LENGTH: 737 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (c)

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..737

(D) OTHER INFORMATION: / Ceres Seq. ID 1575815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3164:

atctctctctc	tgttctatctc	ctcccaagaa	acaagagcca	accagcgctt	cggaactcaa	60
gcgcgcgcgc	aatgtctctg	gcgcgcctca	tccttccat	cgaggtgaag	gtggggcgcg	120
ctctcgtctc	tcctccacac	cgtctcatgc	cggtctctgc	ggatgtcagg	agctccaagg	180
caagaggccc	cattccggaa	ctctgcggcg	ctcgcTgtg	gccaccgcca	ccgattgcaac	240
ccaagacgac	ggctctgttc	actctcccca	ccctgtcgca	gcctccgaca	cccgtagaac	300
ccgctgtctc	accacagctc	tgcgcgcga	tgcacacct	tctctgagcg	aagccaagtT	360
cgccacagac	ccagatcgcg	atgacggctg	ctggggccat	cgatctggag	taccagagaa	420
aggtgcgcaa	gcagctcgag	gagtaactga	agagaagaaa	ctgtggagag	gcgcgaccgg	480
ctcgtctttt	cgagcttcgc	ccaacaaagt	agatttccaa	cggaaagggtg	gccattgttg	540
ggttctgcagt	agggatgcta	acagagtatc	caaacagctt	ggattttgct	cagcaaatga	600
agatctcttc	ctccaaattt	ggaattgtgg	actctgatta	atgtggagct	tttgtgttgt	660
tcgttatgta	caagctcttt	aaatgtaatg	tacttactct	atatgtgata	tagaaaattt	720
caattatcac	attgtctc					

(2) INFORMATION FOR SEQ ID NO:3165:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1575816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3165:

Leu	Leu	Ser	Val	His	Ser	Leu	Pro	Arg	Asn	Lys	Ser	Gln	Pro	Ala	Leu
1				5					10					15	
Ala	Asn	Ser	Ser	Ala	Ala	Ala	Met	Ser	Leu	Ala	Pro	Ser	Ile	Pro	Ser
			20					25					30		
Ile	Lys	Val	Lys	Val	Gly	Ala	Val	Ser	Val	Ala	Pro	Pro	His	Arg	Ala
			35				40					45			
Cys	Arg	Ser	Phe	Ala	Val	Ile	Arg	Ser	Ser	Lys	Ala	Glu	Gly	Pro	Ile
						55					60				
Arg	Arg	Pro	Ala	Ala	Pro	Pro	Leu	Ser	Pro	Pro	Pro	Pro	Met	Pro	Pro
65					70					75				80	
Lys	Thr	Pro	Ala	Leu	Ser	Thr	Pro	Pro	Thr	Leu	Ser	Gln	Pro	Pro	Thr
				85					90				95		
Pro	Val	Lys	Pro	Ala	Ala	Pro	Pro	Thr	Ser	Ser	Gln	Pro	Met	Pro	Pro
			100					105				110			

Ser Pro Glu Pro Lys Pro Val Asp Ala Thr Ala Gln Met Arg Lys Pro
115 120 125
Val Ala Gly Ala Met Thr Leu Glu Tyr Gln Arg Lys Val Ala Lys Asp
130 135 140
Leu Gln Glu Tyr Phe Lys Lys Lys Lys Leu Glu Ala Asp Gln Gly
145 150 155 160
Pro Phe Phe Gly Phe Leu Pro Lys Asn Glu Ile Ser Asn Gly Arg Trp
165 170 175
Ala Met Phe Gly Phe Ala Val Gly Met Leu Thr Glu Tyr Ala Thr Gly
180 185 190
Ser Asp Phe Val Gln Gln Met Lys Ile Leu Leu Ser Asn Phe Gly Ile
195 200 205
Val Asp Leu Asp
210

(2) INFORMATION FOR SEQ ID NO:3166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..189
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3166:

Met Ser Leu Ala Pro Ser Ile Pro Ser Ile Lys Val Lys Val Gly Ala
1 5 10 15
Val Ser Val Ala Pro Pro His Arg Ala Cys Arg Ser Phe Ala Val Ile
20 25 30
Arg Ser Ser Lys Ala Glu Gly Pro Ile Arg Arg Pro Ala Ala Pro Pro
35 40 45
Leu Ser Pro Pro Pro Pro Met Pro Pro Lys Thr Pro Ala Leu Ser Thr
50 55 60
Pro Pro Thr Leu Ser Gln Pro Pro Thr Pro Val Lys Pro Ala Ala Pro
65 70 75 80
Pro Thr Ser Ser Gln Pro Met Pro Pro Ser Pro Glu Pro Lys Pro Val
85 90 95
Asp Ala Thr Ala Gln Met Arg Lys Pro Val Ala Gly Ala Met Thr Leu
100 105 110
Glu Tyr Gln Arg Lys Val Ala Lys Asp Leu Gln Glu Tyr Phe Lys Lys
115 120 125
Lys Lys Leu Glu Glu Ala Asp Gln Gly Pro Phe Phe Gly Phe Leu Pro
130 135 140
Lys Asn Glu Ile Ser Asn Gly Arg Trp Ala Met Phe Gly Phe Ala Val
145 150 155 160
Gly Met Leu Thr Glu Tyr Ala Thr Gly Ser Asp Phe Val Gln Gln Met
165 170 175
Lys Ile Leu Leu Ser Asn Phe Gly Ile Val Asp Leu Asp
180 185

(2) INFORMATION FOR SEQ ID NO:3167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3167:

Met Pro Pro Lys Thr Pro Ala Leu Ser Thr Pro Pro Thr Leu Ser Gln
1 5 10 15
Pro Pro Thr Pro Val Lys Pro Ala Ala Pro Pro Thr Ser Ser Gln Pro
20 25 30
Met Pro Pro Ser Pro Glu Pro Lys Pro Val Asp Ala Thr Ala Gln Met
35 40 45
Arg Lys Pro Val Ala Gly Ala Met Thr Leu Glu Tyr Gln Arg Lys Val
50 55 60
Ala Lys Asp Leu Gln Glu Tyr Phe Lys Lys Lys Leu Glu Glu Ala
65 70 75 80
Asp Gln Gly Pro Phe Phe Gly Phe Leu Pro Lys Asn Glu Ile Ser Asn
85 90 95
Gly Arg Trp Ala Met Phe Gly Phe Ala Val Gly Met Leu Thr Glu Tyr
100 105 110
Ala Thr Gly Ser Asp Phe Val Gln Gln Met Lys Ile Leu Leu Ser Asn
115 120 125
Phe Gly Ile Val Asp Leu Asp
130 135

(2) INFORMATION FOR SEQ ID NO:3168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..745

- (D) OTHER INFORMATION: / Ceres Seq. ID 1575822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3168:

atcaaaatag	agttcacacg	cacaaccgcg	cgcgcacgcg	cgggatctcg	atagactctg	60
gctgcgcg	aaagcggaaa	gaaggcaggg	atcgtggcca	agatgcagat	cttcgtgaag	120
acgctgtcgt	cgacaaggac	gatcacgctg	gaggttgagc	cttcggacac	ggtggcggac	180
gtgaaggcca	aggtgtacga	gtcggaggcg	gtcccgccgg	ccgagcagcg	cctcatcttc	240
gcggggaagc	agCtgcgcga	cggctgcacg	ctggctgact	acaacatccc	caaggagacg	300
atgctgtcct	tgtgtgcgCg	cctcctcgga	ggcgGcccca	agaagcgcaa	taggaagacg	360
ttcaccactc	ctaagaaggg	cacgcacgag	cacaagaacc	ccgggctcga	cgccgtgtct	420
ggcggtgaca	ggatcgatga	ggccacgggg	aaggtggaga	ggCtgcgcgt	gcagtgccct	480
aaaccggagt	gcggcccaRg	gcgtgtctcat	ggcgccgcac	gccgaccgcg	acgtctgcgg	540
cagctgcgcg	ctcaccttcg	tcattccagaa	ctagagcgcg	cgagatagct	aggtcgcttc	600
gtactccccc	catttgaat	gacaaagcgt	ttttaccttt	ctagatatgc	acttatgtct	660
agatacatag	attatcttat	acttttttgc	ttctttttta	tttatcgtgt	tttagttaa	720
aataaataa	ttgagtgaat	atggt				

(2) INFORMATION FOR SEQ ID NO:3169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161

- (D) OTHER INFORMATION: / Ceres Seq. ID 1575823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3169:

Met Gln Ile Phe Val Lys Thr Leu Ser Ser Thr Arg Thr Ile Thr Leu
1 5 10 15
Glu Val Glu Pro Ser Asp Thr Val Ala Asp Val Lys Ala Lys Val Tyr
20 25 30
Glu Ser Glu Gly Val Pro Pro Ala Glu Gln Arg Leu Ile Phe Ala Gly

35	40	45	
Lys Gln Leu Arg Asp Gly Cys Thr Leu Ala Asp Tyr Asn Ile Pro Lys			
50	55	60	
Glu Thr Met Leu Ser Leu Cys Cys Arg Leu Leu Gly Gly Pro Lys			
65	70	75	80
Lys Arg Asn Arg Lys Thr Phe Thr Thr Pro Lys Lys Gly Thr His Glu			
	85	90	95
His Lys Asn Pro Gly Leu Asp Ala Val Leu Gly Arg Tyr Arg Ile Asp			
	100	105	110
Glu Ala Thr Gly Lys Val Glu Arg Leu Arg Met Gln Cys Pro Asn Pro			
	115	120	125
Glu Cys Gly Pro Xaa Arg Ala His Gly Gly Ala Arg Pro Ala Arg			
	130	135	140
Leu Arg Gln Leu Arg Pro His Leu Arg His Pro Glu Leu Glu Arg Gly			
	145	150	155
Arg			160

(2) INFORMATION FOR SEQ ID NO:3170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1575824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3170:

Met Leu Ser Leu Cys Cys Arg Leu Leu Gly Gly Pro Lys Lys Arg	
1	5
Asn Arg Lys Thr Phe Thr Thr Pro Lys Lys Gly Thr His Glu His Lys	10
	15
Asn Pro Gly Leu Asp Ala Val Leu Gly Arg Tyr Arg Ile Asp Glu Ala	20
	25
Thr Gly Lys Val Glu Arg Leu Arg Met Gln Cys Pro Asn Pro Glu Cys	30
	35
Gly Pro Xaa Arg Ala His Gly Gly Ala Arg Pro Ala Arg Leu Arg	40
	45
Gln Leu Arg Pro His Leu Arg His Pro Glu Leu Glu Arg Gly Arg	50
	55
	60
	65
	70
	75
	80
	85
	90
	95

(2) INFORMATION FOR SEQ ID NO:3171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 724 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..724

(D) OTHER INFORMATION: / Ceres Seq. ID 1575825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3171:

gttttgaaaa aggaacggcc catgttcagg gagaaggctc cgaactgggctc agggaggcgt	60
aggctatcgc cgccggccgcc gttctctcac ctgctgcac gctgcttcgc cctccgcctc	120
acaagGctac accagatgcc cagattttcg tccggttctt Tctccggcaa cgagcagcca	180
ccaggtgtct tggattttgc aaacagtgac aaaaggttct gCttcgctgt agagtcattg	240
ctgcaaaagt accgctagtg atgaagtctt ttatgagcca aagcaaccag gtctcagggc	300
ttatgccatt cacaaaagag attggactac ctgaatcac agccctgtac accgtgttgc	360
ggtcacctca tatcgataag aagtccaggg aacaattctc gatgcattgc aagaacacgt	420
ttgtggaaca gacagccaaa ccacacgaac ttacaggaa gttcttctgc ttaaaacgcc	480

tgcggatacc tggggctcag tatgaaatcc aaatttcttt caAgacacgt ctccgatatgg 540
cgagcctaag gtcccaagct ccttgctgac tctcagatct tcttaccgt cctgaatggt 600
tgaagtgact tgtatccatc gacatttcac atgttatgaa gacatgctta ttttgatggc 660
ttttgaaaaa aaatgtacct gctaagtctt cattacccttg acagatcact agtcaagaaa 720
atgc

(2) INFORMATION FOR SEQ ID NO:3172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1575826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3172:

Met	Ser	Ala	Lys	Ile	Arg	Val	Val	Met	Lys	Ser	Phe	Met	Ser	Gln	Ser
1			5						10					15	
Asn	Gln	Val	Ser	Gly	Leu	Met	Pro	Phe	Thr	Lys	Lys	Ile	Gly	Leu	Pro
			20						25				30		
Glu	Ser	Arg	Ala	Leu	Tyr	Thr	Val	Leu	Arg	Ser	Pro	His	Ile	Asp	Lys
			35				40					45			
Lys	Ser	Arg	Glu	Gln	Phe	Ser	Met	His	Val	Lys	Lys	Gln	Phe	Val	Glu
			50				55				60				
Gln	Thr	Ala	Lys	Pro	His	Glu	Leu	His	Arg	Lys	Phe	Phe	Trp	Leu	Lys
			65				70				75			80	
Arg	Leu	Arg	Ile	Pro	Gly	Ala	Gln	Tyr	Glu	Ile	Gln	Ile	Ser	Phe	Lys
			85						90				95		
Thr	Arg	Leu	Asp	Met	Ala	Ser	Leu	Arg	Ser	Gln	Ala	Pro	Cys		
			100						105				110		

(2) INFORMATION FOR SEQ ID NO:3173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1575827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3173:

Met	Lys	Ser	Phe	Met	Ser	Gln	Ser	Asn	Gln	Val	Ser	Gly	Leu	Met	Pro
1			5						10					15	
Phe	Thr	Lys	Lys	Ile	Gly	Leu	Pro	Glu	Ser	Arg	Ala	Leu	Tyr	Thr	Val
			20						25				30		
Leu	Arg	Ser	Pro	His	Ile	Asp	Lys	Lys	Ser	Arg	Glu	Gln	Phe	Ser	Met
			35				40					45			
His	Val	Lys	Lys	Gln	Phe	Val	Glu	Gln	Thr	Ala	Lys	Pro	His	Glu	Leu
			50				55				60				
His	Arg	Lys	Phe	Phe	Trp	Leu	Lys	Arg	Leu	Arg	Ile	Pro	Gly	Ala	Gln
			65				70				75			80	
Tyr	Glu	Ile	Gln	Ile	Ser	Phe	Lys	Thr	Arg	Leu	Asp	Met	Ala	Ser	Leu
			85						90				95		
Arg	Ser	Gln	Ala	Pro	Cys										
			100												

(2) INFORMATION FOR SEQ ID NO:3174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1575828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3174:

Met Ser Gln Ser Asn Gln Val Ser Gly Leu Met Pro Phe Thr Lys Lys
1 5 10 15
Ile Gly Leu Pro Glu Ser Arg Ala Leu Tyr Thr Val Leu Arg Ser Pro
20 25 30
His Ile Asp Lys Lys Ser Arg Glu Gln Phe Ser Met His Val Lys Lys
35 40 45
Gln Phe Val Glu Gln Thr Ala Lys Pro His Glu Leu His Arg Lys Phe
50 55 60
Phe Trp Leu Lys Arg Leu Arg Ile Pro Gly Ala Gln Tyr Glu Ile Gln
65 70 75 80
Ile Ser Phe Lys Thr Arg Leu Asp Met Ala Ser Leu Arg Ser Gln Ala
85 90 95
Pro Cys

(2) INFORMATION FOR SEQ ID NO:3175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 815 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..815

(D) OTHER INFORMATION: / Ceres Seq. ID 1575844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3175:

catagaactg atggtggggc cagaacatgg gataacacta cacctgtaaa caatgtggat 60
ctctgccaatg ttgtctctgca ggggtggtgaa gctccccgca cagctgcaaa tactactagt 120
gagGatTgca tccaaAcagG tacaccaAag tccaggtagt cctcaggtTg ttTggcaaga 180
caacatTgac cctgacaata tgacatatga ggaactcttg gatttgggtg aggcagttgg 240
aaccacagac cgtgtgtctct cccaagaatg catttctgtg ctctcccatca ctaagtataa 300
gtgtggattc ttttcaagga agaaacacgc ccgtgaaagg tgtgtgattt gccaaatgga 360
gtacaggaga ggaaatttgc agattacgct tccatgcaag catgtatacc atgccagctg 420
cgtgacaaga tggcttagca taaacaaggt atgccctgtt tgccttgcgt aagttcctg 480
cgaggattct cagaggcaat gattcatcag ttgtgatgcc actatgaagt tgctgtctgt 540
ggtactgcgc ccccaatgga cgcgatgatt ctttgaagcg agcttgttgt cccacttta 600
gaattgtgta tttagcgcat attaccaaat aggtatttac ttatcagatg tatttagtta 660
gtgtttgtgt tcggaatatg gttagatgga gtcactttgc tctaattta ttgtgtttg 720
aattgtttt atgtaggaca tagtaactct aaaattggaa aaactatgct taaatactga 780
atcatctgac tcccacaaat cttttggacg gagac

(2) INFORMATION FOR SEQ ID NO:3176:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1575845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3176:

Met Trp Ile Leu Pro Met Leu Ser Cys Arg Val Val Lys Leu Pro Ala

1		5		10		15
Gln	Leu	Gln	Ile	Leu	Val	Arg
		20				25
Ser	Pro	Gly	Ser	Pro	Gln	Val
		35				40
Asn	Met	Thr	Tyr	Glu	Glu	Leu
		50				55
Gln	Ser	Arg	Gly	Leu	Ser	Gln
		65				70
Lys	Tyr	Lys	Cys	Gly	Phe	Phe
			85			
Cys	Val	Ile	Cys	Gln	Met	Glu
			100			105
Leu	Pro	Cys	Lys	His	Val	Tyr
			115			120
Ser	Ile	Asn	Lys	Val	Cys	Pro
			130			135

Asp Ser Gln Arg Gln

145

(2) INFORMATION FOR SEQ ID NO:3177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3177:

Met	Leu	Ser	Cys	Arg	Val	Val	Lys	Leu	Pro	Ala	Gln	Leu	Gln	Ile	Leu
1			5						10					15	
Leu	Val	Arg	Ile	Ala	Ser	Lys	Gln	Val	His	Gln	Ser	Pro	Gly	Ser	Pro
			20						25					30	
Gln	Val	Val	Trp	Gln	Asp	Asn	Ile	Asp	Pro	Asp	Asn	Met	Thr	Tyr	Glu
			35						40					45	
Glu	Leu	Leu	Asp	Leu	Gly	Glu	Ala	Val	Gly	Thr	Gln	Ser	Arg	Gly	Leu
			50						55					60	
Ser	Gln	Glu	Cys	Ile	Ser	Leu	Leu	Pro	Ile	Thr	Lys	Tyr	Lys	Cys	Gly
			65						70					75	
Phe	Phe	Ser	Arg	Lys	Lys	Thr	Arg	Arg	Glu	Arg	Cys	Val	Ile	Cys	Gln
				85					90					95	
Met	Glu	Tyr	Arg	Arg	Gly	Asn	Leu	Gln	Ile	Thr	Leu	Pro	Cys	Lys	His
				100					105					110	
Val	Tyr	His	Ala	Ser	Cys	Val	Thr	Arg	Trp	Leu	Ser	Ile	Asn	Lys	Val
				115					120					125	
Cys	Pro	Val	Cys	Phe	Ala	Glu	Val	Pro	Gly	Glu	Asp	Ser	Gln	Arg	Gln
				130					135					140	

(2) INFORMATION FOR SEQ ID NO:3178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1575847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3178:

Met Thr Tyr Glu Glu Leu Leu Asp Leu Gly Glu Ala Val Gly Thr Gln
1 5 10 15
Ser Arg Gly Leu Ser Gln Glu Cys Ile Ser Leu Leu Pro Ile Thr Lys
20 25 30
Tyr Lys Cys Gly Phe Phe Ser Arg Lys Lys Thr Arg Arg Glu Arg Cys
35 40 45
Val Ile Cys Gln Met Glu Tyr Arg Arg Gly Asn Leu Gln Ile Thr Leu
50 55 60
Pro Cys Lys His Val Tyr His Ala Ser Cys Val Thr Arg Trp Leu Ser
65 70 75 80
Ile Asn Lys Val Cys Pro Val Cys Phe Ala Glu Val Pro Gly Glu Asp
85 90 95
Ser Gln Arg Gln
100

(2) INFORMATION FOR SEQ ID NO:3179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..923
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3179:

gtcatcgctct cgttcctctg ctcccttttg caacctccct tcatataggc cactgtgacc 60
tgcttccctt tcgcagttgc tcatctccat agccacctcg gaagctcgag gccgaggatc 120
cacatatata gcatctgtct tttatactaa taggttttag tttttgggag aatctacaca 180
cgcgagaagc taggtagctt tcttcaataa ctggggtcca gtccagcaag ctccaccttg 240
ccctccatcg accgatcgac ctgctgcggg ccagagagaca tccatccatc catcttcctc 300
tccctggctgt aagaagagga gatggtctca tggccgtgat ctacatcGc ggagcGCTcg 360
tcgcggccgt gtcctctctg ctctctctcg Gcgcgcgcac cagcatccGc caccgcgacg 420
ttttccctt ctcaggagaa cctggcggag gacaagtgcg ggctgggggtc gacgcgccgcg 480
atctgccgca accgggtcgag cgcttgcaac ccttgcatgc ccgtgcaggt gacgaccgcg 540
cccgccgggg tcggggcgcg gccccgcgtc accgacgcgc acgcccacgc cgacgcgggtg 600
gcggcttct ccgctactc cgactacaag ccgctgggggt ggaaatgcgg ctgcgacggc 660
cgccctgtag acccttagcc gagcgtgcaa cgccagtga ctcgtctccg gtcgcgttagg 720
gtggggagaga ctggaggcca tccaggttct tcgtgtcatc tgttcttggt ttttgcccat 780
gggcatggc ggcttgcttg cattgcagct tgtaccgccc gtacccgtag ccattttttt 840
ttgctctctg ctgaacaat tttactctg cgtgtaaaga gtaaccgtga ccgtgagcac 900
taaaaaattgt agtggttacc gcc

(2) INFORMATION FOR SEQ ID NO:3180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3180:

Met Ala Val Ile Ser His Arg Gly Ala Leu Val Ala Ala Val Ser Leu
1 5 10 15
Cys Leu Leu Leu Gly Ala Ala Thr Ser Ile Pro His Arg Asp Val Phe
20 25 30
Pro Phe Ser Gly Glu Pro Gly Gly Gln Val Ala Ala Gly Val Asp

35	40	45
Ala Ala Asp Leu Pro Gln Pro Val Gln Arg Leu Gln Pro Leu His Ala		
50	55	60
Arg Ala Gly Asp Asp Arg Ala Arg Gly Ala Arg Ala Arg Gly Pro Arg		
65	70	75
His Arg Arg Arg Arg Arg Arg Arg Arg Gly Gly Arg Leu Leu Pro Leu		
85	90	95
Leu Arg Leu Gln Ala Ala Gly Val Glu Met Arg Leu Arg Arg Pro Pro		
100	105	110
Val Arg Pro Leu Ala Glu Arg Ala Thr Pro Val His Ser Ala Pro Val		
115	120	125

Arg

(2) INFORMATION FOR SEQ ID NO:3181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..904
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3181:

gaaggagttc aaggtggagg tggaaagcaat cggctcgtgtt cggcacaaaa atctcgtcag	60
gttgctcggc tactgcgtag aggggtgctta caggatgctt gtgtatgagt atgtggacaa	120
tggtaatctt gaccagtggc ttcattggtga tgttggcgaa gtgagccac tgacatggga	180
catcaggatg aacatcatgc ttgcaccgcg taaagggctg gcctacctcc acgaggggct	240
ggaaccgaa ttgntccacc gcgacatcaa gctagcaac atcctctctg accagcagt	300
gaacgcgaaa gtatcggatt tcgggctcgc gaaGctgttg tgctcggaga gaagctacgt	360
tacgaccogt gtcattggaa mcttcgggta cgtggcgctt gagtacgcca gaacgggcat	420
gctgaacgag aggagcgtat tgatatgctt cggcgctcgt ataatggaga tcatcaccg	480
cagatctcct gtggattaca caagggcgcg tggagagtg cactgggtg agtggctcaa	540
gaacatggtg gccgagagga aagcggagga ggtagtggac agtaagatgg ccgagaggcc	600
tcctcccaag acgtggaagc gggcgctcct ggtgngsstc cgctgcgtgg accctgacgc	660
gaacaagcgg cctaagatgg ggcatgtgat ccacatgctc gaaatggacg acctccagtt	720
ccgagatagg tacagtccca agctaggtgg aggaagggag cctcagcaag cgcgagcacc	780
agcgtcggta cagatgagat gattgtcatt agagagtagc gatattaac atgttatttt	840
tttcccgcta gtaaatcat tcttcccaa ctcgttccat cgattctcaa tggttytcga	900

ttkt

(2) INFORMATION FOR SEQ ID NO:3182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3182:

Lys Glu Phe Lys Val Glu Val Glu Ala Ile Gly Arg Val Arg His Lys	
1	15
Asn Leu Val Arg Leu Leu Gly Tyr Cys Val Glu Gly Ala Tyr Arg Met	
20	30
Leu Val Tyr Glu Tyr Val Asp Asn Gly Asn Leu Asp Gln Trp Leu His	
35	45
Gly Asp Val Gly Glu Val Ser Pro Leu Thr Trp Asp Ile Arg Met Asn	
50	60


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Ile Met Leu Ala Thr Ala Lys Gly Leu Ala Tyr Leu His Glu Gly Leu
65      70      75      80
Glu Pro Lys Leu Xaa His Arg Asp Ile Lys Ala Ser Asn Ile Leu Leu
      85      90      95
Asp Gln Gln Trp Asn Ala Lys Val Ser Asp Phe Gly Leu Ala Lys Leu
      100      105      110
Leu Cys Ser Glu Arg Ser Tyr Val Thr Thr Arg Val Met Gly Xaa Phe
      115      120      125
Gly Tyr Val Ala Pro Glu Tyr Ala Ser Thr Gly Met Leu Asn Glu Arg
      130      135      140
Ser Asp Val Tyr Ser Phe Gly Val Leu Ile Met Glu Ile Ile Thr Gly
145      150      155      160
Arg Ser Pro Val Asp Tyr Thr Arg Ala Ala Gly Glu Val His Leu Val
      165      170      175
Glu Trp Leu Lys Asn Met Val Ala Glu Arg Lys Ala Glu Glu Val Val
      180      185      190
Asp Ser Lys Met Ala Glu Arg Pro Pro Lys Thr Leu Lys Arg Ala
      195      200      205
Leu Leu Val Xaa Xaa Arg Cys Val Asp Pro Asp Ala Asn Lys Arg Pro
210      215      220
Lys Met Gly His Val Ile His Met Leu Glu Met Asp Asp Leu Gln Phe
225      230      235      240
Arg Asp Arg Tyr Ser Ser Lys Leu Gly Gly Arg Glu Pro Gln Gln
      245      250      255
Ala Arg Ala Pro Ala Ser Val Gln Met Arg
      260      265

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(2) INFORMATION FOR SEQ ID NO:3183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..235

(D) OTHER INFORMATION: / Ceres Seq. ID 1575937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3183:

```

Met Leu Val Tyr Glu Tyr Val Asp Asn Gly Asn Leu Asp Gln Trp Leu
1      5      10      15
His Gly Asp Val Gly Glu Val Ser Pro Leu Thr Trp Asp Ile Arg Met
      20      25      30
Asn Ile Met Leu Ala Thr Ala Lys Gly Leu Ala Tyr Leu His Glu Gly
      35      40      45
Leu Glu Pro Lys Leu Xaa His Arg Asp Ile Lys Ala Ser Asn Ile Leu
50      55      60
Leu Asp Gln Gln Trp Asn Ala Lys Val Ser Asp Phe Gly Leu Ala Lys
65      70      75      80
Leu Leu Cys Ser Glu Arg Ser Tyr Val Thr Thr Arg Val Met Gly Xaa
      85      90      95
Phe Gly Tyr Val Ala Pro Glu Tyr Ala Ser Thr Gly Met Leu Asn Glu
      100      105      110
Arg Ser Asp Val Tyr Ser Phe Gly Val Leu Ile Met Glu Ile Ile Thr
      115      120      125
Gly Arg Ser Pro Val Asp Tyr Thr Arg Ala Ala Gly Glu Val His Leu
130      135      140
Val Glu Trp Leu Lys Asn Met Val Ala Glu Arg Lys Ala Glu Glu Val
145      150      155      160
Val Asp Ser Lys Met Ala Glu Arg Pro Pro Lys Thr Leu Lys Arg
      165      170      175
Ala Leu Leu Val Xaa Xaa Arg Cys Val Asp Pro Asp Ala Asn Lys Arg

```

180	185	190
Pro Lys Met Gly His Val Ile	His Met Leu Glu Met Asp	Asp Leu Gln
195	200	205
Phe Arg Asp Arg Tyr Ser Ser Lys Leu Gly Gly	Gly Arg Glu Pro Gln	
210	215	220
Gln Ala Arg Ala Pro Ala Ser Val Gln Met Arg		
225	230	235

(2) INFORMATION FOR SEQ ID NO:3184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1575938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3184:

Met Asn Ile Met Leu Ala Thr Ala Lys Gly Leu Ala Tyr Leu His Glu	
1 5 10 15	
Gly Leu Glu Pro Lys Leu Xaa His Arg Asp Ile Lys Ala Ser Asn Ile	
20 25 30	
Leu Leu Asp Gln Gln Trp Asn Ala Lys Val Ser Asp Phe Gly Leu Ala	
35 40 45	
Lys Leu Leu Cys Ser Glu Arg Ser Tyr Val Thr Thr Arg Val Met Gly	
50 55 60	
Xaa Phe Gly Tyr Val Ala Pro Glu Tyr Ala Ser Thr Gly Met Leu Asn	
65 70 75 80	
Glu Arg Ser Asp Val Tyr Ser Phe Gly Val Leu Ile Met Glu Ile Ile	
85 90 95	
Thr Gly Arg Ser Pro Val Asp Tyr Thr Arg Ala Ala Gly Glu Val His	
100 105 110	
Leu Val Glu Trp Leu Lys Asn Met Val Ala Glu Arg Lys Ala Glu Glu	
115 120 125	
Val Val Asp Ser Lys Met Ala Glu Arg Pro Pro Lys Thr Leu Lys	
130 135 140	
Arg Ala Leu Leu Val Xaa Xaa Arg Cys Val Asp Pro Asp Ala Asn Lys	
145 150 155 160	
Arg Pro Lys Met Gly His Val Ile His Met Leu Glu Met Asp Asp Leu	
165 170 175	
Gln Phe Arg Asp Arg Tyr Ser Ser Lys Leu Gly Gly Arg Glu Pro	
180 185 190	
Gln Gln Ala Arg Ala Pro Ala Ser Val Gln Met Arg	
195 200	

(2) INFORMATION FOR SEQ ID NO:3185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 841 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..841

(D) OTHER INFORMATION: / Ceres Seq. ID 1575954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3185:

acaagcaaaag cagcagcaac agccaacacc taaactaaaag aacagtagta gtccctgtgt	60
acgtctagca acgatccgca ccgagctcgc cagttttgct cgttagtttg grgacrgcga	120
tggcgtccgg tcaggaaagc agggaggagc tggcgccgat ggccaggagg gggcagacgc	180
tcgtccccgg cggcaccggc ggcaagacc ctagggcgca ggagcacctc gccgaarggc	240

gcagtcacgg cgggcagacc cggagtgagc agctggggcca tgaggggtac agcgagatgg 300
gcagcaaggg cgggcagacc cgcaagagc agctggggcca cgaagggtac agcgagatgg 360
ggaggaaagg cggtctgagc accatgcagg agtccgcgcg cgagcgcgcc gCccgggagg 420
gcacgcagat cgacgagtcc aagttcagga ccaagtccta gatctgatgc gtgccccgcg 480
ttagcatgta gtacgtagct gcaggaatgt agtgtcgtcg tagtagtagg gtatgctgtac 540
gacgtgcgcc tcctcgtttg gcacgtgtgc cctgaataat gtatgctgtg cagtgcgtgt 600
cctagcacgc gtgtaggaga ccatacgtgc gcgtatgac atgcgtgttc gcttcagtta 660
ggtttctgat ttggtcgtcg tcaccgtgtt tgaagcaggc aggtctcttc aggttttgtc 720
gtcgtacgag cctgtgttct agctctacga ccccatctc atagcgtgtg gtgtggggtc 780
gtgatgcctt aaggtctcgc agtttgtatc cgtgcttgtt tcgttaaggt agtttggttc 840
t

(2) INFORMATION FOR SEQ ID NO:3186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3186:

Met Ala Ser Gly Gln Glu Ser Arg Glu Leu Ala Arg Met Ala Glu
1 5 10 15
Glu Gly Gln Thr Val Val Pro Gly Gly Thr Gly Gly Lys Thr Leu Glu
20 25 30
Ala Gln Glu His Leu Ala Glu Xaa Arg Ser His Gly Gly Gln Thr Arg
35 40 45
Ser Glu Gln Leu Gly His Glu Gly Tyr Ser Glu Met Gly Ser Lys Gly
50 55 60
Gly Gln Thr Arg Lys Glu Gln Leu Gly His Glu Gly Tyr Ser Glu Met
65 70 75 80
Gly Arg Lys Gly Gly Leu Ser Thr Met Gln Glu Ser Gly Gly Glu Arg
85 90 95
Ala Ala Arg Glu Gly Ile Glu Ile Asp Glu Ser Lys Phe Arg Thr Lys
100 105 110
Ser

(2) INFORMATION FOR SEQ ID NO:3187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3187:

Met Ala Glu Glu Gly Gln Thr Val Val Pro Gly Gly Thr Gly Gly Lys
1 5 10 15
Thr Leu Glu Ala Gln Glu His Leu Ala Glu Xaa Arg Ser His Gly Gly
20 25 30
Gln Thr Arg Ser Glu Gln Leu Gly His Glu Gly Tyr Ser Glu Met Gly
35 40 45
Ser Lys Gly Gly Gln Thr Arg Lys Glu Gln Leu Gly His Glu Gly Tyr
50 55 60
Ser Glu Met Gly Arg Lys Gly Gly Leu Ser Thr Met Gln Glu Ser Gly
65 70 75 80

Gly Glu Arg Ala Ala Arg Glu Gly Ile Glu Ile Asp Glu Ser Lys Phe
85 90 95

Arg Thr Lys Ser
100

(2) INFORMATION FOR SEQ ID NO:3188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..620
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3188:

atcttttcgag	atgaacgaac	agtcacagaac	ccactgctcg	aaaccgcagc	cactggccag	60
tcgatgccca	tgactgcrgt	gccacgagacc	ggcccccggtt	gcctgggggtc	gccgcgggct	120
caggctctgt	cgagctcaact	agccgggggtt	caaggcgccc	cgaagcgact	ggcgcatcg	180
aagccgtcgt	ggatcggtcg	cactgagtc	aacgtgagga	gggagagagc	aaaacgacct	240
gatccctctt	gcaccatctg	caagggcaca	gggagaatag	actgccgcaa	ctgctttggc	300
cgaggaaaga	caaaccatgc	cgatgtggcc	atgcttcga	acggcgaatg	gccacaatg	360
tgtcgaaatt	gtgtgtgtag	tggactggat	tactgcctcc	gggtccatgg	aactgtgtg	420
tatcgtgaac	ccatgggctt	ccaattcact	gtccaaagaa	aatgagttag	gtgggatggc	480
cttgatgct	acgatgcagc	gcaGcTgvgN	gggacatcgt	agCccactca	gcattgttct	540
ccactgtctc	tcagaactca	gatgatttat	gtctaggsst	aacgtgtgaa	taacgttgct	600
tcataaaagg	aaaaaatgtc					

(2) INFORMATION FOR SEQ ID NO:3189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3189:

Ile	Phe	Arg	Asp	Glu	Arg	Thr	Val	Gln	Asn	Pro	Leu	Leu	Glu	Thr	Ala
1		5						10					15		
Ala	Thr	Gly	Gln	Ser	Met	Pro	Met	Thr	Xaa	Val	Pro	Arg	Thr	Gly	Pro
		20					25					30			
Gly	Cys	Leu	Gly	Ser	Pro	Pro	Ala	Gln	Ala	Leu	Ser	Ser	Ser	Leu	Ala
		35					40				45				
Gly	Val	Gln	Gly	Ala	Pro	Lys	Arg	Leu	Gly	Ala	Ser	Lys	Pro	Ser	Trp
		50				55				60					
Ile	Val	Arg	Thr	Glu	Ser	Asn	Val	Arg	Arg	Glu	Arg	Ala	Lys	Arg	Pro
65						70				75			80		
Asp	Pro	Pro	Cys	Thr	Ile	Cys	Lys	Gly	Thr	Gly	Arg	Ile	Asp	Cys	Arg
			85					90					95		
Asn	Cys	Phe	Gly	Arg	Gly	Arg	Thr	Asn	His	Ala	Asp	Val	Ala	Met	Leu
			100				105					110			
Pro	Asn	Gly	Glu	Trp	Pro	Gln	Trp	Cys	Arg	Ile	Cys	Gly	Gly	Ser	Gly
		115				120						125			
Leu	Asp	Tyr	Cys	Leu	Arg	Cys	His	Gly	Thr	Gly	Glu	Tyr	Arg	Glu	Pro
		130				135					140				
Met	Gly	Phe	His	Phe	Thr	Val	Gln	Arg	Lys						
145						150									

(2) INFORMATION FOR SEQ ID NO:3190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..133
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1575965
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3190:

Met Pro Met Thr Xaa Val Pro Arg Thr Gly Pro Gly Cys Leu Gly Ser
1 5 10 15
Pro Pro Ala Gln Ala Leu Ser Ser Ser Leu Ala Gly Val Gln Gly Ala
20 25 30
Pro Lys Arg Leu Gly Ala Ser Lys Pro Ser Trp Ile Val Arg Thr Glu
35 40 45
Ser Asn Val Arg Arg Glu Arg Ala Lys Arg Pro Asp Pro Pro Cys Thr
50 55 60
Ile Cys Lys Gly Thr Gly Arg Ile Asp Cys Arg Asn Cys Phe Gly Arg
65 70 75 80
Gly Arg Thr Asn His Ala Asp Val Ala Met Leu Pro Asn Gly Glu Trp
85 90 95
Pro Gln Trp Cys Arg Ile Cys Gly Gly Ser Gly Leu Asp Tyr Cys Leu
100 105 110
Arg Cys His Gly Thr Gly Glu Tyr Arg Glu Pro Met Gly Phe His Phe
115 120 125
Thr Val Gln Arg Lys
130

(2) INFORMATION FOR SEQ ID NO:3191:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131

- (D) OTHER INFORMATION: / Ceres Seq. ID 1575966
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3191:

Met Thr Xaa Val Pro Arg Thr Gly Pro Gly Cys Leu Gly Ser Pro Pro
1 5 10 15
Ala Gln Ala Leu Ser Ser Ser Leu Ala Gly Val Gln Gly Ala Pro Lys
20 25 30
Arg Leu Gly Ala Ser Lys Pro Ser Trp Ile Val Arg Thr Glu Ser Asn
35 40 45
Val Arg Arg Glu Arg Ala Lys Arg Pro Asp Pro Pro Cys Thr Ile Cys
50 55 60
Lys Gly Thr Gly Arg Ile Asp Cys Arg Asn Cys Phe Gly Arg Gly Arg
65 70 75 80
Thr Asn His Ala Asp Val Ala Met Leu Pro Asn Gly Glu Trp Pro Gln
85 90 95
Trp Cys Arg Ile Cys Gly Gly Ser Gly Leu Asp Tyr Cys Leu Arg Cys
100 105 110
His Gly Thr Gly Glu Tyr Arg Glu Pro Met Gly Phe His Phe Thr Val
115 120 125
Gln Arg Lys
130

(2) INFORMATION FOR SEQ ID NO:3192:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 855 base pairs

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3192:

(2) INFORMATION FOR SEO ID NO:3193:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1575993

(xi) SEQUENCE DESCRIPTION: SEO ID NO:3193:

[illegible]

(2) INFORMATION FOR SEO ID NO:3194:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(18) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1575994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3194:

Met	Asn	Gly	Thr	Leu	Arg	Tyr	His	Val	Gln	Thr	Ala	Ser	Ala	Glu	Ala
1				5					10					15	
Val	Ser	Ser	Cys	Arg	Thr	Phe	Ser	Asp	Glu	Ala	Trp	Ser	Gln	Gln	Trp
			20					25					30		
Leu	Thr	Pro	Pro	Gln	Gly	Ile	Gln	Gln	Arg	Thr	Ser	Leu	Asp	Gly	Lys

cgcacatctc	ccgcgcgcgc	gcagccttcc	ctccctccct	tcctccgttc	catcgctcgc	60
cgtcgagacc	ttctgccgac	ttaacacttc	gatgcgcgcc	cgctccgcga	taccgccgct	120
ctcgcggggt	gtgcttcccc	aaaccttct	atccccccgg	tcgcgcgcgc	cgcaggctgc	180
acgcgtggcc	tcctcatctc	cgcggctctc	cttgttgctg	tcctccctgc	ggatcactca	240
caataatccc	ccgcctgatg	caagtgcgca	agctcgagaa	cgcgagcctg	tcactgcttc	300
agatgaatcc	gaagaggagg	tgggcgcagg	gtctgtcgat	gtggcgcgag	gggagaagcc	360
gacgcgcgcc	agcaaacgca	agGttaatg	cggcgaaata	attgggactc	tgaataatcc	420
gttcattgag	gaggctgaga	agctgaagac	tgtacccggt	ctbagccctg	gcgataatcc	480
gtagcttagg	atGcaacgcy	ccacaaaaac	gagattgtgc	ctctttaagg	ccataatcat	540
cgcgaagcac	aaagctggtg	ttcacaccac	aatccgtgtc	agaagaaata	ttgctgggtg	600
aggagtgtgag	attacctctc	cagtgctatc	accaggatc	aaggaaatac	cggttatcag	660
gcacaagaaa	gtgaggagag	caaatgtgtg	ctacctgaaa	cgaaagcttc	ccgctcttcc	720
aaacttcaag	tgaatacaga	tatgtcgaca	gaacgacttc	tttcaccacc	atctcagttt	780
ctcttcaaaa	tttttttttc	accttccctc	cgatatcatt	attatccact	gtaatcctgt	840
tgdtatcagat	gtgtaatact	tacagcttta	tatcatactt	ggcttagtgc	aatgttttgt	900
tttdttctctg	gttcaaaaat	ctactactac	acctttttat	tatgaatttg	caaataatcc	960

gttatgc

(2) INFORMATION FOR SEQ ID NO:3197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..243

(D) OTHER INFORMATION: / Ceres Seq. ID 1576003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3197:

Pro	Ile	Leu	Pro	Pro	Xaa	Arg	Arg	Leu	Pro	Leu	Pro	Pro	Ser	Ser	Val
1			5					10					15		
Pro	Cys	Ser	Ala	Ala	Asp	Thr	Leu	Ala	Arg	Leu	Asn	Leu	Thr	Met	Ala
			20				25					30			
Ala	Ala	Ser	Ala	Ile	Thr	Ala	Val	Ser	Gly	Val	Val	Leu	Pro	Gln	Thr
			35				40					45			
Phe	Leu	Ser	Pro	Arg	Ser	Pro	Pro	Gln	Val	Leu	Ala	Val	Ala	Ser	
			50			55				60					
Ser	Phe	Arg	Arg	Leu	Ser	Leu	Cys	Ala	Ser	Pro	Arg	Arg	Ile	Thr	His
65					70				75					80	
Ile	Ile	Pro	Arg	Ala	Asp	Ala	Ser	Ala	Glu	Ala	Gly	Glu	Pro	Glu	Pro
					85				90					95	
Val	Thr	Ala	Ser	Asp	Glu	Ser	Glu	Glu	Glu	Val	Ala	Glu	Gly	Ser	Val
			100					105					110		
Ala	Val	Ala	Glu	Gly	Glu	Glu	Pro	Thr	Pro	Pro	Ser	Lys	Pro	Lys	Val
			115				120					125			
Lys	Phe	Gly	Glu	Ile	Ile	Gly	Ile	Leu	Asn	Lys	Gln	Phe	Ile	Glu	Glu
			130			135					140				
Ala	Glu	Lys	Val	Lys	Thr	Val	Pro	Asp	Leu	Arg	Pro	Gly	Asp	Ile	Ile
145					150				155					160	
Glu	Leu	Arg	Met	Gln	Arg	Pro	Asn	Lys	Arg	Arg	Leu	Ser	Leu	Phe	Lys
			165					170						175	
Gly	Ile	Ile	Ile	Ala	Lys	His	Lys	Ala	Gly	Val	His	Thr	Thr	Ile	Arg
			180					185						190	
Val	Arg	Arg	Ile	Ile	Ala	Gly	Val	Gly	Val	Glu	Ile	Thr	Phe	Pro	Val
			195				200					205			
Tyr	Ser	Pro	Arg	Ile	Lys	Glu	Ile	Thr	Val	Ile	Arg	His	Lys	Lys	Val
			210			215					220				
Arg	Arg	Ala	Lys	Leu	Tyr	Tyr	Leu	Lys	Asp	Lys	Leu	Pro	Arg	Phe	Ser
225					230					235				240	
Thr	Phe	Lys													

(2) INFORMATION FOR SEQ ID NO:3198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213

(D) OTHER INFORMATION: / Ceres Seq. ID 1576004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3198:

Met	Ala	Ala	Ala	Ser	Ala	Ile	Thr	Ala	Val	Ser	Gly	Val	Val	Leu	Pro
1				5				10						15	
Gln	Thr	Phe	Leu	Ser	Pro	Arg	Ser	Pro	Pro	Pro	Gln	Val	Leu	Ala	Val
			20				25					30			

Ala Ser Ser Phe Arg Arg Leu Ser Leu Cys Ala Ser Pro Arg Arg Ile
35 40 45
Thr His Ile Ile Pro Arg Ala Asp Ala Ser Ala Glu Ala Gly Glu Pro
50 55 60
Glu Pro Val Thr Ala Ser Asp Glu Ser Glu Glu Val Ala Glu Gly
65 70 75 80
Ser Val Ala Val Ala Glu Gly Glu Glu Pro Thr Pro Pro Ser Lys Pro
85 90 95
Lys Val Lys Phe Gly Glu Ile Ile Gly Ile Leu Asn Lys Gln Phe Ile
100 105 110
Glu Glu Ala Glu Lys Val Lys Thr Val Pro Asp Leu Arg Pro Gly Asp
115 120 125
Ile Ile Glu Leu Arg Met Gln Arg Pro Asn Lys Arg Arg Leu Ser Leu
130 135 140
Phe Lys Gly Ile Ile Ile Ala Lys His Lys Ala Gly Val His Thr Thr
145 150 155 160
Ile Arg Val Arg Arg Ile Ile Ala Gly Val Gly Val Glu Ile Thr Phe
165 170 175
Pro Val Tyr Ser Pro Arg Ile Lys Glu Ile Thr Val Ile Arg His Lys
180 185 190
Lys Val Arg Arg Ala Lys Leu Tyr Tyr Leu Lys Asp Lys Leu Pro Arg
195 200 205
Phe Ser Thr Phe Lys
210

(2) INFORMATION FOR SEQ ID NO:3199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..967
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3199:

cttaaaaaacc	tctgctcggg	cctagggttt	cctcccagtc	gtcatcgctt	ggcgctccgcc	60
ttagccccgcc	gccaggagag	ccggctcggg	cggttcgtcg	aagatcccgg	atctgctctg	120
tcacgaggctc	tctcggcggg	tgttgtctcg	cgaggtgtag	cgagccaagg	tctggtcgcc	180
ttttcaggag	agtttcgaga	agctgaaatg	gtctcctaaag	ctgctcctgc	caagaagggt	240
gatgccaaaga	cccaggcctt	gaagggtgcc	aaggctgtga	agtctgggtc	agtaaaagag	300
accaagaaga	tccgcacgtc	cgtagacatt	caccgcccca	agaccctgaa	gaaggctagg	360
gaccccaagt	accacaagaat	cagcactacc	ggaaggaaca	agcttgatca	gtaccaaat	420
ctcaagtatc	ccctcaccac	agaatcggcg	atgaagaaga	ttgaagataa	caacactctt	480
gtcttctattg	tgcacctcaa	ggcagacaag	ragaagatca	Aggctgctgt	caagaagatg	540
tatgacattc	agggccaaga	ggcacaaccc	ctgatcaggc	ctgatggaaa	gaagaaggct	600
tacgtgaagc	ttatgctgta	ctatgatgct	cttgatgtgg	ccaacaaaat	cgggcatcatc	660
taaaagtacc	ggctcaggca	tctgctgtgc	tctatttcca	tgtgaaacca	gagtttttgt	720
agctatggct	cagtggctcc	atgacctatg	cttatgcaca	cttacgaatt	tgatatcatc	780
caagtcacag	gttgctctca	tcaactctg	gatactatca	cttattcgta	tggggttggt	840
ctttggctct	cacatttctt	tgtattgggt	tgggtttttg	atctcacctt	tcttcgcatt	900
gggttggtct	ttgggaattg	gaactcggcc	tgatagctgt	tggagtatag	tgtatggatc	960
tgcgttc						

(2) INFORMATION FOR SEQ ID NO:3200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..220

(D) OTHER INFORMATION: / Ceres Seq. ID 1576027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3200:

Leu Lys Asn Leu Cys Ser Gly Leu Gly Phe Pro Pro Ser Arg His Arg
1 5 10 15
Leu Ala Ser Ala Leu Ala Arg Arg Gln Glu Ser Arg Leu Gly Arg Phe
20 25 30
Val Glu Asp Pro Gly Ser Ala Leu Ser Arg Gly Leu Ser Ala Gly Val
35 40 45
Val Ser Arg Gly Val Ala Ser Gln Gly Leu Val Ala Phe Ser Gly Glu
50 55 60
Phe Arg Glu Ala Glu Met Ala Pro Lys Ala Ala Pro Ala Lys Lys Gly
65 70 75 80
Asp Ala Lys Thr Gln Ala Leu Lys Val Ala Lys Ala Val Lys Ser Gly
85 90 95
Ser Val Lys Lys Thr Lys Lys Ile Arg Thr Ser Val Thr Phe His Arg
100 105 110
Pro Lys Thr Leu Lys Lys Ala Arg Asp Pro Lys Tyr Pro Arg Ile Ser
115 120 125
Thr Thr Gly Arg Asn Lys Leu Asp Gln Tyr Gln Ile Leu Lys Tyr Pro
130 135 140
Leu Thr Thr Glu Ser Ala Met Lys Lys Ile Glu Asp Asn Asn Thr Leu
145 150 155 160
Val Phe Ile Val Asp Leu Lys Ala Asp Lys Xaa Lys Ile Lys Ala Ala
165 170 175
Val Lys Lys Met Tyr Asp Ile Gln Ala Lys Lys Val Asn Thr Leu Ile
180 185 190
Arg Pro Asp Gly Lys Lys Lys Ala Tyr Val Lys Leu Met Pro Asp Tyr
195 200 205 210 215 220

(2) INFORMATION FOR SEQ ID NO:3201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1576028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3201:

Met Ala Pro Lys Ala Ala Pro Ala Lys Lys Gly Asp Ala Lys Thr Gln
1 5 10 15
Ala Leu Lys Val Ala Lys Ala Val Lys Ser Gly Ser Val Lys Lys Thr
20 25 30
Lys Lys Ile Arg Thr Ser Val Thr Phe His Arg Pro Lys Thr Leu Lys
35 40 45
Lys Ala Arg Asp Pro Lys Tyr Pro Arg Ile Ser Thr Thr Gly Arg Asn
50 55 60
Lys Leu Asp Gln Tyr Gln Ile Leu Lys Tyr Pro Leu Thr Thr Glu Ser
65 70 75 80
Ala Met Lys Lys Ile Glu Asp Asn Asn Thr Leu Val Phe Ile Val Asp
85 90 95
Leu Lys Ala Asp Lys Xaa Lys Ile Lys Ala Ala Val Lys Lys Met Tyr
100 105 110
Asp Ile Gln Ala Lys Lys Val Asn Thr Leu Ile Arg Pro Asp Gly Lys
115 120 125
Lys Lys Ala Tyr Val Lys Leu Met Pro Asp Tyr Asp Ala Leu Asp Val

130 135 140
Ala Asn Lys Ile Gly Ile Ile
145 150
(2) INFORMATION FOR SEQ ID NO:3202:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..115
(D) OTHER INFORMATION: / Ceres Seq. ID 1576029
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3202:
Met Met Leu Met Met Trp Pro Thr Lys Ser Ala Ser Ser Lys Val Thr
1 5 10 15
Ala Ser Gly Ile Cys Cys Ala Leu Phe Pro Cys Glu Thr Arg Val Phe
20 25 30
Val Ala Met Ala Gln Trp Leu His Asp His Val Leu Cys Thr Leu Thr
35 40 45
Asn Leu Ile Ser Ser Lys Ser Gln Val Val Leu Ile Asn Thr Trp Ile
50 55 60
Leu Ser Leu Ile Arg Ile Gly Leu Val Phe Gly Ser His Ile Ser Leu
65 70 75 80
Tyr Trp Val Gly Val Leu Ile Ser Pro Phe Phe Ala Leu Gly Trp Ser
85 90 95
Leu Glu Ile Gly Thr Arg Pro Asp Ser Cys Trp Ser Ile Val Tyr Gly
100 105 110
Ser Ala Phe
115

(2) INFORMATION FOR SEQ ID NO:3203:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1041 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1041
(D) OTHER INFORMATION: / Ceres Seq. ID 1576041
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3203:
atcaacttgac ttgcgagcga ccgcggctca cgtcgggtgc ataaattgct tcgtagacta 60
mgaccacaca gttttgcaga aggggagagg tagagggttc gaggtagaga gataganang 120
mnagagaagra gggcgaggcg gcggatccgt cactcgcgtc ttctccgctg atctggagga 180
aggargcgarg gggagttgca aatccatcaa tggccactcc aaccaccctat tcagtcgccga 240
tatctctcgga gaccacacaag attgaagcct ggggtggtgc tgacgaagct ttggccaggc 300
aactcgagga dgaggagaac acgcgtgcamg ctrctgccga caccagagaa gtrccggcca 360
atgtaccctt ggagtcacgt tcaccggctg ttgartacag gctgcacag aatgcagctc 420
agggtgcaag ggaagacaat gtgGaccacg ataatatGt catatGagc aactacaagc 480
attaggggaa gcagtaggaa ttcagtcacg agggttatct gatgagctga tatcttattt 540
ggagccattt aggaacaaagt gcactttctt ctccaggaaa aagaacagtg aggaatgtgt 600
gatctcgcaag acaacatata gaagccggca gaaattgata agactaccct gcagccactg 660
ttatcacgca gattgcataa ctctgtggct taagatcaac aaggcatgcc cagtctgcaa 720
cgaggaggtg tttgtagtaa ctgcaaggtt ctggccagat gctgcggttt catcgtaact 780
tgcttgcggc atgcttttga gaagacgttg gaocgataag gtccattggt tgtgattatg 840
ttgtgagcct agttttgtgc cctttgctta agaggactgg ctctgccccat gcacgggttg 900
gtctacacgt gtgctagttaa ctggaccagg tcgcgttttg tgatgcgtct atccatcttg 960
gttttatcac aaatttgatg atctgtgtg tgggtgatgt ggttgccgtt ttctgaatat 1020
aatggatggt gtttttggcc c

(2) INFORMATION FOR SEQ ID NO:3204:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1576042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3204:

Met	Ala	Thr	Pro	Thr	Thr	Tyr	Ser	Val	Arg	Ile	Ser	Ser	Glu	Thr	His	
1			5					10					15			
Lys	Ile	Glu	Ala	Trp	Val	Val	Ser	Asp	Glu	Ala	Leu	Ala	Arg	Gln	Leu	
			20					25					30			
Gln	Xaa	Glu	Glu	Asn	Thr	Arg	Xaa	Ala	Xaa	Ala	Asp	Thr	Arg	Glu	Val	
			35					40					45			
Xaa	Gly	Asn	Val	Pro	Leu	Glu	Ser	Ser	Ser	Pro	Ala	Val	Xaa	Tyr	Arg	
			50					55					60			
Xaa	Ala	Gln	Asn	Ala	Ala	Gln	Val	Ala	Arg	Glu	Asp	Asn	Val	Asp	Pro	
			65					70					75		80	
Asp	Asn	Met	Val	Ile	Trp	Ser	Asn	Tyr	Lys	His						
			85						90							

(2) INFORMATION FOR SEQ ID NO:3205:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1576043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3205:

Met	Tyr	Pro	Trp	Ser	His	Arg	His	Arg	Leu	Leu	Xaa	Thr	Xaa	Leu	His	
1			5						10					15		
Arg	Met	Gln	Leu	Arg	Leu	Gln	Gly	Lys	Thr	Met	Trp	Thr	Gln	Ile	Ile	
			20					25					30			
Trp	Ser	Tyr	Gly	Ala	Thr	Thr	Ser	Ile	Arg	Gly	Ser	Ser	Arg	Asn	Ser	
			35					40					45			
Val	Gln	Arg	Val	Ile												
			50													

(2) INFORMATION FOR SEQ ID NO:3206:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1576044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3206:

Met	Glu	Gln	Leu	Gln	Ala	Leu	Gly	Glu	Ala	Val	Gly	Ile	Gln	Ser	Arg	
1			5						10					15		
Gly	Leu	Ser	Asp	Glu	Leu	Ile	Ser	Tyr	Leu	Glu	Pro	Phe	Arg	Asn	Lys	
			20					25					30			
Cys	Thr	Phe	Phe	Ser	Arg	Lys	Lys	Asn	Ser	Glu	Glu	Cys	Val	Ile	Cys	

	35		40		45		
Lys Thr Thr Tyr Arg Ser Arg Gln Lys Leu Ile Arg Leu Pro Cys Ser							
50		55		60			
His Cys Tyr His Ala Asp Cys Ile Thr Arg Trp Leu Lys Ile Asn Lys							
65	70		75		80		
Ala Cys Pro Val Cys Asn Glu Glu Val Phe Gly							
	85		90				

(2) INFORMATION FOR SEQ ID NO:3207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 769 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..769
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3207:

cccaaaaacgc ccaccacgccc gccactcgca accgcacacc agccctcgca acccaccacc	60
acgtcccgaga cgtccgagat ggagttcttc gccgcgtacc tgcgtccgtg cctggcgccc	120
ggcccgccccc ccaagctccc gaccaaggac gacgtgcgtc gcatcctgag atccgtcaag	180
gcgcaggtgg aggaggaccg cctcgacctg Gtcttcgccc tcctagaggt taaggacatc	240
gcgcagctga tcGccacggg cggggagcat ctgcctacg ccgcgtcagg agccgctgct	300
gcgctcgttg ccaactcctgc cgctgcgcag gtcgaggagg agggccacgaa ggaggaggat	360
gaggacatcg cctcttctaa cctcttcgac accctacgtg ccgtccggga	420
ccgcggggcaa ccaaggacga gtgcccacgc tacgcgcaca tgaccaccgg acacggcaca	480
cgcaccagc ccaagtgccc ctgatgatat tcattccttc gctctgtctt gcattcgctat	540
gtaatgtata ggctgtgcaa tgcctgcata catgatacat gcctgactc tggatcgccg	600
gatgcctatg catgcttttc actagctatt attactacta ctactactct tctgtcttc	660
ctactgtgtg caccaaagtg agagggacga catgcacggc gatgacatgt cgtgttatgt	720
gcactggcgg ccgctctggcc aggtcataat tcattgctctg tgattgtgt	

(2) INFORMATION FOR SEQ ID NO:3208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3208:

Pro Lys Thr Pro Thr Pro Pro Leu Ala Thr Ala His Gln Pro Ser	
1	5
Gln Pro Thr Thr Thr Ser Glu Thr Ser Glu Met Glu Phe Leu Ala Ala	10
	15
20	25
Tyr Leu Leu Pro Cys Leu Gly Ala Gly Pro Ala Pro Thr Leu Pro Thr	30
35	40
Lys Asp Asp Val Arg Arg Ile Leu Arg Ser Val Ser Ala Glu Val Glu	45
50	55
Glu Asp Arg Leu Asp Leu Val Phe Ala Leu Leu Glu Val Lys Asp Ile	60
65	70
Ala Glu Leu Ile Ala Thr Gly Gly Glu His Leu Ala Tyr Ala Pro Ser	75
	80
85	90
Gly Ala Ala Ala Val Val Ala Thr Pro Ala Ala Ala Glu Val Glu	95
100	105
Glu Glu Ala Thr Lys Glu Glu Asp Glu Asp Ile Ala Leu Phe Asn Leu	110
115	120
Phe Asp	125

130

(2) INFORMATION FOR SEQ ID NO:3209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3209:

Gln	Asn	Ala	His	His	Ala	Ala	Thr	Arg	Asn	Arg	Thr	Pro	Ala	Leu	Ala
1			5					10					15		
Thr	His	His	His	Val	Arg	Asp	Val	Arg	Asp	Gly	Val	Pro	Arg	Arg	Val
			20					25				30			
Pro	Ala	Ala	Val	Pro	Gly	Arg	Arg	Pro	Gly	Pro	His	Ala	Pro	Asp	Gln
			35				40				45				
Gly	Arg	Arg	Ala	Ser	His	Pro	Glu	Ile	Arg	Gln	Arg	Arg	Gly	Gly	Gly
	50					55				60					
Gly	Pro	Pro	Arg	Pro	Gly	Leu	Arg	Pro	Pro	Arg	Gly				
65					70					75					

(2) INFORMATION FOR SEQ ID NO:3210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3210:

Met	Glu	Phe	Leu	Ala	Ala	Tyr	Leu	Leu	Pro	Cys	Leu	Gly	Ala	Gly	Pro
1			5					10					15		
Ala	Pro	Thr	Leu	Pro	Thr	Lys	Asp	Asp	Val	Arg	Arg	Ile	Leu	Arg	Ser
			20					25				30			
Val	Ser	Ala	Glu	Val	Glu	Glu	Asp	Arg	Leu	Asp	Leu	Val	Phe	Ala	Leu
			35				40				45				
Leu	Glu	Val	Lys	Asp	Ile	Ala	Glu	Leu	Ile	Ala	Thr	Gly	Gly	Glu	His
	50				55					60					
Leu	Ala	Tyr	Ala	Pro	Ser	Gly	Ala	Ala	Ala	Ala	Val	Val	Ala	Thr	Pro
65					70					75				80	
Ala	Ala	Ala	Glu	Val	Glu	Glu	Glu	Ala	Thr	Lys	Glu	Glu	Asp	Glu	Asp
					85			90					95		
Ile	Ala	Leu	Phe	Asn	Leu	Phe	Asp								
					100										

(2) INFORMATION FOR SEQ ID NO:3211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..999
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3211:

gagtagcaat	cactgctgcg	cccgataggg	ggcagcgagc	cagcdhmcca	mccgactctg	60
ttccaacgag	cctwccccc	caaacttgca	cgtgcgcgcc	gctctcgcc	cgcgcgcgca	120
tccagatcca	gggtggaata	gggaacggcc	atacaccatg	gggatttct	ccaaggaatc	180
ttgccctctc	gtgaagaaca	ttttacttct	ggattctgaa	ggaaagcgty	ttgctgtaaa	240
gtattttcca	gatgattggc	cgactaatgc	atcaaatgta	gcctacgaaa	agctctgttt	300
tactaaaaact	ctaaaagacaa	atgcacggac	agaagctgag	ataacattgt	ttgatgggta	360
tattgwcgk	tacaagtgtt	tactgacct	tcacttkttt	gtccacgctg	gagatgatga	420
gGaatgagct	catcttagca	agtgtactac	atggtttttc	tgattctggt	ggctctctac	480
tcagggggga	tggttmgagg	cggactgcgc	ttgagaactt	ggatttgata	cttctctgca	540
tcgatgaat	tgtagatggg	ggaatcatcc	tgaaaacaga	tgcaaacacc	attgctggta	600
aggttgcaac	caatgctgtt	gatggttctg	tgcccttttc	tgagcagacg	atatctcaag	660
cactagcaoc	agctaggagg	caccttgcaa	gatctctact	gaaatgaaca	accagcaata	720
tgtagcaact	attatatgac	atatatgtgt	gtaggttggg	ctactgaaat	ttgaggggtc	780
ttgtagacgt	tattgtcccc	aaagtgcctc	tgtagacagag	cctagttgaa	tatccgaggg	840
attggtcaca	tgctcgttaa	attttttttt	tgaaccagtg	agtttgtagc	tgccaatttt	900
caggtaaaaa	ataaaataaa	gagttgtaat	gggtgtgta	ataattttca	ccatacaaaa	960
aaaattcat	ctcaactatc	aaaccatggt	aaaagttc			

(2) INFORMATION FOR SEQ ID NO:3212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3212:

Met	Val	Ile	Leu	Xaa	Xaa	Thr	Ser	Leu	Tyr	Xaa	Thr	Phe	Thr	Xaa	Leu
1			5					10						15	
Ser	Pro	Leu	Glu	Met	Met	Arg	Asn	Glu	Leu	Ile	Leu	Ala	Ser	Val	Leu
			20					25					30		
His	Gly	Phe	Ser	Asp	Ser	Val	Gly	Leu	Leu	Leu	Arg	Gly	Asp	Val	Xaa
			35					40					45		
Lys	Arg	Thr	Ala	Leu	Glu	Asn	Leu	Asp	Leu	Ile	Leu	Leu	Cys	Ile	Asp
			50				55						60		
Glu	Ile	Val	Asp	Gly	Gly	Ile	Ile	Leu	Glu	Thr	Asp	Ala	Asn	Thr	Ile
			65				70						75		80
Ala	Gly	Lys	Val	Ala	Thr	Asn	Ala	Val	Asp	Gly	Ser	Val	Pro	Phe	Ser
			85					90					95		
Glu	Gln	Thr	Ile	Ser	Gln	Ala	Leu	Ala	Thr	Ala	Arg	Glu	His	Leu	Ala
			100					105					110		
Arg	Ser	Leu	Leu	Lys											
			115												

(2) INFORMATION FOR SEQ ID NO:3213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3213:

Met	Met	Arg	Asn	Glu	Leu	Ile	Leu	Ala	Ser	Val	Leu	His	Gly	Phe	Ser
1				5				10					15		
Asp	Ser	Val	Gly	Leu	Leu	Leu	Arg	Gly	Asp	Val	Xaa	Lys	Arg	Thr	Ala
			20					25					30		

Leu Glu Asn Leu Asp Leu Ile Leu Leu Cys Ile Asp Glu Ile Val Asp
35 40 45
Gly Gly Ile Ile Leu Glu Thr Asp Ala Asn Thr Ile Ala Gly Lys Val
50 55 60
Ala Thr Asn Ala Val Asp Gly Ser Val Pro Phe Ser Glu Gln Thr Ile
65 70 75 80
Ser Gln Ala Leu Ala Thr Ala Arg Glu His Leu Ala Arg Ser Leu Leu
85 90 95
Lys

(2) INFORMATION FOR SEQ ID NO:3214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3214:

Met Arg Asn Glu Leu Ile Leu Ala Ser Val Leu His Gly Phe Ser Asp
1 5 10 15
Ser Val Gly Leu Leu Arg Gly Asp Val Xaa Lys Arg Thr Ala Leu
20 25 30
Glu Asn Leu Asp Leu Ile Leu Leu Cys Ile Asp Glu Ile Val Asp Gly
35 40 45
Gly Ile Ile Leu Glu Thr Asp Ala Asn Thr Ile Ala Gly Lys Val Ala
50 55 60
Thr Asn Ala Val Asp Gly Ser Val Pro Phe Ser Glu Gln Thr Ile Ser
65 70 75 80
Gln Ala Leu Ala Thr Ala Arg Glu His Leu Ala Arg Ser Leu Leu Lys
85 90 95

(2) INFORMATION FOR SEQ ID NO:3215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..655
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3215:

gcccgctcat tgcttgctc cagctccag agaacgcgat ttgttctgtt gttcggtccc 60
caatcttcgc ctccgCtccg cccgcgccga cccagatcag gagctgagag atggacgcga 120
acagcgccca aggtgggagt cagcagttgc tggctgcgga gCaggaggct cagcaaatgt 180
tgaatgcggc tagagctgct aagtcagcaa ggcttaggca agcgaagag gaggcagaga 240
gggaaatagc cgaatacgt gccagatagg aggtgagtt ccagaggaag gtccgacaga 300
gcagtggtga ctctggtgc aacgtcaagc gtctcgagga agagacaacg gcgaaaatcg 360
aacagctcaa ccagcaggtg gaaagcatct cccagatgt cattcagatg ctctcgagcg 420
atgtcaccac cgtgaagaac tgagaagtgc tgctcccaaa ctatggctat cggctctattt 480
attttttgtca gagcaggtga ggaataataa tatggccctt gtaccagtaa ttcttttttt 540
aactacggaa taagccgcag cagcttttagc ggcaaccgtg actgttacta ccagaactgtg 600
ccattatttg gtataatcgg caaataataa atattgttt tatattggat ttttg

(2) INFORMATION FOR SEQ ID NO:3216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..60
(D) OTHER INFORMATION: / Ceres Seq. ID 1576068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3216:

Ala Arg Ser Leu Leu Ala Ser Ser Leu Gln Arg Thr Arg Phe Val Leu
1 5 10 15
Leu Phe Gly Pro Gln Ser Ser Pro Pro Leu Arg Pro Pro Arg Pro Arg
20 25 30
Ser Gly Ala Glu Arg Trp Thr Pro Thr Gly Ala Lys Val Gly Phe Ser
35 40 45
Ser Cys Trp Leu Arg Ser Arg Arg Leu Ser Lys Leu
50 55 60

(2) INFORMATION FOR SEQ ID NO:3217:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..63
(D) OTHER INFORMATION: / Ceres Seq. ID 1576069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3217:

Pro Ala His Cys Leu Pro Pro Val Ser Arg Glu Arg Asp Leu Phe Cys
1 5 10 15
Cys Ser Val Pro Asn Leu Arg Leu Arg Ser Ala Arg Pro Asp Pro Asp
20 25 30
Gln Glu Leu Arg Asp Gly Arg Gln Gln Ala Pro Arg Trp Asp Ser Ala
35 40 45
Val Ala Gly Cys Gly Ala Gly Gly Ser Ala Asn Cys Glu Cys Gly
50 55 60

(2) INFORMATION FOR SEQ ID NO:3218:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..110
(D) OTHER INFORMATION: / Ceres Seq. ID 1576070

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3218:

Met Asp Ala Asn Arg Arg Gln Gly Gly Ile Gln Gln Leu Leu Ala Ala
1 5 10 15
Glu Gln Glu Ala Gln Gln Ile Val Asn Ala Ala Arg Ala Ala Lys Ser
20 25 30
Ala Arg Leu Arg Gln Ala Lys Glu Glu Ala Glu Arg Glu Ile Ala Glu
35 40 45
Tyr Arg Ala Gln Met Glu Ala Glu Phe Gln Arg Lys Val Ala Glu Ser
50 55 60
Ser Gly Asp Ser Gly Ala Asn Val Lys Arg Leu Glu Glu Glu Thr Thr
65 70 75 80
Ala Lys Ile Glu Gln Leu Asn Gln Gln Ala Ala Ser Ile Ser Pro Asp

85 90 95
Val Ile Gln Met Leu Leu Arg His Val Thr Thr Val Lys Asn
100 105 110

(2) INFORMATION FOR SEQ ID NO:3219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 892 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..892
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3219:

accgcagcca	cacccaaca	tcaaaacct	cccatctctt	cccctccgcc	gccgtctctg	60
ctctcaagat	cgccatggcg	tcagaaaaga	agcagctcgaa	cccgatgcgg	gagatcaagg	120
tgcagaagct	cgtgctcaat	atctccgttg	gagagagtgg	agatcgactc	accgcgcgcc	180
ccaaggtgtt	ggagcagttg	agtgggcagt	ctccggtttt	ctccaaggca	aggfatactg	240
tgaggtcttt	cggtattctg	cgtaatgaga	agattgcatg	ctatttcaat	cgtgctgtat	300
gcttcttgaa	attgggaaaa	catgatgaga	ccattaaaAg	aatgctcaaa	agcacttgag	360
ctcaatccaa	catacctgaa	agccctgctt	cggaggggcag	aagcgcgatg	aaagcttgaa	420
cattatgatg	aagctattgc	cgatatgaaa	aagggtgttg	aagtggatcc	ttcaaatcaa	480
caagccacga	ggtctctttt	ccgacttgag	cccctggcag	ctgagaagag	ggaaaagatg	540
aaggaagaaa	tgattgcaaa	gctgaaaagt	ctgggggaact	ctgtgctggg	ccgcttcggg	600
atgagtgttg	acaatttcaa	agctgtcaaa	gatccaaaca	ctggctctta	cagcatctaa	660
ttccaaaagt	aacacgacgt	gaagaaagac	atggatgaat	atggctgggg	ggcatatttc	720
agttgtaatt	gttcaaggaa	ctgtgctgtc	acatacctgg	acaatatcca	aacagatatc	780
tgcaaatcga	tctgaagggt	ggacatggaa	gaggaattgg	agtattcggt	cgcggttgca	840
tttgtcgac	gttagactgt	tagagatgct	ttctcgagtg	cgaacttgca	tg	

(2) INFORMATION FOR SEQ ID NO:3220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3220:

Arg Ser His Thr Pro Thr Ser Lys Pro Ser His Leu Phe Pro Ser Ala	
1 5 10 15	
Ala Val Ser Ala Leu Lys Ile Ala Met Ala Ser Glu Lys Lys Gln Ser	
20 25 30	
Asn Pro Met Arg Glu Ile Lys Val Gln Lys Leu Val Leu Asn Ile Ser	
35 40 45	
Val Gly Glu Ser Gly Asp Arg Leu Thr Arg Ala Ala Lys Val Leu Glu	
50 55 60	
Gln Leu Ser Gly Gln Ser Pro Val Phe Ser Lys Ala Arg Tyr Thr Val	
65 70 75 80	
Arg Ser Phe Gly Ile Arg Arg Asn Glu Lys Ile Ala Cys Tyr Ser Asn	
85 90 95	
Arg Ala Val Cys Phe Leu Lys Leu Gly Lys His Asp Glu Thr Ile Lys	
100 105 110	
Arg Met Leu Lys Ser Thr	
115	

(2) INFORMATION FOR SEQ ID NO:3221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1576077

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3221:

Met	Arg	Pro	Leu	Lys	Glu	Cys	Ser	Lys	Ala	Leu	Glu	Leu	Asn	Pro
1			5				10						15	
Thr	Tyr	Leu	Lys	Ala	Leu	Leu	Arg	Arg	Ala	Glu	Ala	His	Glu	Lys
			20				25					30		
Glu	His	Tyr	Asp	Glu	Ala	Ile	Ala	Asp	Met	Lys	Lys	Val	Val	Glu
			35				40					45		
Asp	Pro	Ser	Asn	Gln	Gln	Ala	Thr	Arg	Ser	Leu	Phe	Arg	Leu	Glu
			50				55				60			
Leu	Ala	Ala	Glu	Lys	Arg	Glu	Lys	Met	Lys	Glu	Glu	Met	Ile	Ala
			65			70				75			80	
Leu	Lys	Asp	Leu	Gly	Asn	Ser	Val	Leu	Gly	Arg	Phe	Gly	Met	Ser
			85						90				95	
Asp	Asn	Phe	Lys	Ala	Val	Lys	Asp	Pro	Asn	Thr	Gly	Ser	Tyr	Ser
			100					105					110	
Gln	Phe	Gln	Lys											
			115											

- (2) INFORMATION FOR SEQ ID NO:3222:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1576078

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3222:

Met	Arg	Pro	Leu	Lys	Glu	Cys	Ser	Lys	Ala	Leu	Glu	Leu	Asn	Pro	Thr
1			5				10						15		
Tyr	Leu	Lys	Ala	Leu	Leu	Arg	Arg	Ala	Glu	Ala	His	Glu	Lys	Leu	Glu
			20				25					30			
His	Tyr	Asp	Glu	Ala	Ile	Ala	Asp	Met	Lys	Lys	Val	Val	Glu	Val	Asp
			35				40					45			
Pro	Ser	Asn	Gln	Gln	Ala	Thr	Arg	Ser	Leu	Phe	Arg	Leu	Glu	Pro	Leu
			50				55				60				
Ala	Ala	Glu	Lys	Arg	Glu	Lys	Met	Lys	Glu	Glu	Met	Ile	Ala	Lys	Leu
			65			70				75			80		
Lys	Asp	Leu	Gly	Asn	Ser	Val	Leu	Gly	Arg	Phe	Gly	Met	Ser	Val	Asp
			85						90				95		
Asn	Phe	Lys	Ala	Val	Lys	Asp	Pro	Asn	Thr	Gly	Ser	Tyr	Ser	Ile	Gln
			100					105					110		
Phe	Gln	Lys													
			115												

- (2) INFORMATION FOR SEQ ID NO:3223:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1206
(D) OTHER INFORMATION: / Ceres Seq. ID 1576102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3223:

aaagrararav	ggggaggtcg	acgagacaga	gagagaaggc	caagaggett	cctctcccca	60
ttctctccctt	ccgtgcacct	gccgagccag	ccgcgaggaa	ggagggcatcc	cgcgctctcg	120
cctggcgcccc	gcccgcgcgc	cgacctctcg	ccgcgagcttc	caattgtataa	aagatcatag	180
atttttgtgc	aagagcgagt	ggatatggaa	ccatccccctc	agcctatggg	tgtcgctgoc	240
gggtgggtcac	aagtgtatcc	tgccctctgcc	tatccgcctg	cagcaaacagt	agctcctgct	300
tctgtgtgat	ctgctgggtt	acagtcaggg	cagccattcc	cagccaatcc	tgttcatagt	360
agtgctcagc	accagattgt	ctaccaacaa	gctcaacaat	tccaccaaca	gctccagcag	420
caaccaacaac	agcagcttca	cgagttctgg	gttgaacgca	tgaactgaaat	tgaggcgacg	480
actgattttca	agaaccacaa	cttgcacact	gcgaggataa	agaagatcat	gaagggccgat	540
gaagatgttc	gcatgatctc	agctgaagct	cctgtagtct	ttgcaaagc	ttgtgagata	600
ttcatactgg	agctgacact	taVggtcgtg	gatgcmcaact	gaggwgwaca	agcgccgcac	660
yttgcwaam	aatgacattg	cagcagcgat	cactaggact	gacatttatg	acttcttggt	720
cgacattgtt	cccaggggwtg	agatgaagga	ggmcggaatt	gggcttccca	gggctggtct	780
gccaccctatg	ggagccccag	ctgatgcata	tccatactac	tacatgccac	agcagcaggt	840
gctctggtct	ggaatgggtt	atgggtgccc	gcaagggcac	ccagtgactt	attgtggcca	900
ggagcctcac	caacagcagg	agcaagctcc	tgaagagcag	caatctgcac	gaaagtggtc	960
gagaattattg	ctcagaagct	atcacctgat	tcagagttct	cattttaggt	tgtccaaact	1020
gcaggtttttc	ttagtaatat	cggtgtgtat	caactgaaa	caggcgattc	taagtagggt	1080
gtagcatcat	gttagtttca	tttctgcttg	tgatgttagt	tgaagagata	atgattagt	1140
gctagtggtat	taaagttaac	ataccatttc	cttctatttc	gaaagtgdgy	ttccwtgwgw	1200

(2) INFORMATION FOR SEQ ID NO:3224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1576103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3224:

Arg	Xaa	Xaa	Gly	Arg	Ser	Thr	Arg	Gln	Arg	Glu	Lys	Ala	Lys	Arg	Leu
1			5					10					15		
Pro	Leu	Pro	Ile	Pro	Pro	Phe	Arg	Ala	Leu	Ala	Glu	Pro	Ala	Ala	Arg
			20					25				30			
Lys	Glu	Ala	Ser	Arg	Arg	Leu	Ala	Trp	Arg	Pro	Pro	Val	Gly	Arg	Pro
			35				40					45			
Ser	Ala	Ala	Ala	Ser	Asn	Cys	Lys	Lys	Ile	Ile	Asp	Phe	Cys	Ala	Arg
			50				55					60			
Ala	Ser	Gly	Tyr	Gly	Thr	Ile	Pro	Ser	Ala	Tyr	Gly	Cys	Arg	Cys	Arg
			65				70				75			80	
Trp	Val	Thr	Ser	Val	Ser	Cys	Leu	Cys	Leu	Ser	Ala	Cys	Ser	Asn	Ser
			85				90					95			
Ser	Ser	Cys	Phe	Cys	Cys	Ile	Cys	Trp	Phe	Thr	Val	Arg	Ala	Ala	Ile
			100				105					110			
Pro	Ser	Gln	Ser	Trp	Ser	Tyr	Glu	Cys	Ser	Ala	Pro	Asp	Cys	Leu	Pro
			115				120					125			
Thr	Ser	Ser	Thr	Ile	Pro	Pro	Thr	Ala	Pro	Ala	Ala	Thr	Thr	Thr	Ala
			130				135					140			
Ala	Ser	Ala	Val	Leu	Gly										
			145				150								

(2) INFORMATION FOR SEQ ID NO:3225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1576104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3225:

```
Met Glu Pro Ser Pro Gln Pro Met Gly Val Ala Ala Gly Gly Ser Gln
1      5      10      15
Val Tyr Pro Ala Ser Ala Tyr Pro Pro Ala Ala Thr Val Ala Pro Ala
      20      25      30
Ser Val Val Ser Ala Gly Leu Gln Ser Gly Gln Pro Phe Pro Ala Asn
      35      40      45
Pro Gly His Met Ser Ala Gln His Gln Ile Val Tyr Gln Gln Ala Gln
      50      55      60
Gln Phe His Gln Gln Leu Gln Gln Gln Gln Gln Gln Leu Gln Gln
      65      70      75      80
Phe Trp Val Glu Arg Met Thr Glu Ile Glu Ala Thr Thr Asp Phe Lys
      85      90      95
Asn His Asn Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys Ala Asp
      100      105      110
Glu Asp Val Arg Met Ile Ser Ala Glu Ala Pro Val Val Phe Ala Lys
      115      120      125
Ala Cys Glu Ile Phe Ile Leu Glu Leu Thr Leu Xaa Val Val Asp Xaa
      130      135      140
```

His
145

(2) INFORMATION FOR SEQ ID NO:3226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1576105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3226:

```
Met Gly Val Ala Ala Gly Gly Ser Gln Val Tyr Pro Ala Ser Ala Tyr
1      5      10      15
Pro Pro Ala Ala Thr Val Ala Pro Ala Ser Val Val Ser Ala Gly Leu
      20      25      30
Gln Ser Gly Gln Pro Phe Pro Ala Asn Pro Gly His Met Ser Ala Gln
      35      40      45
His Gln Ile Val Tyr Gln Gln Ala Gln Gln Phe His Gln Gln Leu Gln
      50      55      60
Gln Gln Gln Gln Gln Gln Leu Gln Gln Phe Trp Val Glu Arg Met Thr
      65      70      75      80
Glu Ile Glu Ala Thr Thr Asp Phe Lys Asn His Asn Leu Pro Leu Ala
      85      90      95
Arg Ile Lys Lys Ile Met Lys Ala Asp Glu Asp Val Arg Met Ile Ser
      100      105      110
Ala Glu Ala Pro Val Val Phe Ala Lys Ala Cys Glu Ile Phe Ile Leu
      115      120      125
Glu Leu Thr Leu Xaa Val Val Asp Xaa His
      130      135
```

(2) INFORMATION FOR SEQ ID NO:3227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 773 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..773
(D) OTHER INFORMATION: / Ceres Seq. ID 1576110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3227:

arcgctcgtg	gaaaggagac	gtctctgaac	cgaggctgcg	actgcgaggg	cagcgaggga	60
gatcgagcca	cgcttcttgt	cgctgtaatc	ccctcgagag	ccgcccggcg	ascatggcgc	120
ggccccagcg	cgctctctcc	tcctctacac	cgacacagac	gggatccctc	tcgactcag	180
Gctccacctc	ctcggaatc	gaccgccgcc	gccacagcgc	ggagcggcgg	cggtccgcgt	240
cggaagacga	cagctacagc	acaagctctt	atgacagtga	ccgtgaggtg	tctggcagat	300
ctcgaaaca	taagaagagc	agcagatcaa	gaaagtctag	ggagagggag	cgagCaaag	360
atagacatca	taaacgagac	aagagtaaac	acaaagagaa	gaaagagagt	gagcatgctg	420
atggccctgt	ccagctttcc	aagtttcttg	gacgggacaa	agaaaaggaa	gaaggtactc	480
aacggagtgc	aatatcttgt	aaaaagataa	tgatgaagct	tgagaagaca	aaggaagaca	540
aggcagcaga	gagcaagcga	aacgaactgt	tgaagtttct	gaatgccagt	tacgattgat	600
gtgttcgaat	yGctgacgcg	gaaagtgcag	watgcccttt	tttatcgctc	ttgcactcgt	660
gcttttggtg	atacttaagt	tataaacggt	ttgtttcttg	tctataactt	ggccaccaaa	720
gttttttat	gctcaactag	cgaactgagt	aaggtctaca	tgcaattgat	ttg	

(2) INFORMATION FOR SEQ ID NO:3228:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..198
(D) OTHER INFORMATION: / Ceres Seq. ID 1576111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3228:

Arg	Ser	Trp	Lys	Gly	Asp	Val	Ser	Glu	Pro	Arg	Leu	Arg	Leu	Arg	Gly
1				5				10			15				
Gln	Arg	Gly	Arg	Ser	Ser	His	Ala	Ser	Cys	Arg	Val	Asn	Pro	Leu	Glu
		20					25				30				
Xaa	Arg	Arg	Xaa	Xaa	Met	Ala	Arg	Ser	Pro	Ala	Ala	Ser	Ser	Ser	Ser
		35				40				45					
Tyr	Thr	Asp	Ser	Thr	Gly	Ser	Ser	Ser	Asp	Ser	Gly	Ser	Thr	Ser	Ser
		50				55				60					
Gly	Ile	Asp	Arg	Arg	Arg	His	Glu	Arg	Glu	Arg	Arg	Ser	Ala	Ser	
		65				70				75				80	
Asp	Asp	Asp	Ser	Tyr	Ser	Thr	Ser	Ser	Tyr	Asp	Ser	Asp	Arg	Glu	Val
			85						90					95	
Ser	Gly	Arg	Ser	Arg	Lys	His	Lys	Lys	Ser	Ser	Arg	Ser	Arg	Lys	Ser
			100					105					110		
Arg	Glu	Arg	Glu	Arg	Ser	Lys	Asp	Arg	His	His	Lys	Arg	Asp	Lys	Ser
			115				120					125			
Lys	His	Lys	Glu	Lys	Lys	Glu	Ser	Glu	His	Ala	Asp	Gly	Pro	Val	Gln
			130				135					140			
Leu	Ser	Lys	Phe	Leu	Gly	Arg	Asp	Lys	Glu	Lys	Glu	Glu	Gly	Thr	Gln
			145			150				155					160
Arg	Ser	Ala	Ile	Ser	Gly	Lys	Lys	Ile	Met	Met	Lys	Leu	Glu	Lys	Thr
			165						170					175	
Lys	Glu	Asp	Lys	Ala	Ala	Glu	Ser	Lys	Arg	Asn	Glu	Leu	Leu	Lys	Phe
			180					185					190		
Leu	Asn	Ala	Ser	Tyr	Asp										
			195												

(2) INFORMATION FOR SEQ ID NO:3229: